博淼生物
BIOMIAO BIOLOGICAL
-SINCE2009-
Your own Laboratory
您的专属实验室

Olink Proteomics —新一代「精准」蛋白组学技术及在人群队列及精准医学中的应用

全国统一服务电话：400-6506-908
网址：www.biomiao.com
邮箱： marketing@biomiao.com
地址：北京市丰台区丰管路优橙创新中心

~700	Top 20	~2.4M	>940	100%	Validated	KOLs	Consortia
Biopharma and prestigious academic institutions, as customers	Serving all of the largest 20 biopharma companies (by revenue in 2019).	Samples run on the Olink platform	Peer-reviewed publications	Coverage of all major biological pathways	Complete technical validation of each protein assay	Established strong global KOL networks	Global consortia within proteogenomics, neurology, IBD

基于Olink 蛋白组数据组建的国际大型产学研联盟

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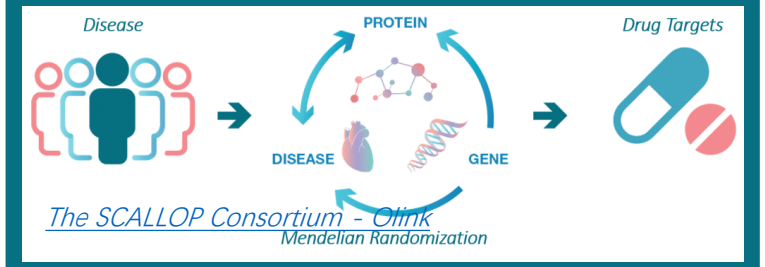
SCALLOP

Anders Malarstig
SCALLOP chair
Senior Researcher at
Director, Pfizer

SCALLOP - genetics of the proteome



The SCALLOP Consortium - Olink

The SCALLOP consortium (Systematic and Combined Analysis of Olink Proteins) is a collaborative framework for discovery and follow-up of genetic associations with proteins on the Olink platform. To date, 33 PI's/28 institutions joined. Summary level data for ~65,000 patients or controls.

- June 2021 SCALLOP launches clinical trial arm

COLLIBRI
Collaborative IBD Biomarker Research Initiative

Jonas Halfvarsson, COLLIBRI chair
Prof. Medical Science, Orebro University Hospital

January 2020

COLLIBRI is a consortium that aims to accelerate progress in the field of inflammatory bowel disease through the use of protein biomarkers

The COLLIBRI consortium - Olink

CORAL

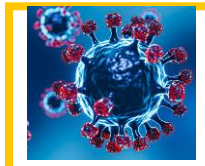
Charlotte Teunissen, CORAL chair
Prof. Neurochemistry, Amsterdam, UMC

June 2021

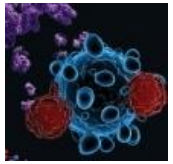
CORAL - the proteome in neurological disease

The CORAL consortium (Community using Olink for Research on Alzheimer's Disease and other neurological diseases) is a collaborative framework. Objective is to accelerate the identification of proteins and mechanisms for neurological diseases, as well as the translation of novel biomarkers for neurological diseases to the clinic.

The CORAL Consortium - Olink



COVID-19



Coming in 2022

Immunotherapy / RNASeq
Genevieve Boland, MGH
Arnav Mehta, MGH and Broad

全球目前最大的蛋白基因组学联盟

To discover pQTLs & 临床相关生物标志物

Acronym	Design	Size	Institute	Country
MadCam_ph2	IBD（慢性肠炎）	200	Pfizer	US
IMPROVE	Prospective, MetSyn	3,403	Karolinska	Sweden
NSPHS	Population isolate	1,000	Uppsala	Sweden
PIVUS	Prospective observational	933	Uppsala	Sweden
STABILITY	Acute coronary syndrome冠心病	3,000	Uppsala	Sweden
STANLEY	Bipolar/depression抑郁	681	Karolinska	Sweden
ULSAM	Prospective observational	730	Uppsala	Sweden
ASAP	Aortic valve surgery	600	Karolinska	Sweden
BioFinder	AD, PD and controls阿尔兹海默症	1,550	Lund	Sweden
RECOMBINE	Rheumatoid arthritis风湿性关节炎	800	Karolinska	Sweden
EpiHealth	Prospective observational	2,500	Uppsala	Sweden
Estonian Biobank	Population based	500	Tartu	Estonia
HELIC MANOLIS	Population isolate	1,475	Helmholtz	Germany
SMCC / SIMPLER	Population based, women	5,000	Uppsala	Sweden
INTERVAL	Blood donors	5,000	Cambridge	UK
China Kadoorie BB	Pancreatic cancer胰腺癌	1,400	Oxford	UK
KORA F4	Population based	1,050	Helmholz	Germany
LifeLines Deep	Population based	1,200	Groeningen	Netherlands
MPP-RES	Heart failure心衰	1,000	Malmo	Sweden
ORCADES	Population isolate	1,000	Edinburgh	UK
VIS	Population isolate	1,000	Edinburgh	UK
PURE	Epidemiological cohort study	5,000	Hamilton	Canada
Aristotle	Atrial fibrillation	4,000	Uppsala	Sweden
PRIDE	Dementia老年痴呆	1,500	Amsterdam	Netherlands
Tromso	Population based	2,000	Tromso	Norway
INSIGHT	HIV patients	1,500	Copenhagen	Denmark
FENLAND	Stroke patients	500	Cambridge	UK
DIRECT consortium	Diabetes糖尿病	5,000		Sweden/UK

>20 academic and industry partners

www.scallop-consortium.com

SCALLOP Systematic and Combined AnaLysis of Olink Proteins

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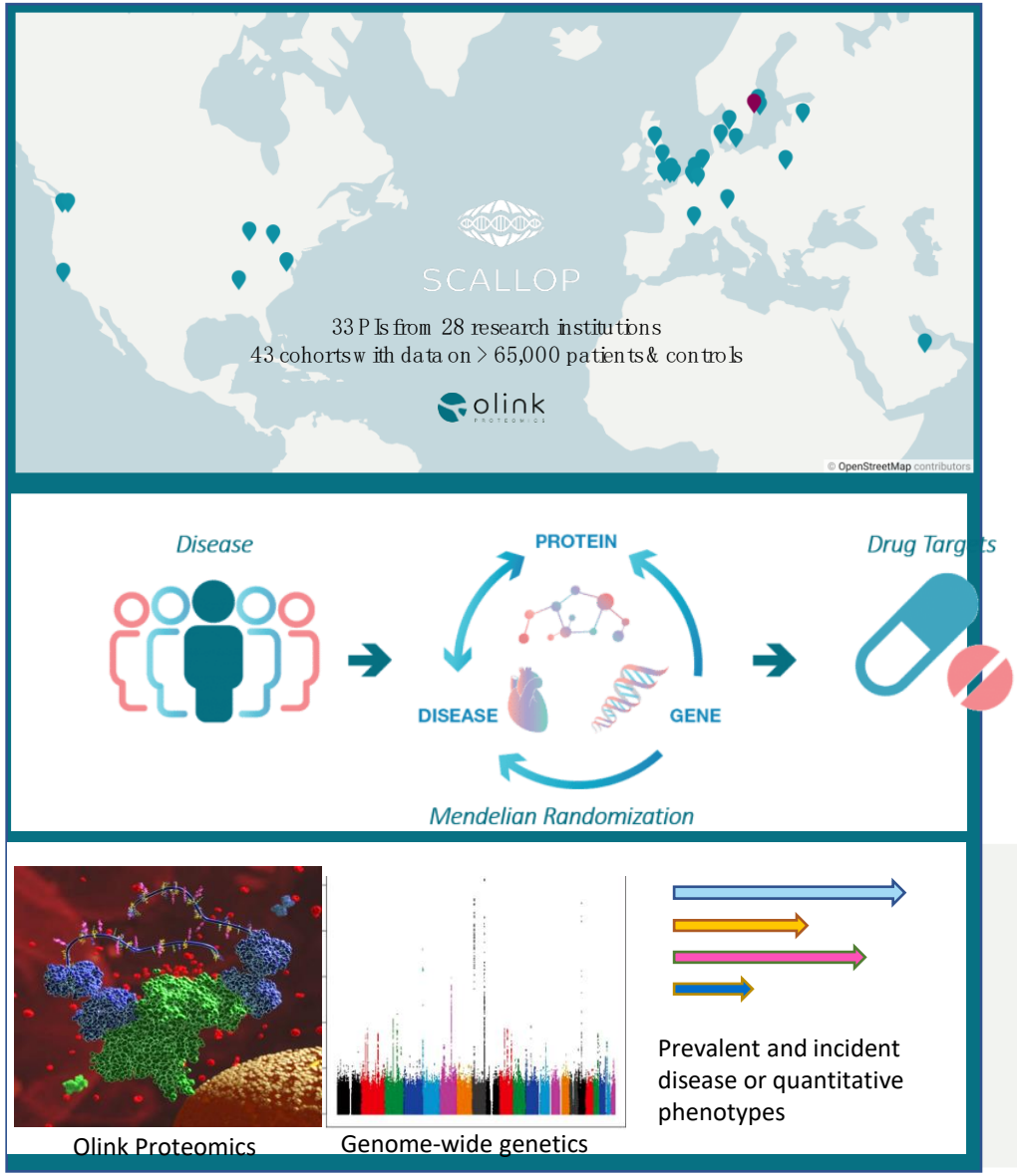
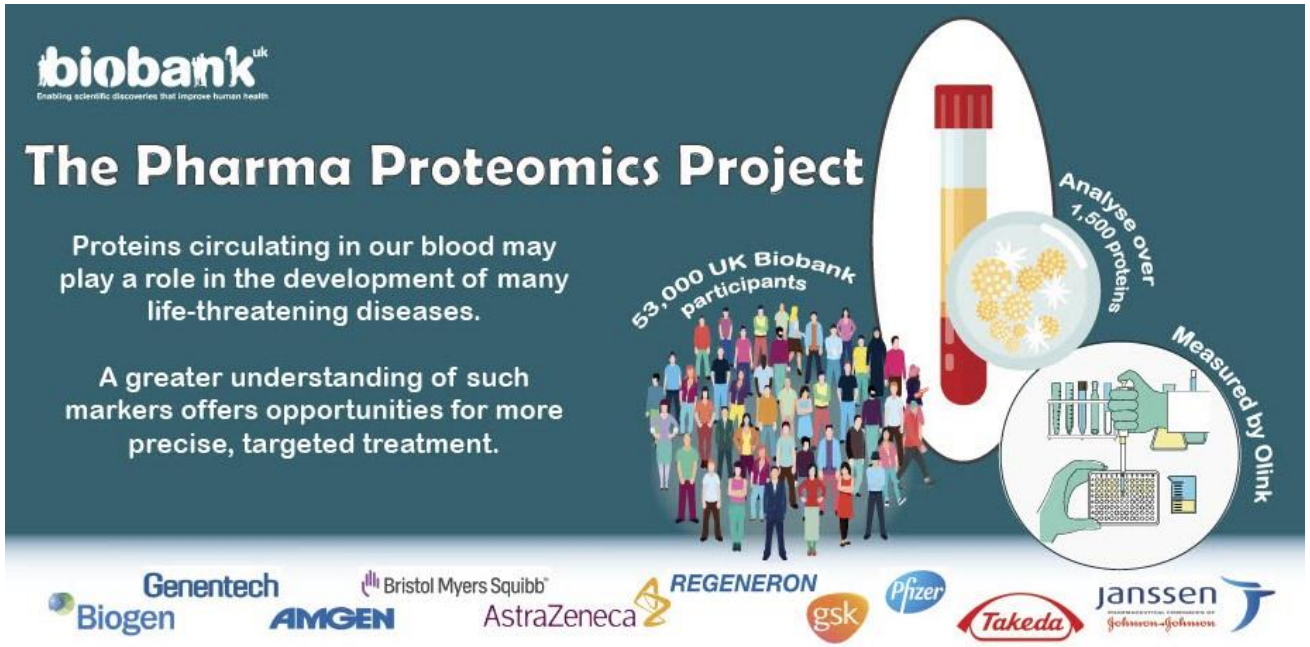


英国生物样本库 & 冰岛生物样本库



- 2020年12月7日，Olink 和UK Biobank一起宣布，将联合Top10生物制药公司启动血液蛋白组研究。
- 采用Olink 蛋白组检测平台，对53,000名参与者的56,000个血浆样品进行检测，从而在20周内获得7百万蛋白标志物数据。
- 这将是迄今为止进行的全球最大的血液蛋白组研究之一，旨在显著增强“蛋白质组学”的领域，使人们对疾病的过程有更好的了解并支持创新药物的开发。

- 2021年7月13日，位于冰岛的生物样本库deCODE genetics引进并在内部落地Olink 蛋白质组平台，对其人群队列样本进行血液蛋白组的高质量检测分析。
- deCODE和Olink共同努力进一步优化Olink的高通量、高质量蛋白质组学，推进其在“国家级人口规模队列”的现代医疗项目中的应用。

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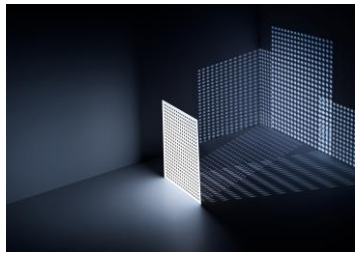
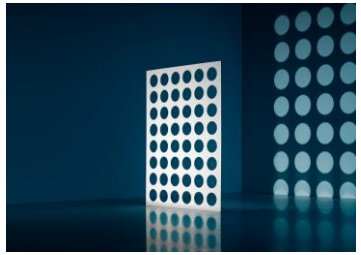
Proteomic screens by Olink



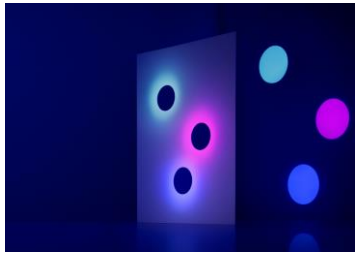
Measure 1,536， 3072proteins,
Soon 4,5k proteins covering the dynamic plasma proteome.

1µl sample for 384 assays



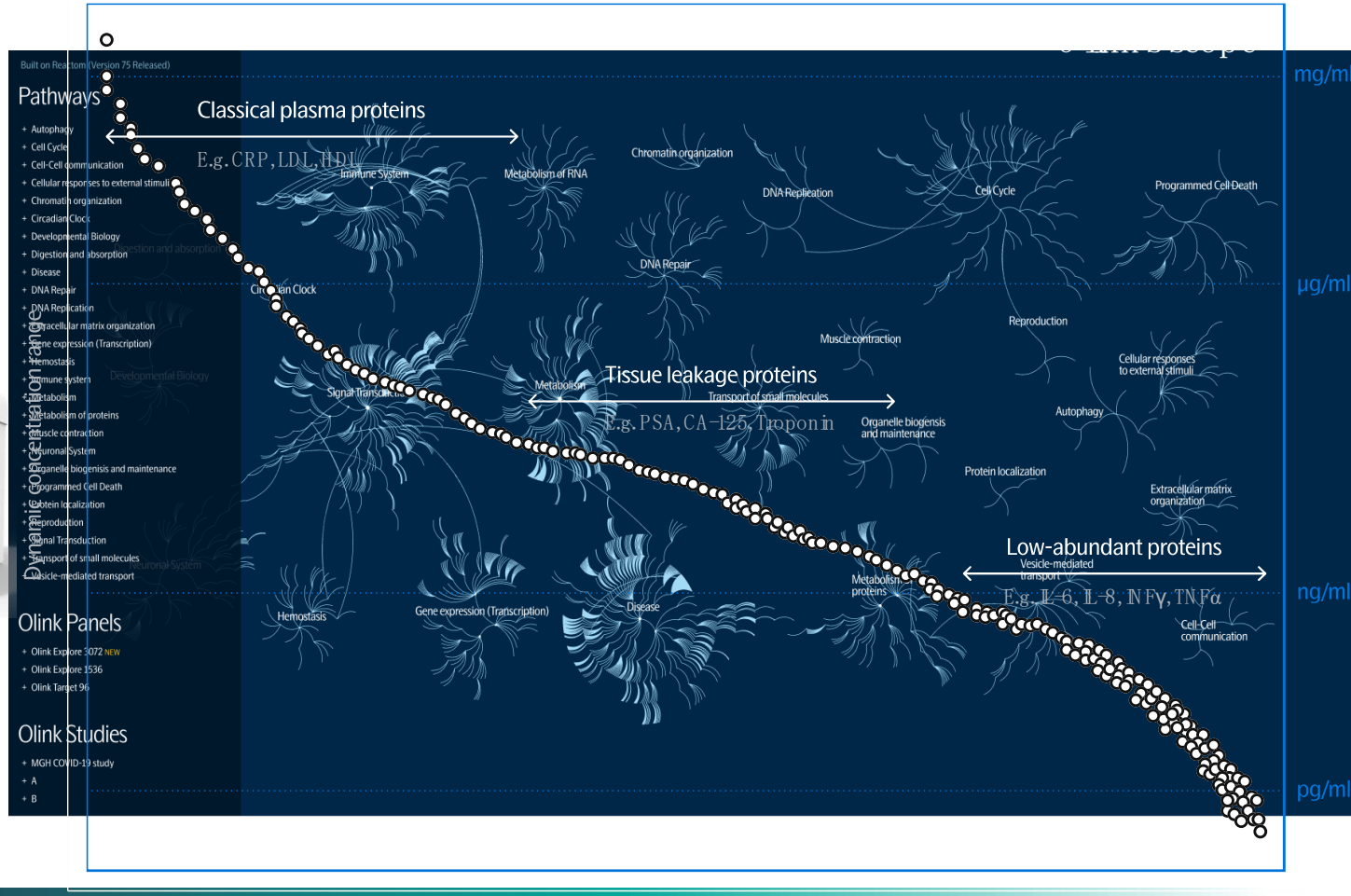
15 panels built for specific area of disease or biology process.

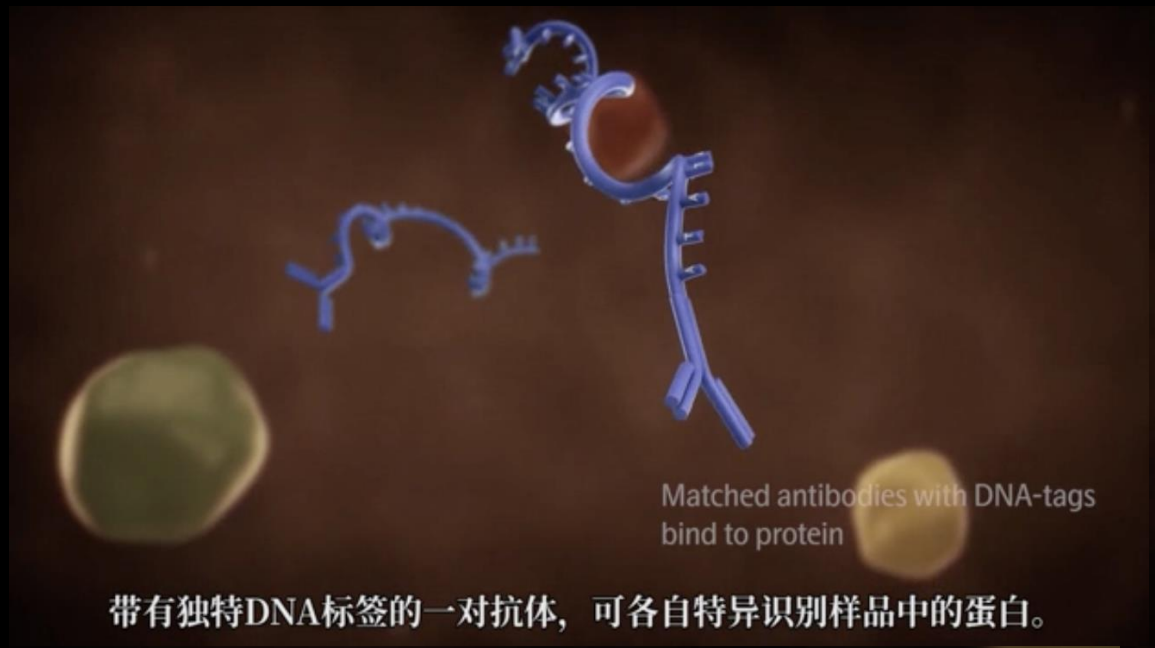
48-plex Cytokine panel with absolute quantification.



Custom-developed product based on protein signature. Relative or absolute quantification for research use only or clinical decision making.

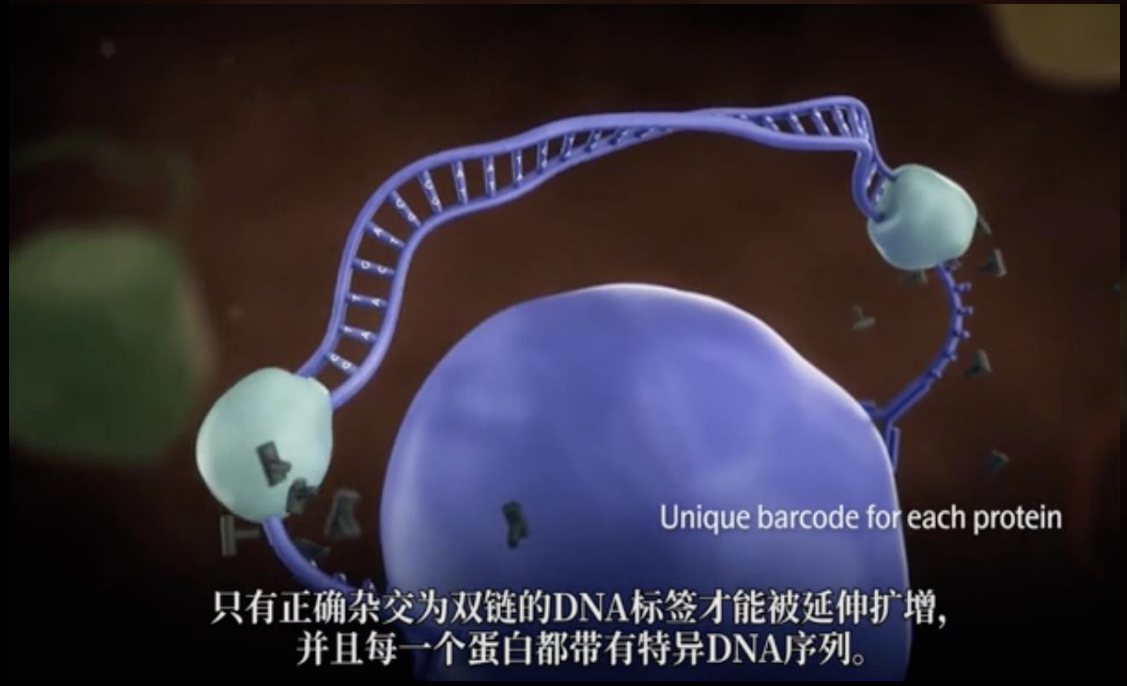
First clinical test LDT) 2021 for monitoring MS progression (in partnership)



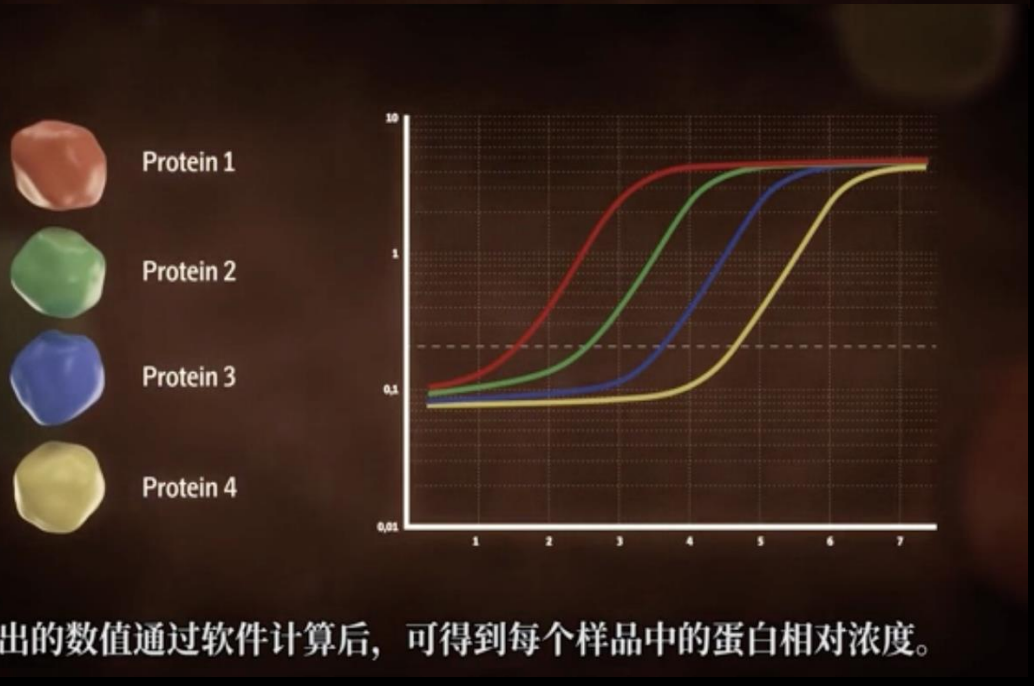


带有独特DNA标签的一对抗体，可各自特异识别样品中的蛋白。

当互补的DNA单链足够接近时，即会杂交形成双链。

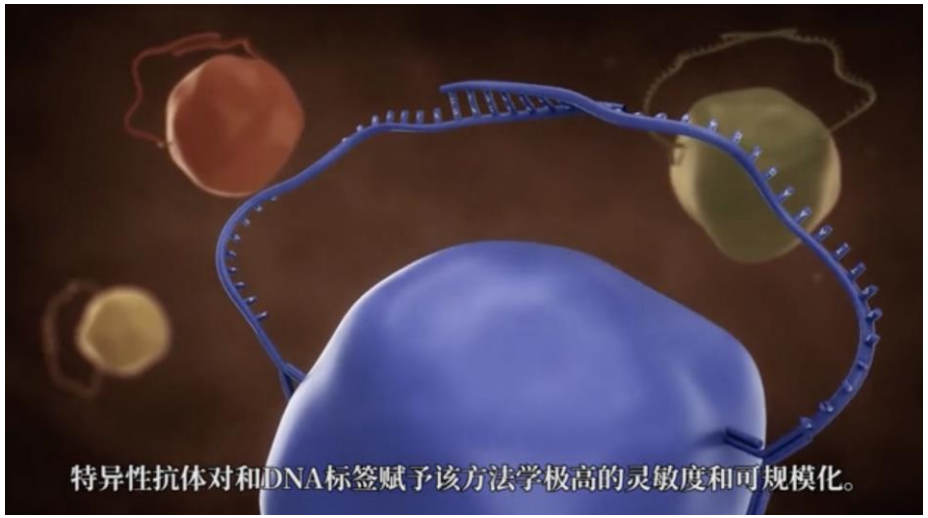


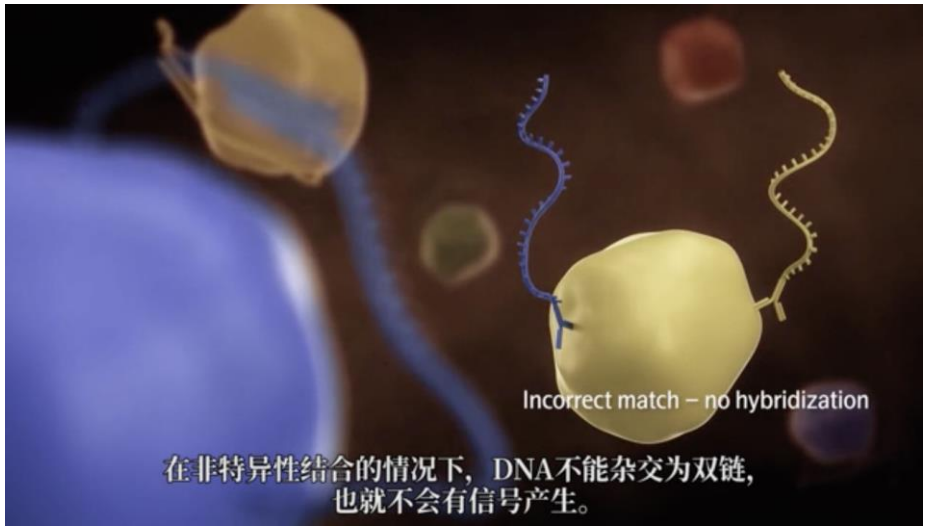
只有正确杂交为双链的DNA标签才能被延伸扩增，
并且每一个蛋白都带有特异DNA序列。

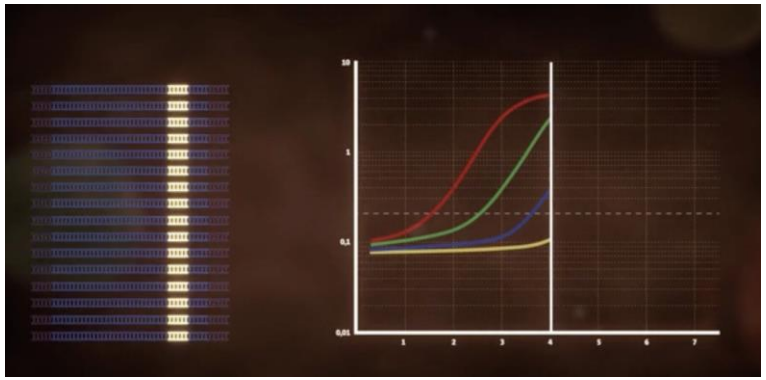


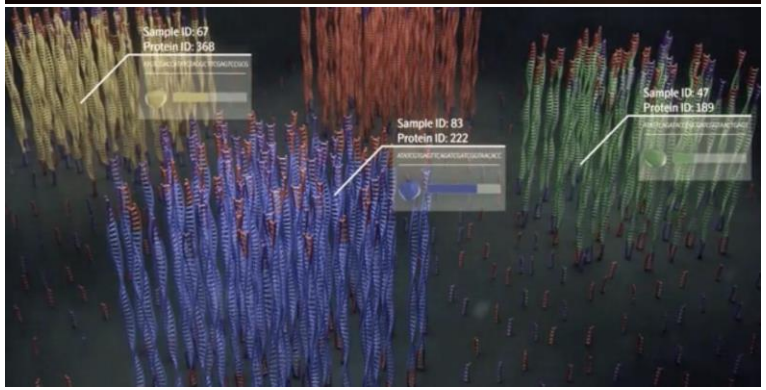
读出的数值通过软件计算后，可得到每个样品中的蛋白相对浓度。

实现了“灵敏度、特异性、高通量”的完美结合







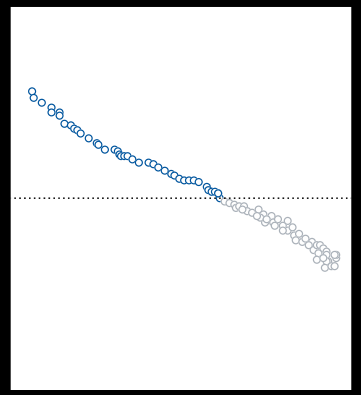


qPCR 检测平台：
96-plex
48-plex

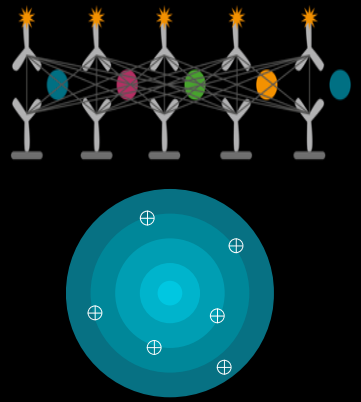
二代测序检测平台：
384-plex、1536-plex、3072-plex或更多

Signature Q100

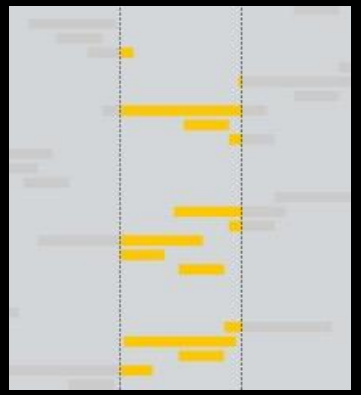
传统蛋白质组技术的挑战 & Olink 蛋白质组技术的突破



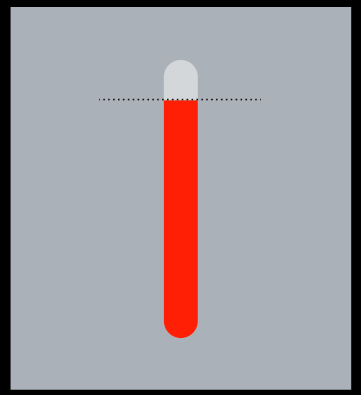
灵敏度不够，无法发现低丰度蛋白



特异性低，导致数据质量差



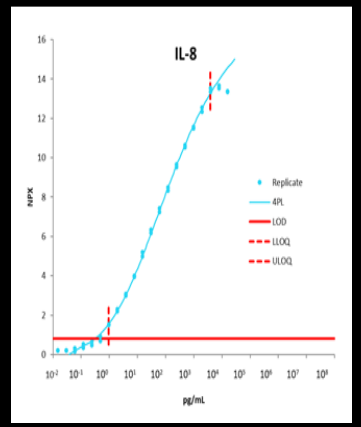
动态范围低，导致无法全面了解血浆蛋白变化



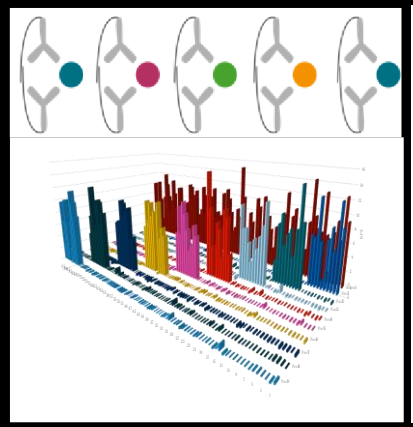
样本量需求大，很多珍稀样本无法检测

通量较低，检测速度慢

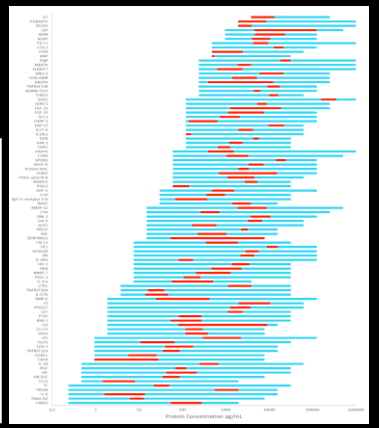
低性价比，重复性差导致的复孔和验证成本高，通量低导致的时间成本高



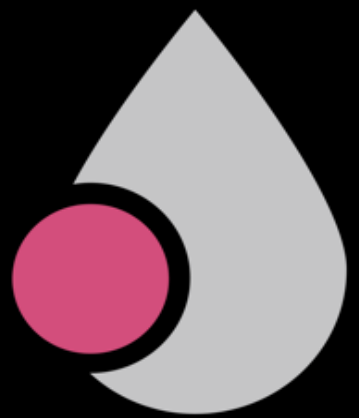
IL8检测到12fg/ml，并且可以有效的检出单个胚胎干细胞的胞内蛋白（见后文）



经过多个大型研究组织评估，FDA验证，最佳的特异性保证业内最高数据质量



PEA技术覆盖10个数量级的动态范围，高中低丰度无偏检测

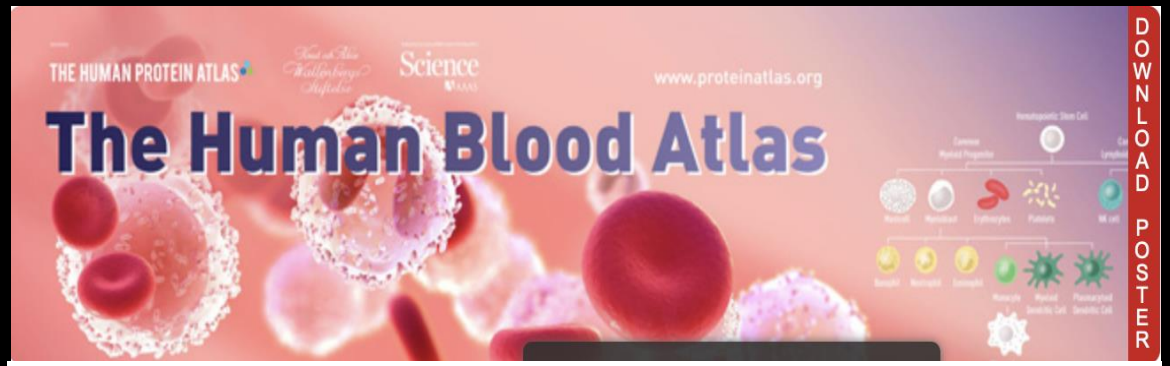


PEA技术仅需1-6ul血浆（体液），可以检测21-3072个蛋白

凭借高通量测序和成熟的qPCR技术，可以在一周检测1300左右样本

使用Olink技术的药物或诊断相关biomarker研发成功率高，性价比高

PEA技术——人类血浆蛋白组官网推荐



THE HUMAN PROTEIN ATLAS

MENU HELP NEWS

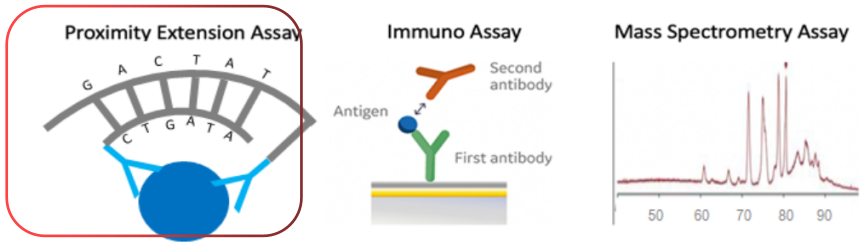
HUMAN PROTEIN ATLAS SECTIONS : BLOOD PROTEIN > METHOD

Blood Protein - Methods summary

- Summary
- Key publication
- What can you learn from the Blood Proteins section?
- How has the data been generated?
- How was the classification of the human secretome done?
- What is presented in the section?

How has the data been generated?

The plasma proteome levels from healthy individuals were measured using proximity extension assay (PEA). The healthy individuals were followed longitudinal for two years and the plasma proteome levels were measured every three months. Data generated by proximity extension assays was normalized within and between plates followed by transformation using a predetermined correction factor and provided in the arbitrary unit Normalized Protein eXpression (NPX). The Blood Atlas also contain information of proteins detected by mass spectrometry-based proteomics, based on publicly available data on the Peptide Atlas. The mass-spectrometry based data was filtered to include only the minimal, non-redundant list of proteins derived from the set of identified peptides and exclude entries labelled as contaminants. In addition, the concentration of actively secreted proteins was annotated using publicly available literature. The Blood proteins section also contains an annotation of the human secretome classified into different categories, including secreted to blood, secreted locally and matrix proteins.



NCI CANCER MOONSHOT
A program of the National Cancer Institute of the National Institutes of Health

CIMAC-CIDC Immuno-Oncology Biomarkers Network

临床试验技术指南 第一梯队方法

Tier 1 (Planned for most trials)	Tier 2 (Planned for selected trials)	Tier 3 (Novel and exploratory)
• CyTOF • Olink • WES • RNA-seq or nCounter (NanoString) • Multiplex IHC/IF • Singleplex IHC	• CyTOF Phosphoflow • Grand Serology ELISA • ctDNA • ATAC-seq • scTCR-seq • TCR-seq • MIBI • Microbiome sequencing	• ELISPOT • HLA tetramers • scRNA-seq • CITE-Seq • Other assays

Cytokines/serum analytes

O-link Serum Cytokine Analysis

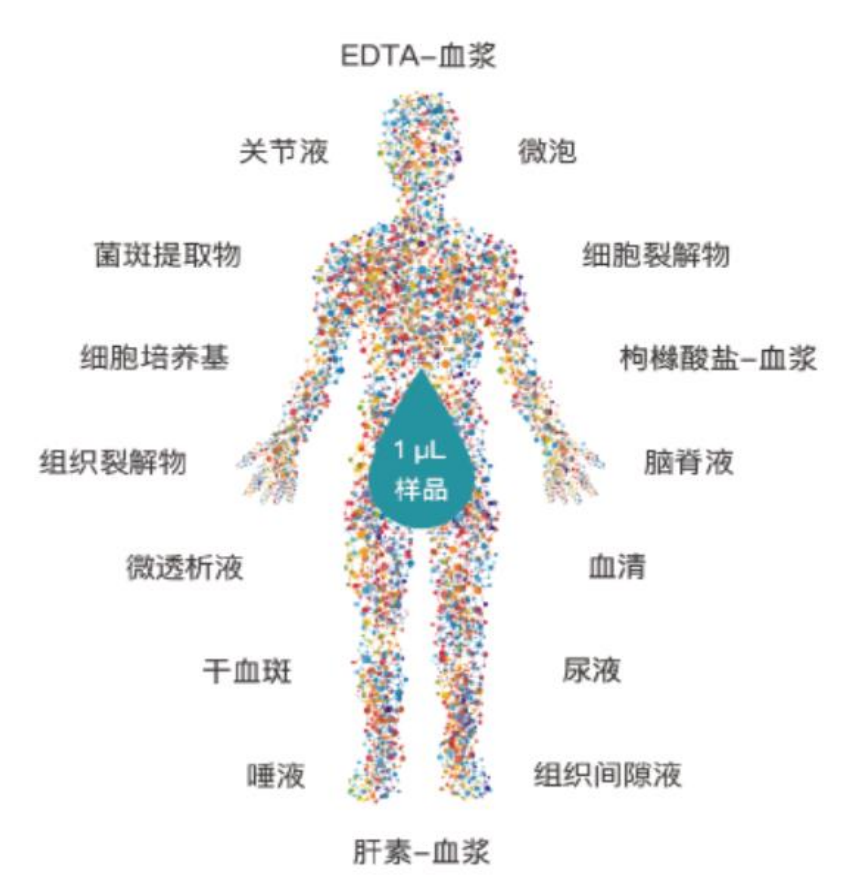
O-link is a technique for detection and quantification of soluble proteins. It can be used for the profiling of cytokines, chemokines, and growth factors, as well as the detection of circulating immune co-stimulatory and inhibitory molecules. Cytokines are key factors regulating immune response and intercellular communication in the tumor microenvironment. As such, cytokines possess diagnostic and prognostic potential, and cytokine production may reflect effects of immunotherapies. Cytokines may also be used in cancer therapy and to modulate immune response.

- SOP Olink Analysis
- SOP Olink proseek kit

https://www.proteinatlas.org/humanproteome/blood

适用各种样本类型

1-6 ul 样品可同时检测 **48-3072** 种蛋白

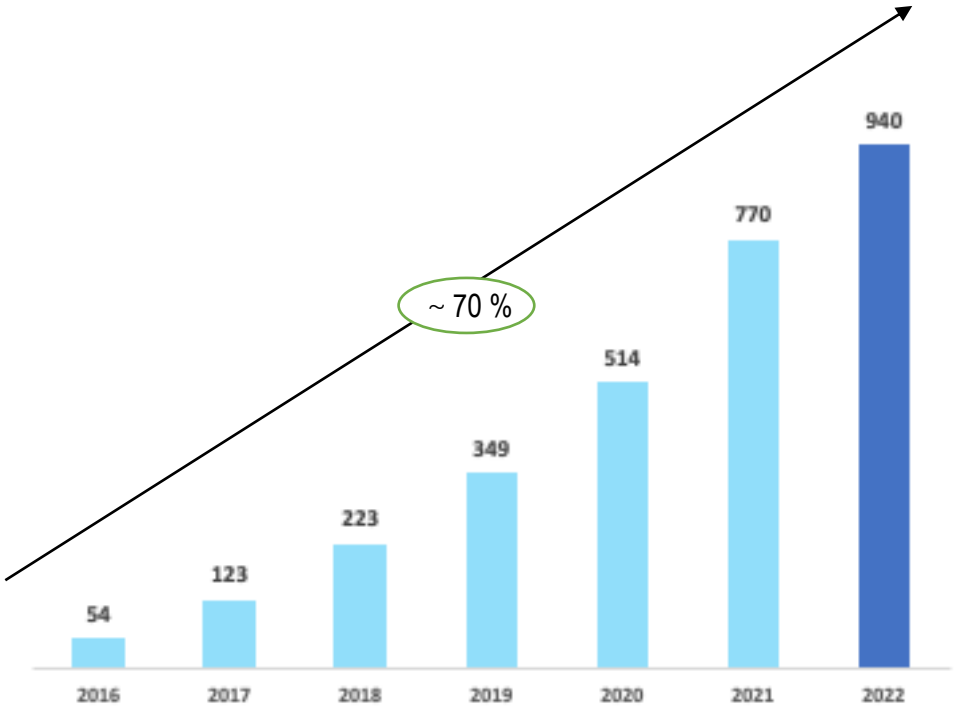


Olink 蛋白质组学panel检测类型

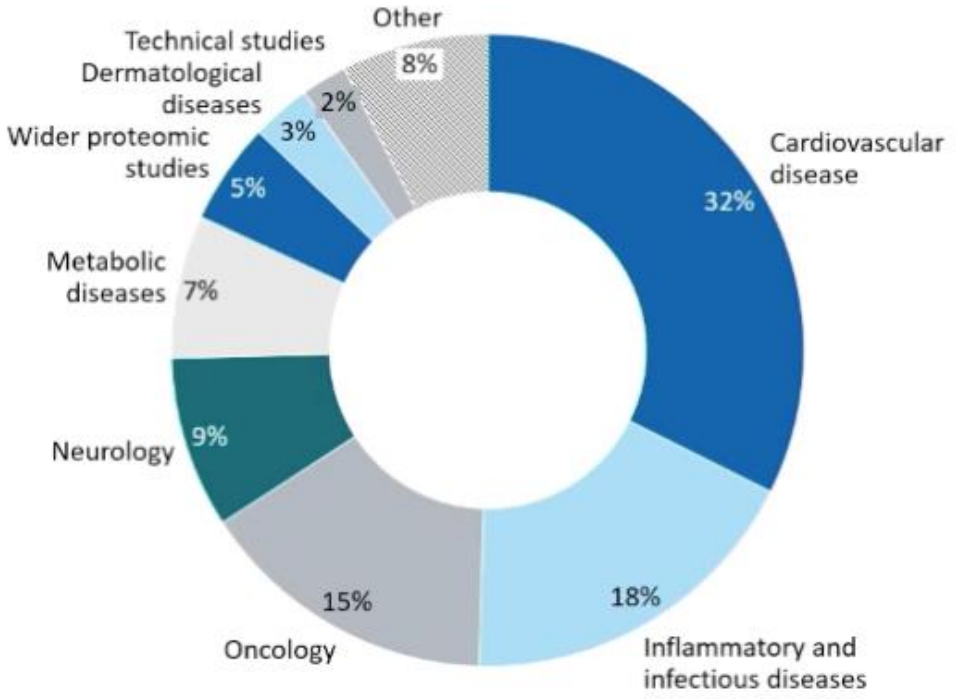
Olink is driving the Proteomics conversion

Evolution of Publication based on PEA (as of 27 July 2022)

Number of publications (accumulated)



Publications by diseases



Olink 蛋白质组学近期代表性文章

博淼生物 BIO MIAO BIOLOGICAL SINCE 2009

1
杂志｜Nature（IF=49.962）2022
文章｜肥胖如何改变免疫系统及个体治疗的响应差异
关键词｜肥胖、特应性皮炎 、队列研究

2
杂志｜Nature Communications （IF= 14.919）2022
文章｜宋尔卫院士团队新作三阴性乳腺癌治疗临床II期研究
关键词｜三阴性乳腺癌、药物响应、蛋白标志物

3
杂志｜Nature （IF=49.962) 2021
文章｜多组学研究mRNA疫苗BNT162B2人体免疫应答
关键词｜新冠、mRNA疫苗 、再次免疫

4
杂志｜Cell Research （IF= 25.617）2021
文章｜中国学者首发新冠病毒无症状感染组免疫学特征和蛋白标志物
关键词｜新冠、队列研究、患者分层

5
杂志｜Science （IF = 47.728）2021
文章｜Olink超灵敏血浆蛋白组挑战基因与疾病间之鸿沟
关键词｜蛋白组学、多组学、pQTL

6
杂志｜Alzheimers‘ Dementia （IF=21.566）2021
文章｜叶玉如院士借助 Olink 19-plex panel更准确地筛查并分期AD
关键词｜阿尔茨海默症 AD、蛋白标志物、无创检测

7
杂志｜Cell （IF = 41.582）2021
文章｜多组学研究揭示发酵食品可降低人体炎症标志物
关键词｜多组学、宏基因组、肠道菌群

8
杂志｜Annals of Oncology （IF = 32.976）2021
文章｜Olink助力预测免疫检验点阻断剂抵抗的全新生物标志物
关键词｜ICB、癌症治疗耐药、生物标志物

9
杂志｜Lancet Respir Med（IF =30.7）2022
文章｜Olink助力多中心队列研究首发PFILD肺病蛋白组特征
关键词｜进行性肺纤维化、蛋白组学、Machine Learning

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杂志｜JACC （IF = 24.094）2021
文章｜Olink蛋白质组联合机器自学习显著提高死亡风险预测有效性
关键词｜心血管、蛋白质组、Machine Learning

应用场景

Olink 蛋白质组在精准医学中的应用

nature COMMUNICATIONS

应用分享：olink血浆蛋白质组在人群队列中分析监测健康和疾病

ARTICLE

https://doi.org/10.1038/s41467-021-22767-z OPEN

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Next generation plasma proteome profiling to monitor health and disease

Wen Zhong [1], Fredrik Edfors [1], Anders Gummesson [2,3], Göran Bergström [2,4], Linn Fagerberg [1] & Mathias Uhlén [1,5]✉

发表期刊：Nature communication

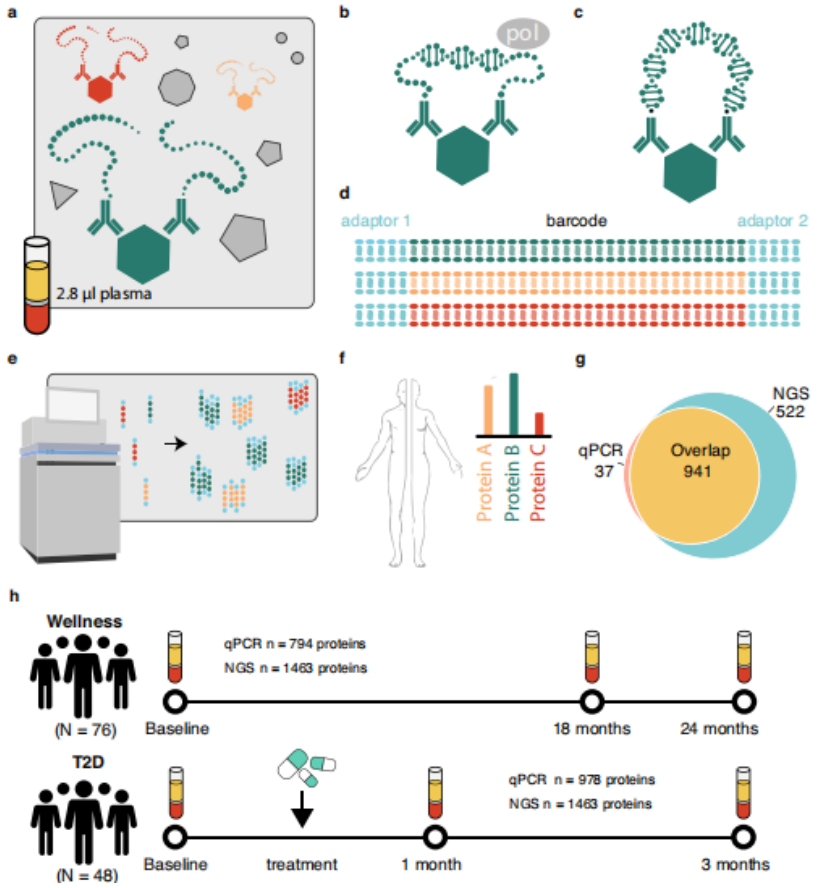
影响因子：14.919

发表时间：2021

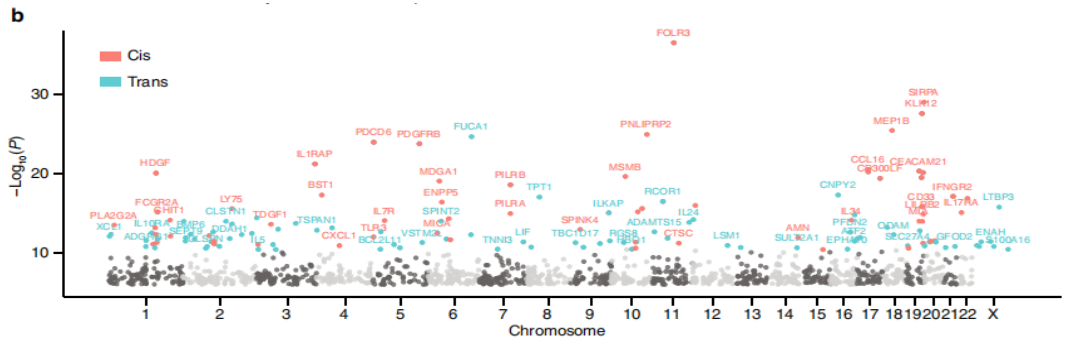
样本选择：76例健康对照、48例T2D患者

多组学平台：Olink蛋白组 / 二代测序

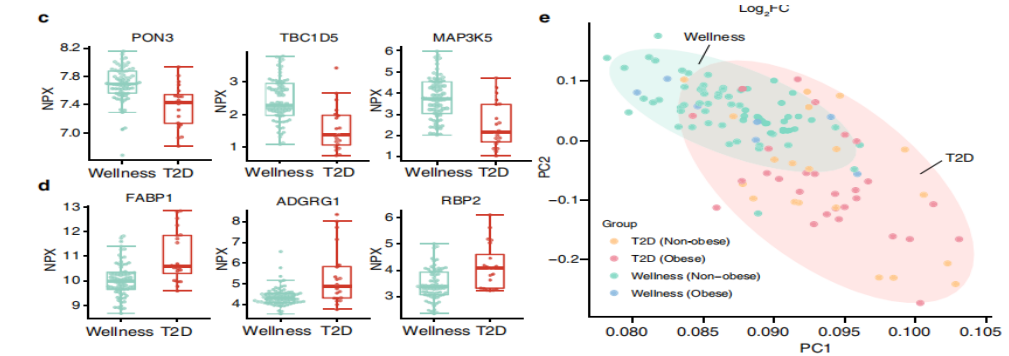
研究方案



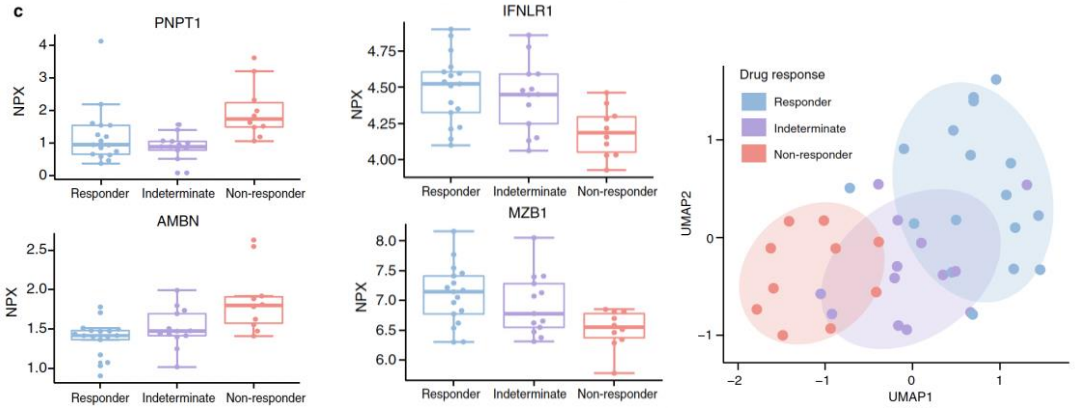
结果



多组学药物靶点发现（pQTLs）：通过基于基因组检测的数据和血浆蛋白质组，使用多重分析鉴定了69个先前未描述的遗传变异(pQTLs)，确定多组学和疾病表型的因果关联，发现疾病致病机理



二型糖尿病（T2D）诊断标志物开发：分析比较T2D病患和健康人队列的血浆蛋白组，发现了一系列蛋白质标志物，未来可能开发糖尿病的液态活检试剂盒；



疗效预测生物标志物开发：检测了T2D患者在二甲双胍治疗前后的差异蛋白质组。在治疗有效，无效和介于中间的患者中找到表达有显著差异的蛋白标志物，可用于药物伴随诊断开发

应用1：疾病的精准诊断及液态活检生物标志物开发

To perform successful biomarker research ending with validated assays that are suitable for clinical application requires collaboration between academic centers and industry with considerable investments of time and money

Bioinformatics and Statistics: Computational Validation of Functional Biomarkers 245

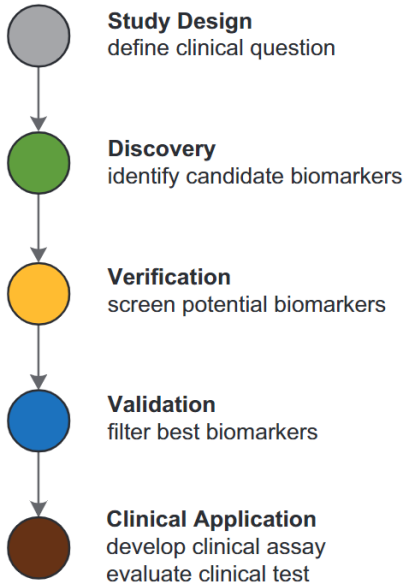


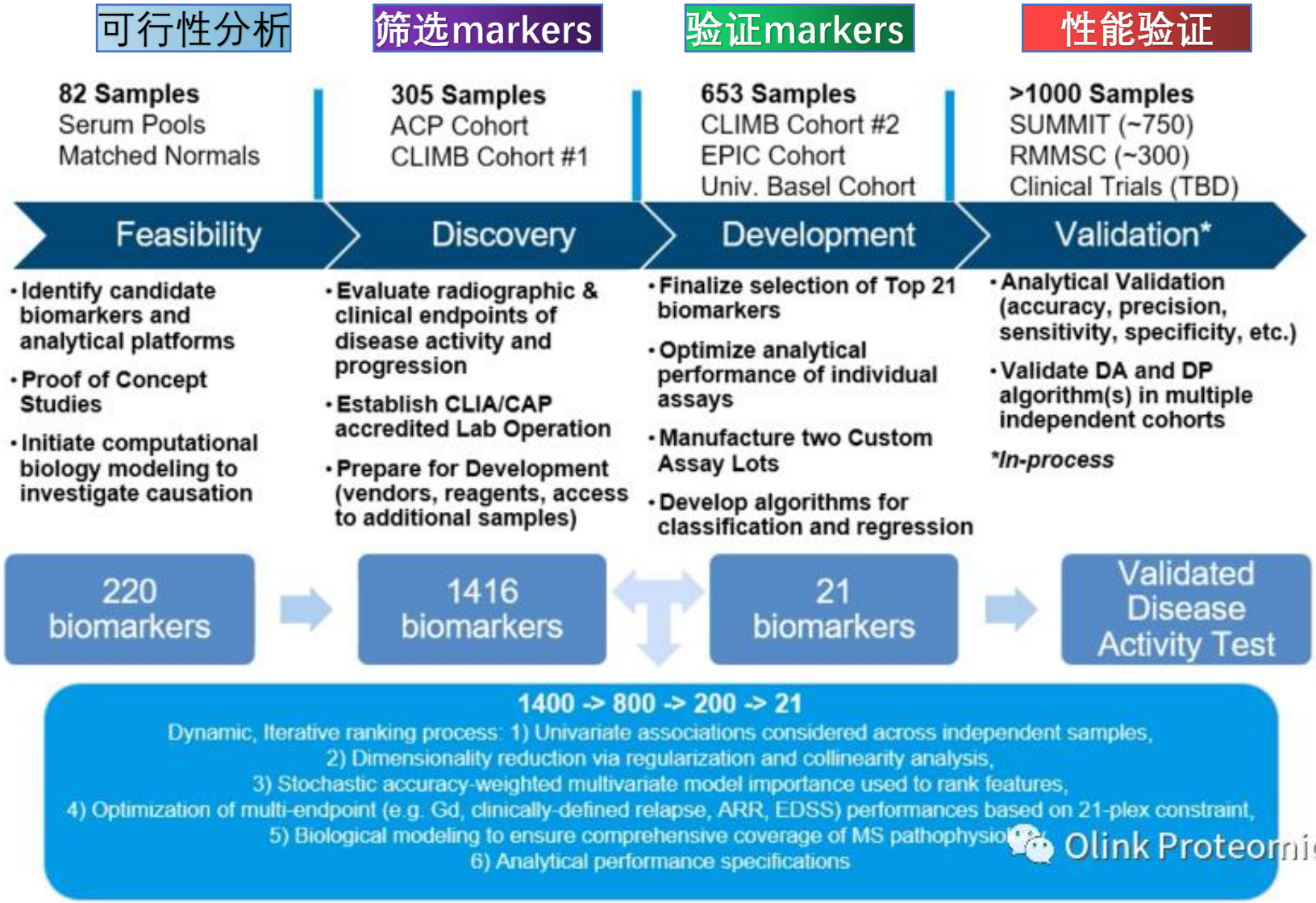
Figure 9.1 Biomarker development workflow overview.

Comprehensive Biomarker Discovery and Validation for Clinical Application

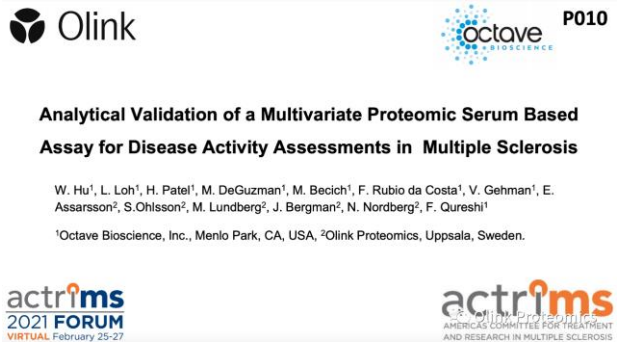
Author: Péter Horvatovich, Rainer Bischoff

Date: 2013

Olink技术生物标志物的筛选以及进行定制化开发流程图



美国Octave公司与Olink公司合作，研发和验证了通过血清蛋白组分析来进行多发性硬化症（以下简称MS）的伴随诊断试剂盒，建立了精准无创液体活检的伴随诊断方法。

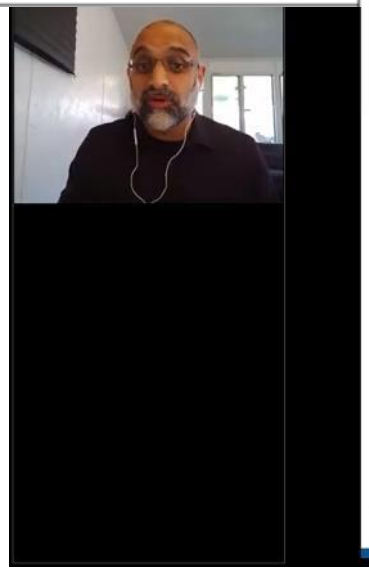


Count	Marker	Name (Alias)	Associated Pathways, Cell Types
1	APLP1	Amyloid Beta Precursor Like Protein 1	synaptic maturation during cortical development, regulation of neurite outgrowth
2	CCL20	MIP-3 alpha	immunoregulatory and inflammatory processes
3	CD6	Cluster of Differentiation 6	T cell, Th1, Th17
4	CDCP1	CUB domain-containing protein 1	T cell migration
5	CNTN2	Contactin 2	cell adhesion, proliferation, migration, and axon guidance of neurons
6	COL4A1	Collagen alpha-1(IV) chain	cell proliferation, migration, ECM
7	CXCL13	C-X-C Motif Chemokine Ligand 13, BLC	immune activation, B cell homing
8	CXCL9	Monokine Induced by Gamma Interferon, MIG	Immune Response, Inflammation
9	FLRT2	Leucine-rich repeat transmembrane protein	cell-cell adhesion, cell migration and axon guidance
10	GFAP	Glial Fibrillary Acidic Protein	demyelination and neuroaxonal injury
11	GH	Somatotropin, Growth Hormone	growth, cell reproduction and regeneration
12	IL-12B	Interleukin 12B	innate & adaptive immunity, Th1, overexpression observed in CNS in MS
13	MOG	Myelin-oligodendrocyte glycoprotein	oligodendrocyte, immune-mediated demyelination
14	NEFL	Neurofilament Light, NFL	Neurodegeneration
15	OPG	Osteoprotegerin, TNFRSF11B	inflammation, T cell activation, IFN-B treatment
16	OPN	Osteopontin	Immune modulation
17	PRTG	Protogenin	neurogenesis, demyelinating
18	SERPINA9	Serpin Family A Member 9	B cell
19	TNFRSF10A	TRAILR1, DR5 - Death Receptor 5	Cell Signaling and Apoptosis
20	TNFSF13B	BAFF	B cell, Inflammation
21	VCAN	Versican, versican proteoglycan	cell motility, growth and differentiation, cell adhesion, proliferation, migration and angiogenesis

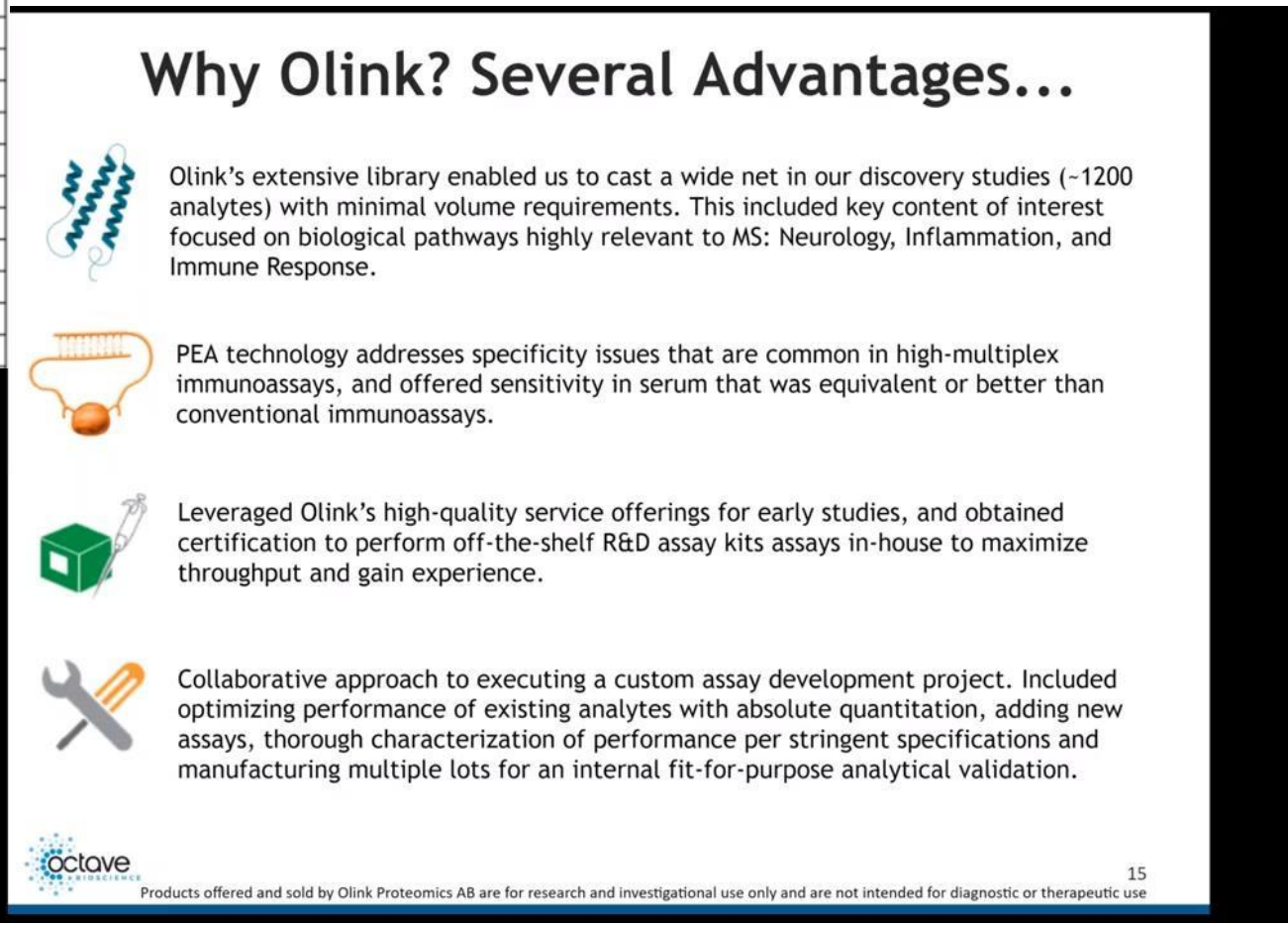
Olink Proteomics

Olink Focus panel for Octave

蛋白标志物详细列表

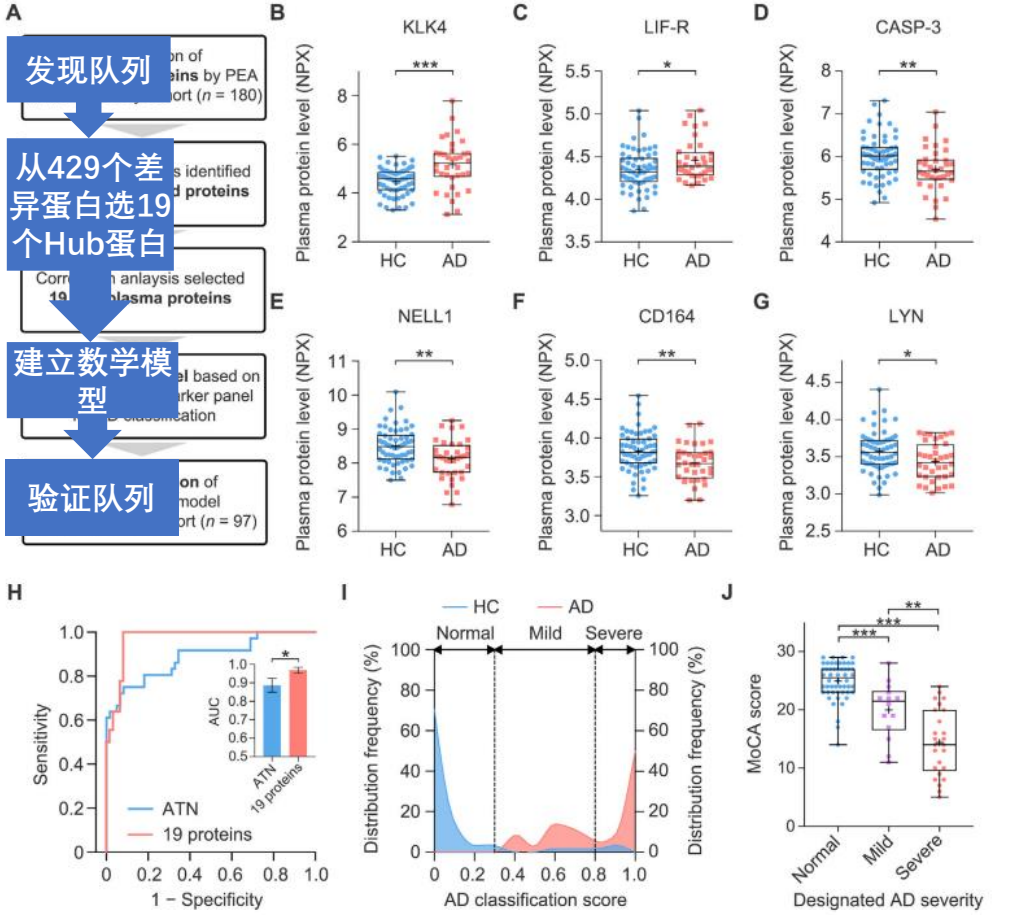


PEA技术在Biomarker discovery中的优势



案例：阿尔兹海默症液态活检诊断标志物开发

This study comprehensively profiled the AD plasma proteome and serves as a foundation for a high-performance, blood-based test for clinical AD screening and staging.Individual AD classification scores were calculated using a linear regression model that included age, sex, and the plasma levels of the 19-protein biomarker panel as candidate factors



DOI: 10.1002/alz.12369, Alzheimer's Dement. 2021;1–15.

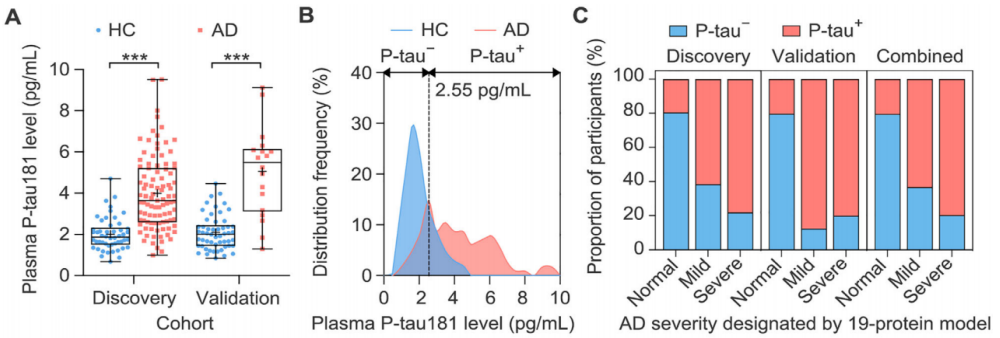
Received: 24 November 2020 | Revised: 29 March 2021 | Accepted: 5 April 2021
DOI: 10.1002/alz.12369

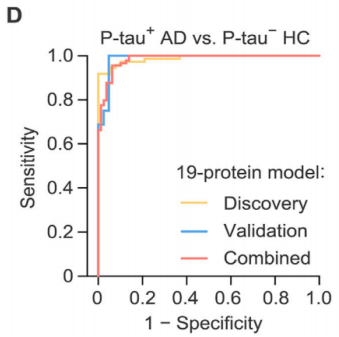
FEATURED ARTICLE

Alzheimer's & Dementia® THE JOURNAL OF THE ALZHEIMER'S ASSOCIATION

Large-scale plasma proteomic profiling identifies a high-performance biomarker panel for Alzheimer's disease screening and staging

Yuanbing Jiang[1] | Xiaopu Zhou[1,2,3] | Fanny C. Ip[1,2,3] | Philip Chan[1] | Yu Chen[1,2,3,4] | Nicole C.H. Lai[1] | Kit Cheung[1] | Ronnie M.N. Lo[1] | Estella P.S. Tong[1] | Bonnie W.Y. Wong[1] | Andrew L.T. Chan[5] | Vincent C.T. Mok[6] | Timothy C.Y. Kwok[7] | Kin Y. Mok[1,2,8,9] | John Hardy[2,8,9] | Henrik Zetterberg[2,8,9,10,11] | Amy K.Y. Fu[1,2,3] | Nancy Y. Ip[1,2,3]





E

AUCs of 19-protein model

Cohorts	Overall AD vs. HC#	P-tau⁺ AD vs. P-tau⁻ HC#	p†
Discovery	0.9816 ± 0.0083	0.9881 ± 0.0071	0.5518
Validation	0.9690 ± 0.0151	0.9863 ± 0.0115	0.3620
Combined	0.9594 ± 0.0107	0.9844 ± 0.0069	**0.0495**

#AUC is denoted as mean ± SEM
†DeLong test

.鉴定了429个在血浆中调节失调的蛋白质。我们选择了19个代表阿尔兹海默症血浆蛋白概况的"中心蛋白"，这形成了准确分类AD（曲线=0.9690–0.9816下的面积）和相关内表型的评分系统的基础。此外，特异性中心蛋白表现出疾病阶段依赖性调节失调，可以描述区分AD阶段。

应用2
在人类免疫图谱研究中的相关应用

应用分享：多组学联用评估mRNA疫苗BNT162B2人体免疫应答

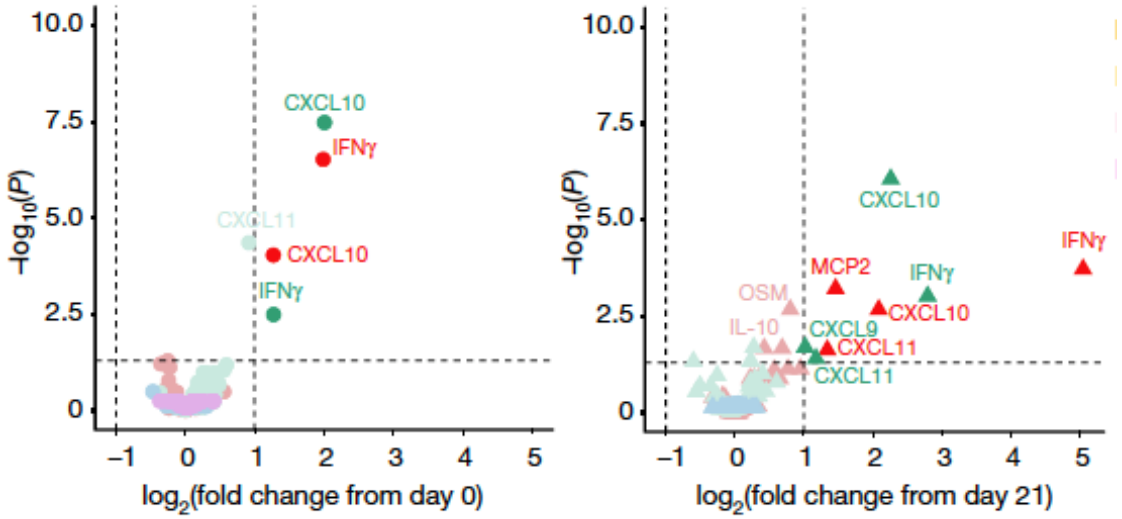
Systems vaccinology of the BNT162b2 mRNA vaccine in humans

Prabhu S. Arunachalam, Madeleine K. D. Scott, ... Bali Pulendran + Show authors

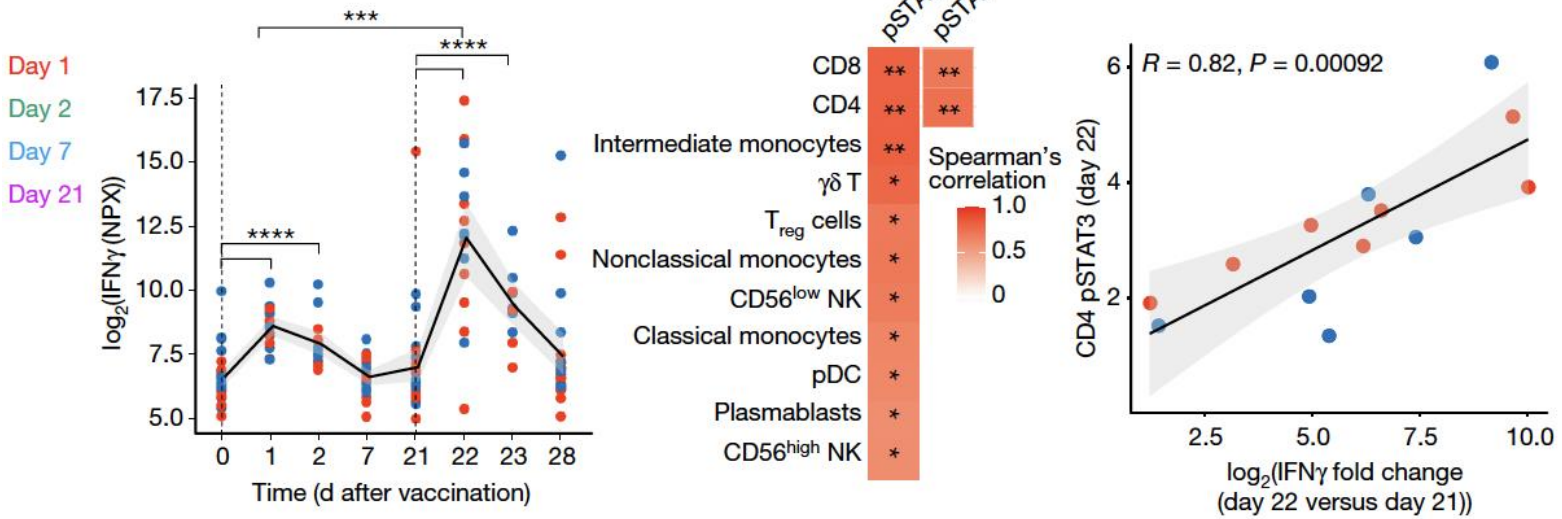
Nature **596**, 410–416 (2021) | Cite this article

发表期刊：Nature
影响因子：49.962
发表时间：2021
样本选择：56例志愿者（31例进行olink分析）
多组学平台：Olink 免疫蛋白组/ 10X 单细胞转录组

斯坦福医学院团队在《自然》杂志发表研究，借助Olink免疫验证蛋白组学分析和单细胞转录组学平台，详细阐述了Pfizer-BioNTech mRNA疫苗BNT162B2再次注射后，人体免疫系统对SRAS-CoV-2野生型病毒及突变株的天然免疫应答和获得性免疫应答。

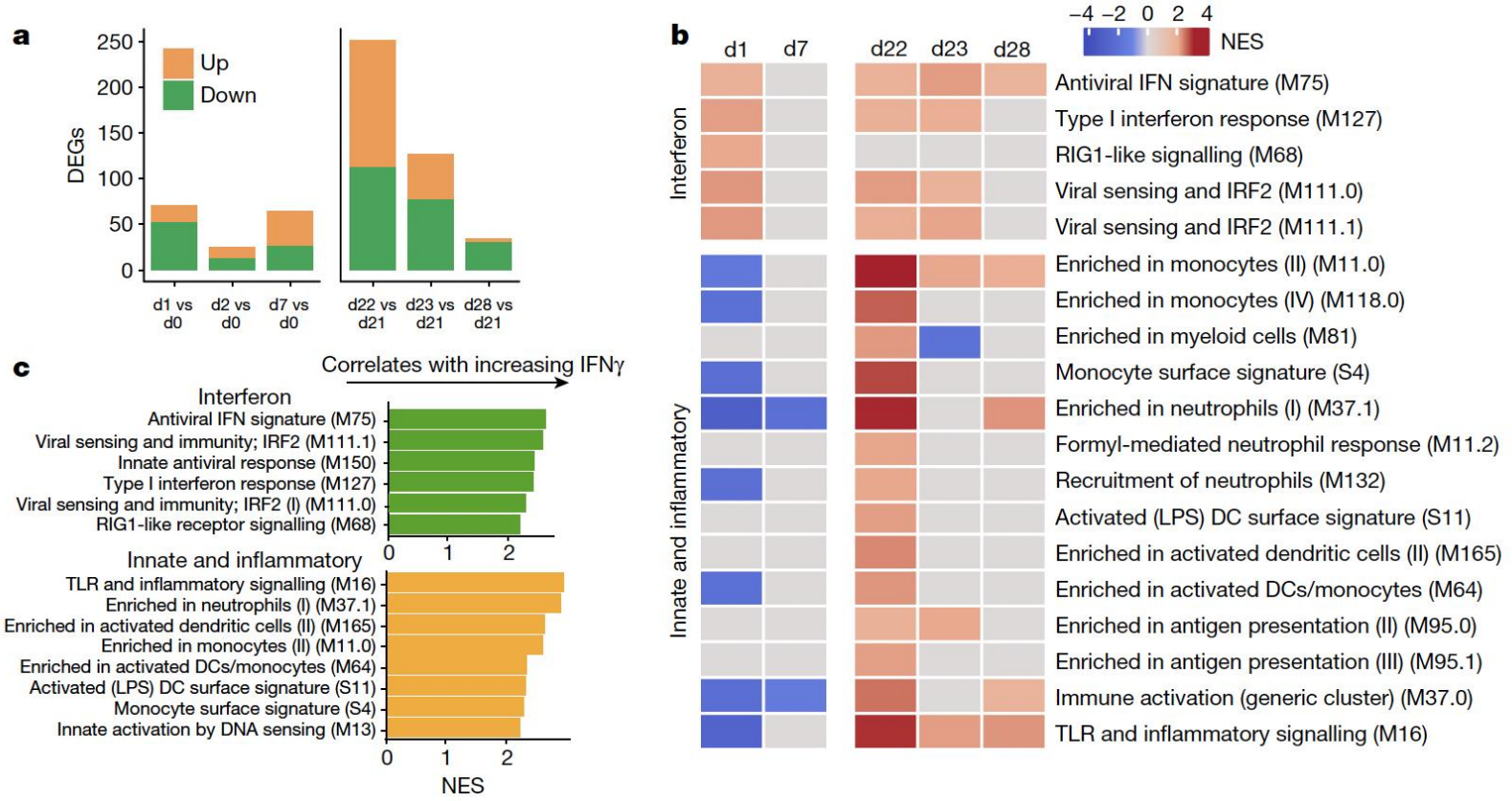


采用Olink血浆蛋白组学平台的免疫炎症Panel，对31例免疫者的血浆样品进行多重细胞因子检测分析，在初次（左）和二次（右）疫苗接种后分别与第0天和第21天相比，火山图显示血浆中细胞因子表达的变化。



将第1天到第22天的INFγ细胞因子数据进行时间轴的系统分析，并分析INFγ表达水平和不同细胞类型中的pSTAT磷酸化的相关性，

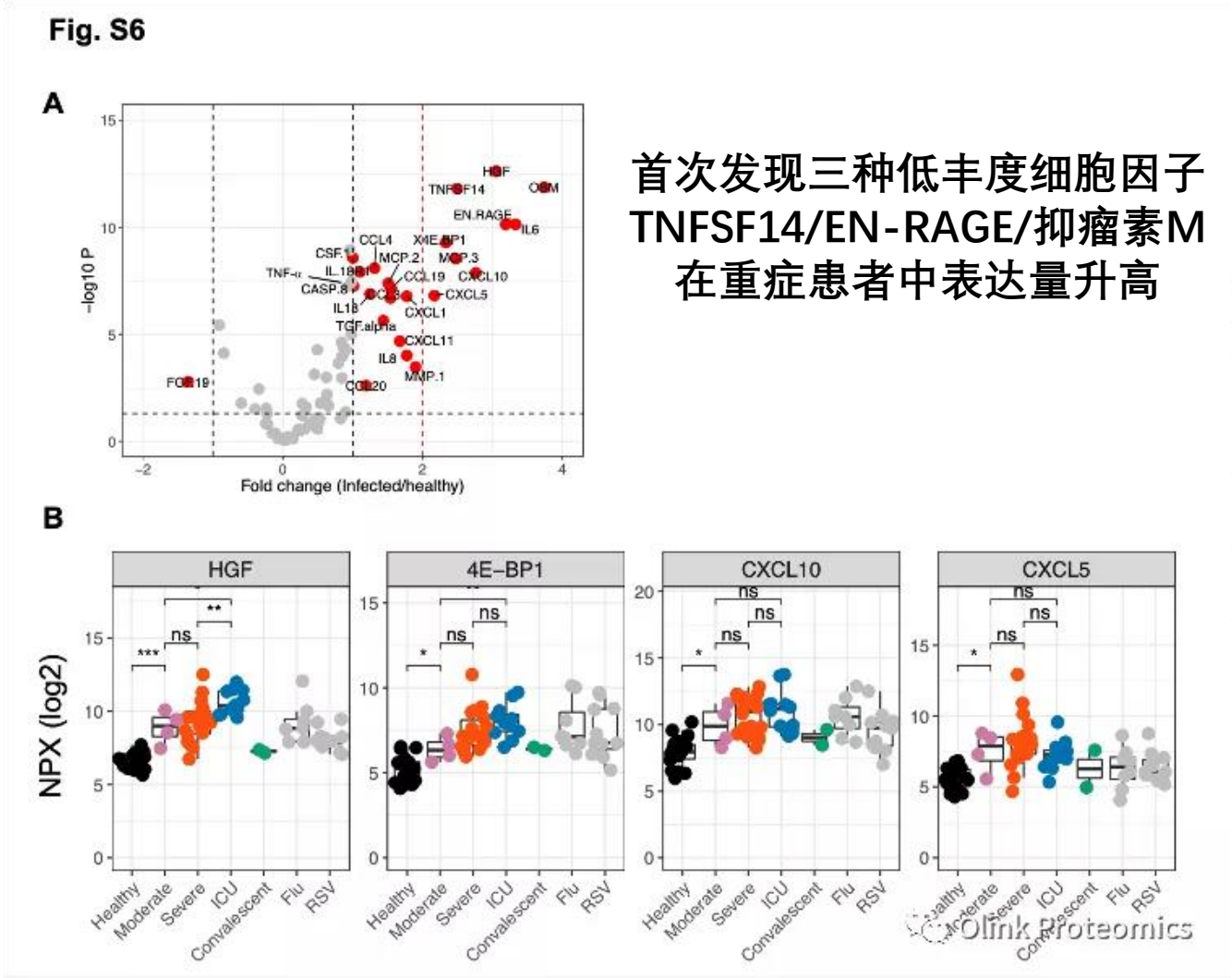
结果



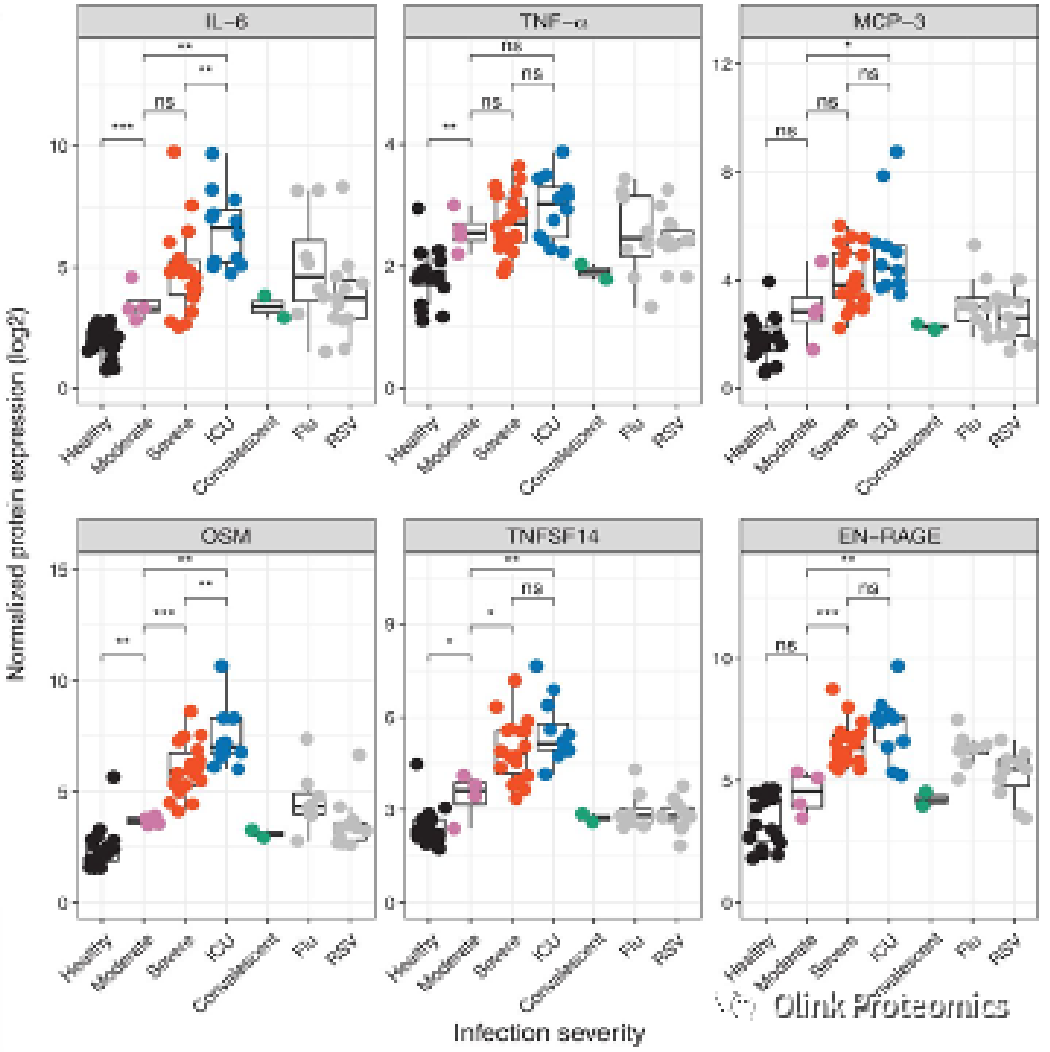
采用单细胞转录组学技术对免疫者样品进行了系统分析，结合之前的Olink蛋白组学数据进行相关性分析

最后得出结论：BNT162B2疫苗在二次免疫后可显著提升以INFγ为代表的先天免疫防御；随着INFγ浓度持续显著提高，“细胞因子反馈”调节进一步激活免疫系统；二次免疫后，骨髓细胞出现mRNA免疫后独特转录学特征标签C8簇，这一特征与天然免疫中INF介导的HLA-DR低表达现象截然不同。

Science | 根据免疫系统应答对中/重症新冠患者进行分层



首次发现三种低丰度细胞因子
TNFSF14/EN-RAGE/抑瘤素M
在重症患者中表达量升高



Cell Research ｜新冠病毒无症状感染组免疫学特征和蛋白标志物

Cell Research

www.nature.com/cr
www.cell-research.com

ARTICLE OPEN

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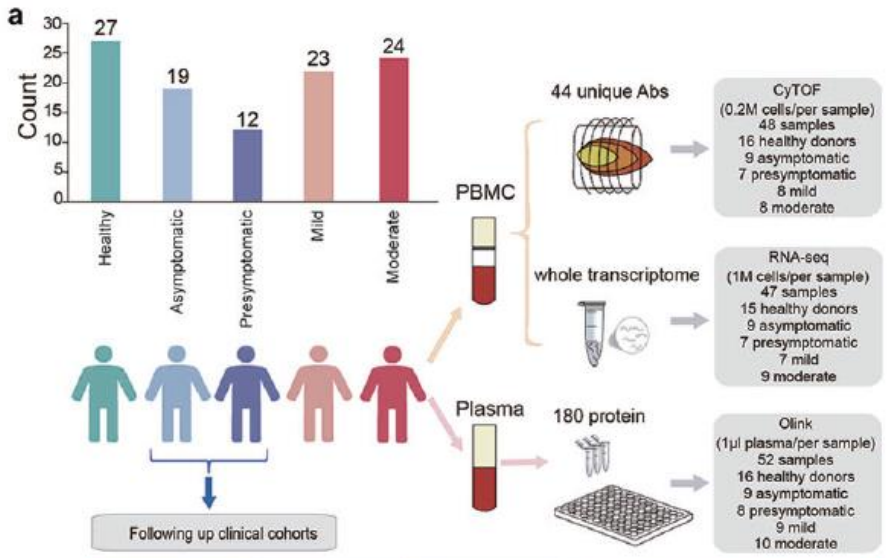
Distinct immune signatures discriminate between asymptomatic and presymptomatic SARS-CoV-2^{pos} subjects

Shanhe Yu[1,3,8], Caixia Di[2,3,8], Shijun Chen[1,8], Mingquan Guo[4,8], Jiayang Yan[2,3,8], Zhaoqin Zhu[4], Li Liu[5], Ruixue Feng[1], Yinyin Xie[1], Ruihong Zhang[1], Juan Chen[1], Mengxi Wang[1], Dong Wei[3,6], Hai Fang[1], Tong Yin[1], Jinyan Huang[1], Saijuan Chen[1], Hongzhou Lu[5] ✉, Jiang Zhu[1,3] ✉ and Jieming Qu[2,3,7] ✉

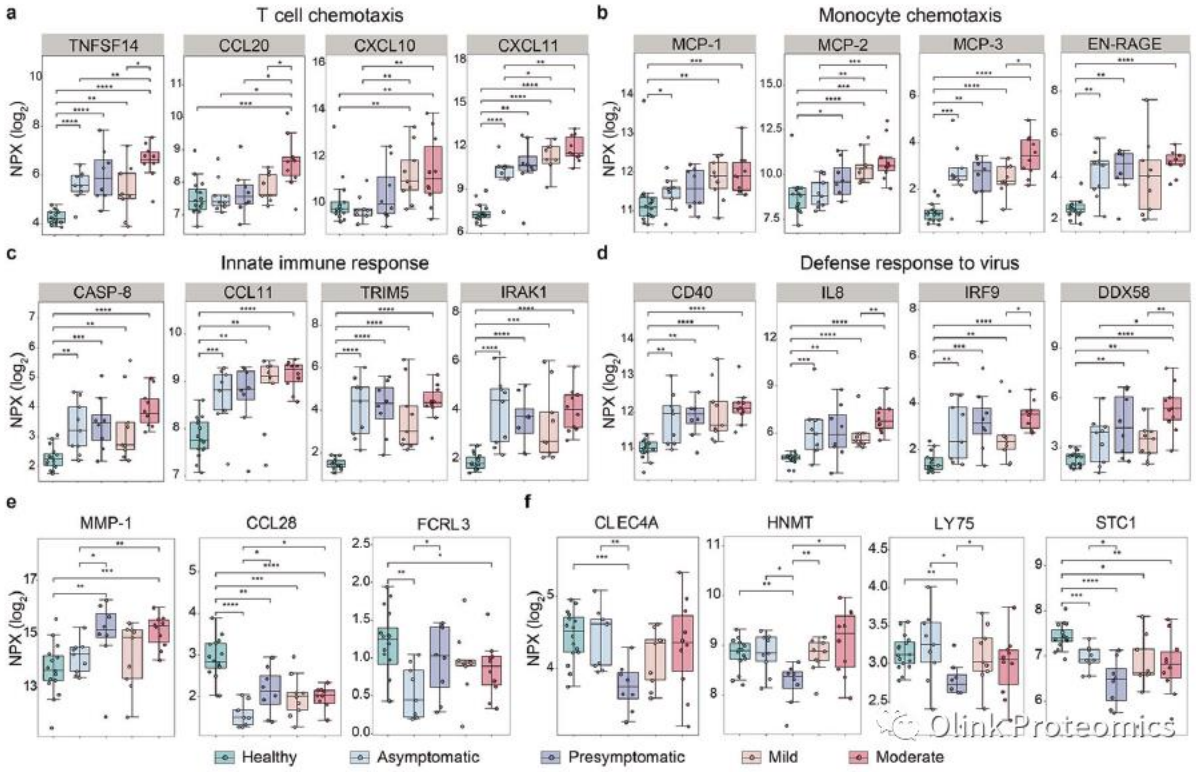


	Healthy	Asymptomatic	Presymptomatic	Mild	Moderate
Age (yr)	26.00 (24.00-29.00)	23.00 (20.00-31.00)	29.50 (23.25-36.00)	23.00 (21.00-26.00)	25.00 (23.00-29.50)
Gender (F/M)	14 (51.9%)/13 (48.1%)	8 (42.1%)/11 (57.9%)	7 (58.3%)/5 (41.7%)	7 (30.4%)/16 (69.6%)	12 (50.0%)/12 (50.0%)
BMI	21.08 (19.37-23.89)	20.98 (19.23-22.84)	21.48 (18.70-23.65)	22.07 (19.13-23.67)	21.55 (19.32-24.41)
Comorbidities *	N/A	N/A	N/A	N/A	N/A

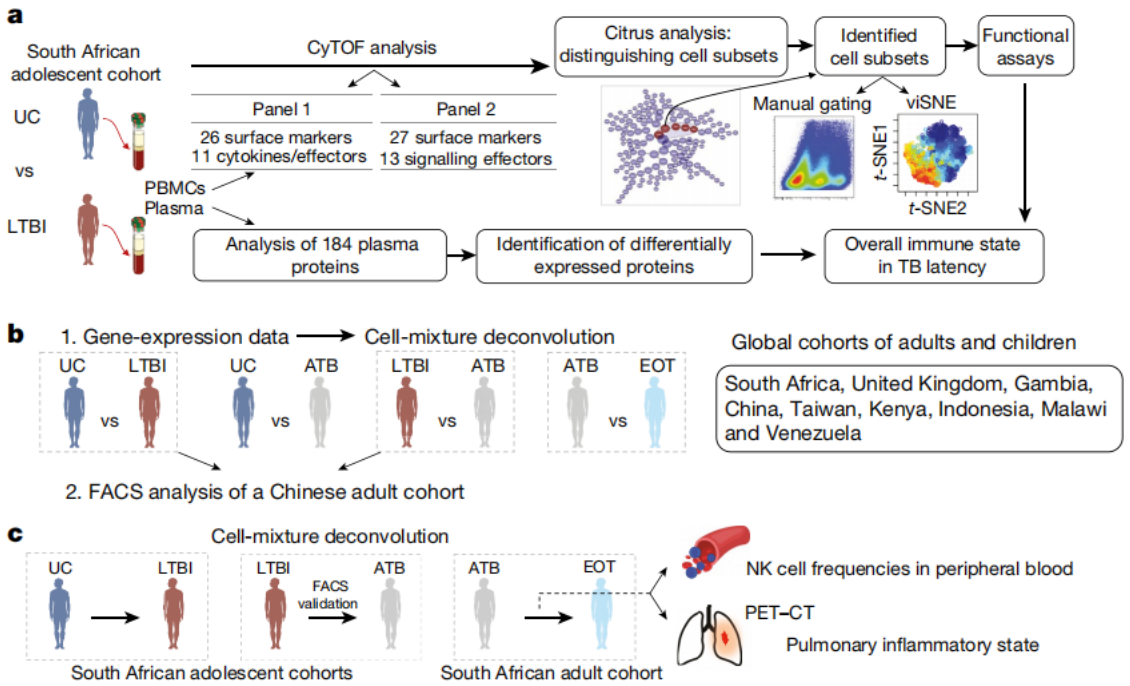
*Comorbidities include all coexisting disorders shown in Table S1.

Overall Immune State：细胞学研究+Olink炎症蛋白质组+转录组

- 新冠病毒感染静默期SSIS无症状感染人群，运用「多维度多组学」方法进行系统性人群队列研究，首次发现细胞水平和分子水平特异性免疫学特征，可区分持续无症状感染者和潜伏期无症状感染者；并针对潜伏期感染者在感染静默期的免疫机制进行了系列研究，发现导致静默期SSIS两种相反疾病进展的免疫机制；
- 基于Olink血浆蛋白组学结论，研究团队又进一步通过酶联免疫ELISA技术，对发现的两个重要的单核细胞相关标志物STC1和MMP-1，做了进一步验证。ELISA结果在之前的第1队列研究和全新的第2组队列研究中，都与Olink血浆蛋白学有很好的一致性，STC1和MMP-1标志物可在静默期SSIS中将潜伏期感染者和持续无症状感染人群区分开来。

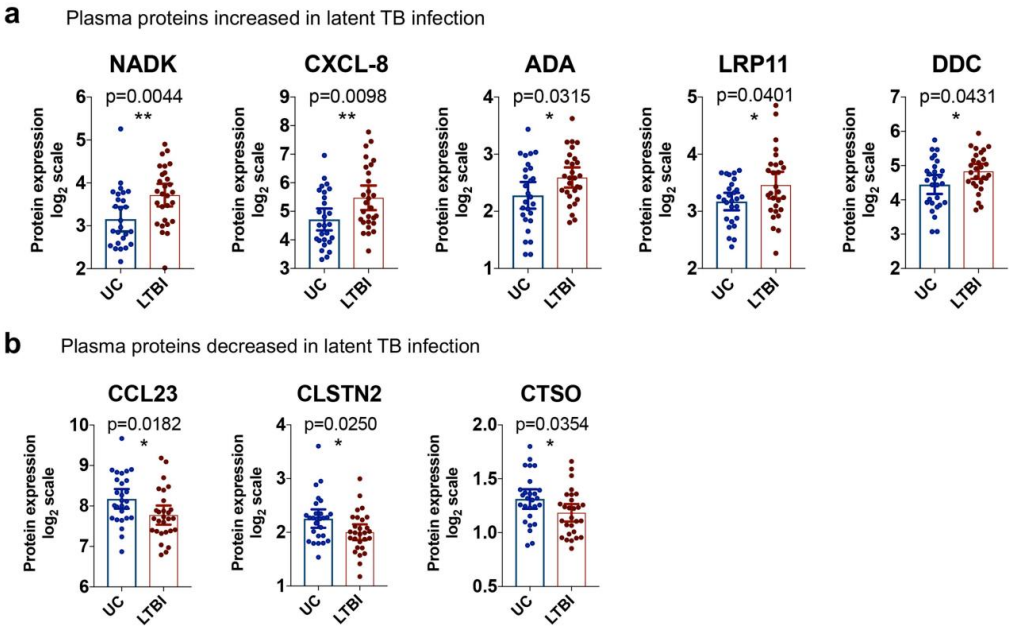


Nature｜结核杆菌感染的潜伏期感染个体的免疫特征



Overall Immune State：细胞学研究+Olink炎症蛋白质组+转录组

从南非青少年队列中区分未感染和潜伏感染个体的免疫特征。



- 大多数结核分枝杆菌(Mtb)感染表现为临床无症状的状态，称为潜伏结核感染，影响约四分之一的全球人口
- 这个研究为结核病潜伏期的潜在病理生理学提供了关键的见解，并确定了可能影响感染结果的因素。找到了潜伏期差异显著的蛋白质生物标志物。
- Olink Metabolism panel&Inflamation Panel

Chowdhury et al. "A multi-cohort study of the immune factors associated with M. tuberculosis infection outcomes." Nature, vol. 560, no. 7720, Aug. 2018, pp. 644+.

应用3

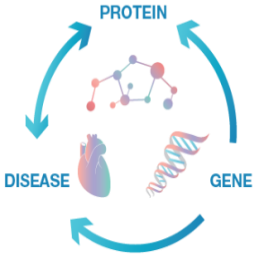
药物研发和临床实验

Olink Proteomics可以应用于药物研发全流程中的蛋白检测

博淼生物 BIO MIAO BIOLOGICAL SINCE 2009

- 精准药物、精准剂量、精准病人——实现精准治疗

临床前研发 → I期临床 → II 期临床 → III期临床 → 药物上市后研究



转化医学生物标志物发现

- 药物靶点发现和验证
- 利用多组学联合分析因果关系挖掘创新药物靶点
- 更好理解生物学和生理病理进程

病人分层、精准治疗

- 发现疾病致病机理以及相关信号通路
- 开发疾病早筛及伴随诊断标志物
- 寻找和筛选易感人群

药物临床实验

- 药物的安全性及有效性评估及风险监测
- 拓展药物的新适应症
- 筛选更好的疾病预测和预后标

利用临床样本和数据进行新靶标发现，在整个临床实验中评估药物安全性和有效性，寻找最合适药物剂量，筛选易感人群，开发伴随诊断拓展新的适应症，加速药物研发进程，最终达致精准医学。

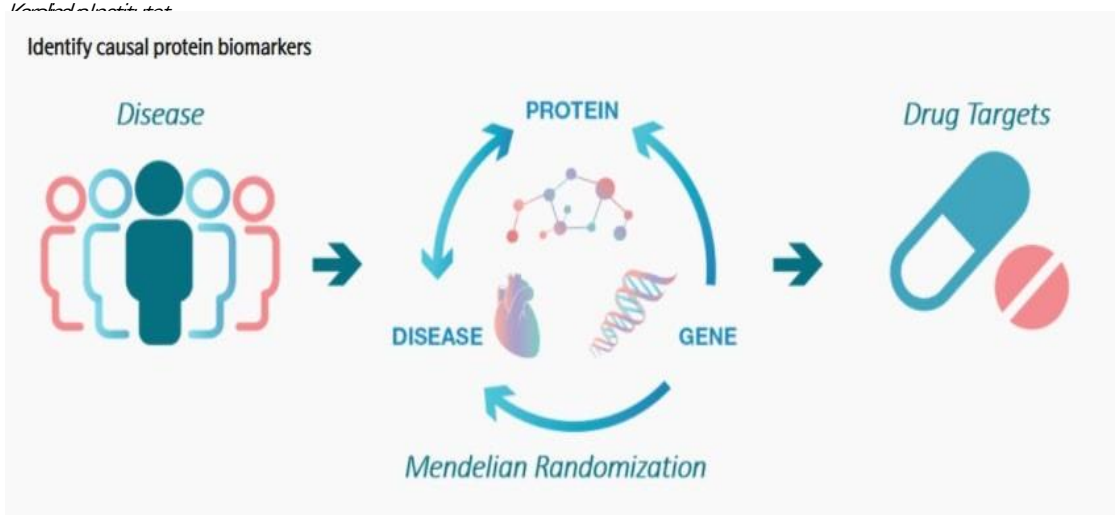
1.挖掘药物靶点：SCALLOP 联盟基于基因组和 olink 蛋白组数据

“在SCALLOP联盟成立之初，我们并不知道将人类遗传学与Olink蛋白组学相结合是否能够达到如此规模，更不知道我们的方法是否会对疾病生物学产生新的见解。基于这篇论文，我预测我们将看到下一代有效的药物从类似的方法中出现——**基于对蛋白生物标志物进行仔细的孟德尔随机化研究**。这项工作的功劳应该归于CVD-I编写组和SCALLOP联盟成员“.

Anders Mälarstig, Director at

Pfizer and researcher at

SCALLOP




nature metabolism
Articles
Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals

- n=30,931 from 15 GWAS studies
- Mapped 451 pQTLs linked to 85 cardiovascular proteins (CVD I)
- Using MR and 38 common diseases,they identified 25 proteins (of which 11 were previously unidentified) as causal in various diseases
- Identified candidates for target validation, repositioning, target-mediated safety, and new target candidates

Olink蛋白质组+GWAS+MR因果推断算法

Nat Metab **2,** 1135–1148 (2020)

Combining Olink and Genetic data lead to significant insights to guide drug development

- 25 causal proteins identified, including 5 novel findings.
- Strong causal evidence shown for targets In phase 2（2期中验证了因果性）
- Alternative indications suggested in some cases
- Monitoring of safety risks also suggested for some targets（某些靶点的安全性风险监控提示）

20 已知靶点

5 新靶点

Overview of gene products targeted by compounds or antibodies that have been in clinical development

				Mendelian randomization strong evidence (pan-pQTLs) (SE)
Gene	**Stage**	**Indication**	**Drug name or generic class**	**Causal Strong Evidence**
ADM	Preclinical	Oncology		Waist-hip ratio
CASP8	Preclinical	Oncology		Breast cancer
CD40	Phase-2	Autoimmune disease,Renal		IBD,RA
CHI3L1	Preclinical	Oncology		Atrial fibrillation
CSF1	Phase-3	Oncology		Waist-hip ratio
CX3CL1	Phase-2	IBD,RA,PBC	E6011	Bone fracture,SLE
CXCL16	Preclinical	Oncology		
DKK1	Phase-2	Osteoporosis,Oncology		Bone fracture
FAS	Phase-2	Oncology		IBD
GDF15	Preclinical	Cachexia	Recombinant also in ph1 dev	HDL-C
HGF	Phase-2	Oncology		Triglycerides
IL18	Phase-2	Oncology,T2D		
IL1RN	Launched	Autoimmune disease	Anakinra	Total cholesterol
IL6R	Launched	Rheumatoid Arthritis	Tocilizumab	Asthma,Eczema
MMP12	Preclinical	COPD		Eczema
PGF	Phase-2	Diabetic retinopathy		
AGER	Phase-3	Alzheimer's disease		Triglycerides,total cholsterol, prostate cancer,schizophrenia
IL1RL1	Phase-2	Asthma,COPD		IBD
TNFRSF1(	Phase-2	Oncology		Prostate cancer
TNFSF11	Launched	Osteoporosis	Denosumab	eBMD
EGF	**na**			**eBMD**
F3	**na**			**HbA1C**
IL16	**na**			**2h-glucose**
PAPPA	**na**			**Diabetes**
SPON1	**na**			**Afib**

SCALLOP

https://www.olink.com/scallop/
Contact: Anders.Mälarstig@pfizer.com

Supplemental Table 7 from
Folkersen L, Gustafsson S, Wang Q, et al. Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. *Nat Metab*. 2020; 2(10):1135-1148. doi:10.1038/s42255-020-00287-2.

应用分享：Olink 联合多组学助力发现免疫治疗预后标志物

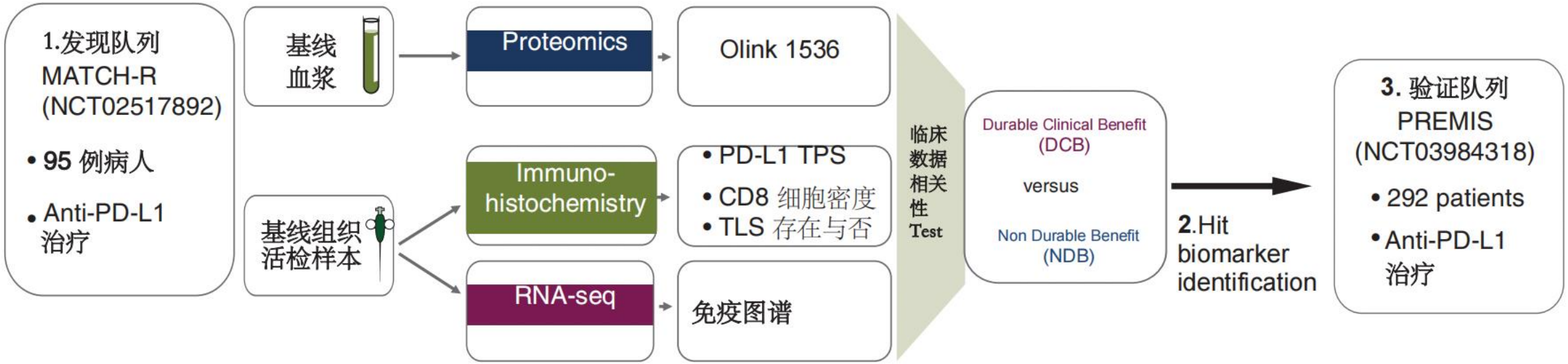
Plasma proteomics identifies leukemia inhibitory factor (LIF) as a novel predictive biomarker of immune-checkpoint blockade resistance

Y. Loriot[1†], A. Marabelle[2†], J. P. Guégan[3], F. X. Danlos[2], B. Besse[1,4], N. Chaput[5,6,7], C. Massard[2], D. Planchard[1], C. Robert[1], C. Even[1], M. Khettab[1], L. Tselikas[8], L. Friboulet[9], F. André[1,4], I. Nafia[3], F. Le Loarer[10,11], J. C. Soria[1], A. Bessede[3‡] & A. Italiano[2,11,12*‡]

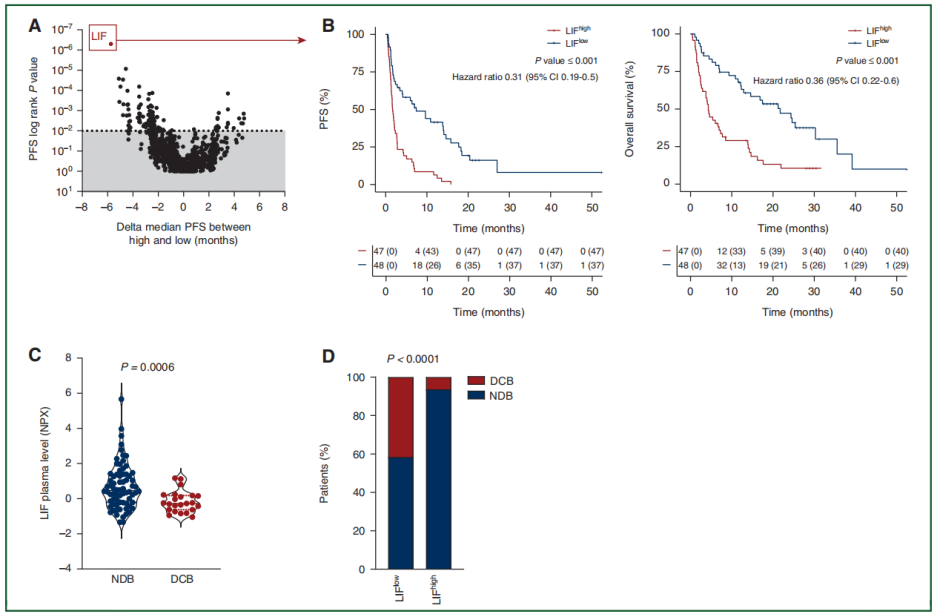
发表期刊：ANNALS of ONCOLOGY
影响因子：32.976
发表时间：2021
样本选择：活检组织（基线，59例）
血浆样本（发现队列n = 95，验证队列n = 292）
多组学平台：Olink / RNA-seq / m(IHC)

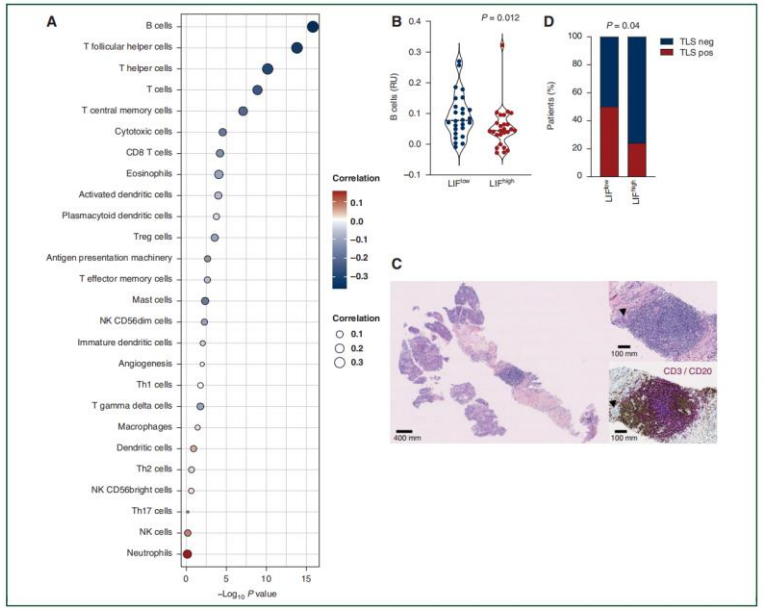
法国Institut Bergonie的Antoine研究组基于Olink技术对两个独立接受ICB治疗的癌症患者前瞻性队列基线血浆样本（发现队列n = 95，验证队列n = 292）进行了无偏血浆蛋白组分析，。然后，研究者通过Cox比例风险模型研究了血浆蛋白水平与临床获益率、无进展生存期(PFS)、总生存期(OS)以及与PD-L1表达水平、CD8+T细胞浸润密度、三级淋巴结构TLS的相关性。

研究方案


1.发现队列
MATCH-R
(NCT02517892)
• 95 例病人
• Anti-PD-L1
治疗
基线
血浆
基线组织
活检样本
Proteomics
Immuno-
histochemistry
RNA-seq
Olink 1536
• PD-L1 TPS
• CD8 细胞密度
• TLS 存在与否
免疫图谱
临床
数据
相关
性
Test
Durable Clinical Benefit
(DCB)
versus
Non Durable Benefit
(NDB)
2.Hit
biomarker
identification
3. 验证队列
PREMIS
(NCT03984318)
• 292 patients
• Anti-PD-L1
治疗

结果

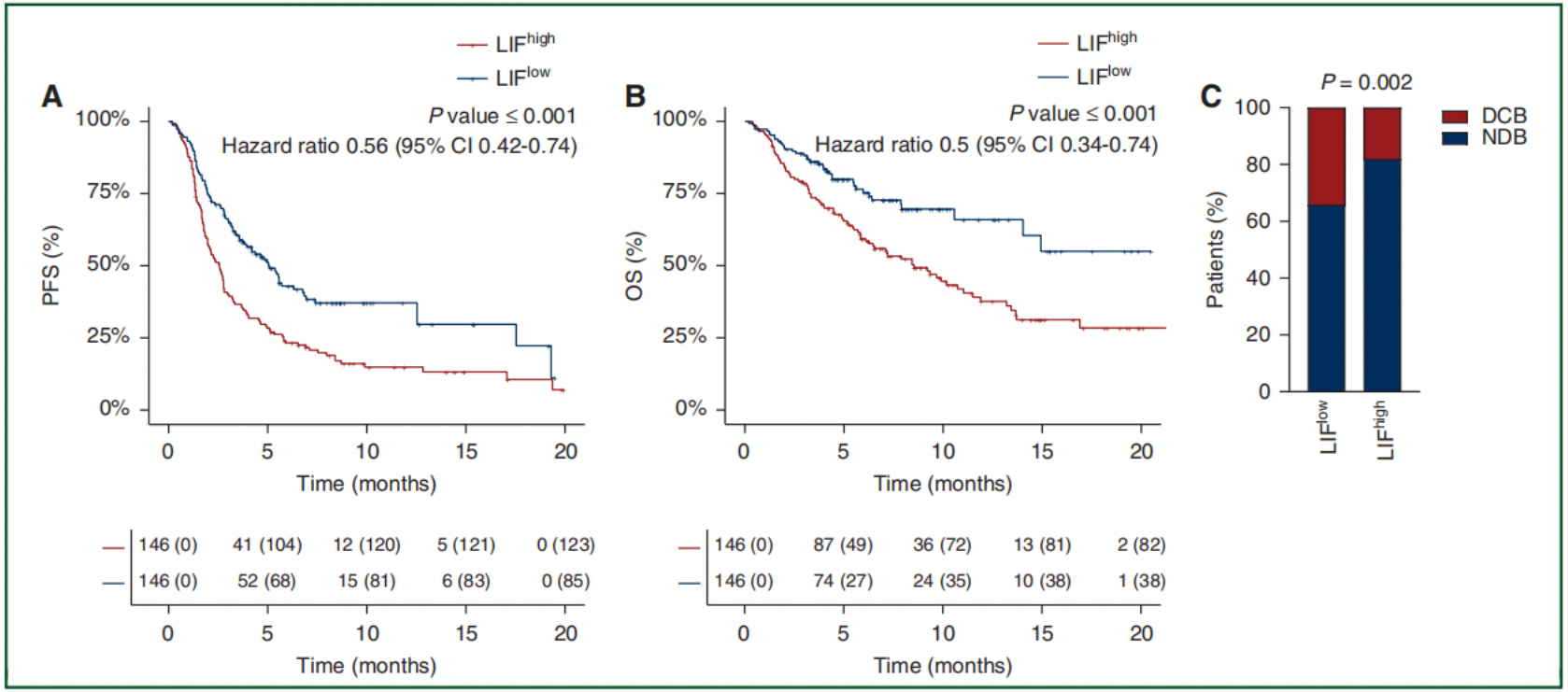




利用Olink Explore 1536 Panel对发现队列入组患者基线时血浆样本进行蛋白质组检测，通过Cox比例风险分析研究血浆蛋白表达水平与无进展生存期（PFS）、总生存期(OS)的关系，发现白血病抑制因子(LIF)的基线血浆表达水平与接受免疫检查点阻断剂治疗癌症患者的不良临床结局相关性最显著。具体而言，LIF Low较LIF High的患者在PFS和OS显著延长。

利用免疫组化和多重免疫组化对59例患者的PD-L1表达和CD8+ T细胞密度浸润程度，关联分析显示：白血病抑制因子(LIF)可独立于PD-L1表达状态预测免疫检查点阻断剂治疗癌症患者的效果；CD8+ T细胞密度与LIF水平以及预后无显著相关性；白血病抑制因子(LIF)水平与肿瘤微环境三级淋巴结构也存在相关性。

结果



基于发现队列，研究人员认为LIF有可能是一个HIT Biomarker，进一步在292例患者的验证队列中进行验证，在接受免疫检查点阻断剂治疗的癌症患者验证队列中，白血病抑制因子（LIF）的基线表达水平独立于其他预后因素预测患者结局。

nature COMMUNICATIONS

应用案例：Olink联合多组学平台助力三阴性乳腺癌治疗临床II期研究

Multicenter phase II trial of Camrelizumab combined with Apatinib and Eribulin in heavily pretreated patients with advanced triple-negative breast cancer

Jieqiong Liu[1,6], Ying Wang[1,6], Zhenluan Tian[1,6], Ying Lin[2,6], Hengyu Li[3], Zhaowen Zhu[1], Qiang Liu[1], Shicheng Su[1], Yinduo Zeng[1], Weijuan Jia[1], Yaping Yang[1], Shengqiang Xu[4], Herui Yao[1], Wen Jiang[5] & Erwei Song[1]✉

发表期刊：Nature communication
影响因子：14.919
发表时间：2022
样本选择：46名局部晚期或转移性TNBC患者
多组学平台：Olink蛋白组 / m(IHC) / Flow cell

中山大学孙逸仙纪念医院宋尔卫院士和刘洁琼教授团队发起的一项关于晚期三阴性乳腺癌（aTNBC）患者治疗的临床II期研究工作（NCT04303741），正式发表在Nature Communications杂志（IF = 14.919）。该研究是一项探索卡瑞利珠单抗（Camrelizumab）联合阿帕替尼（Apatinib）、艾瑞布林（Eribulin）治疗晚期三阴性乳腺癌患者的多中心、单臂的临床试验。

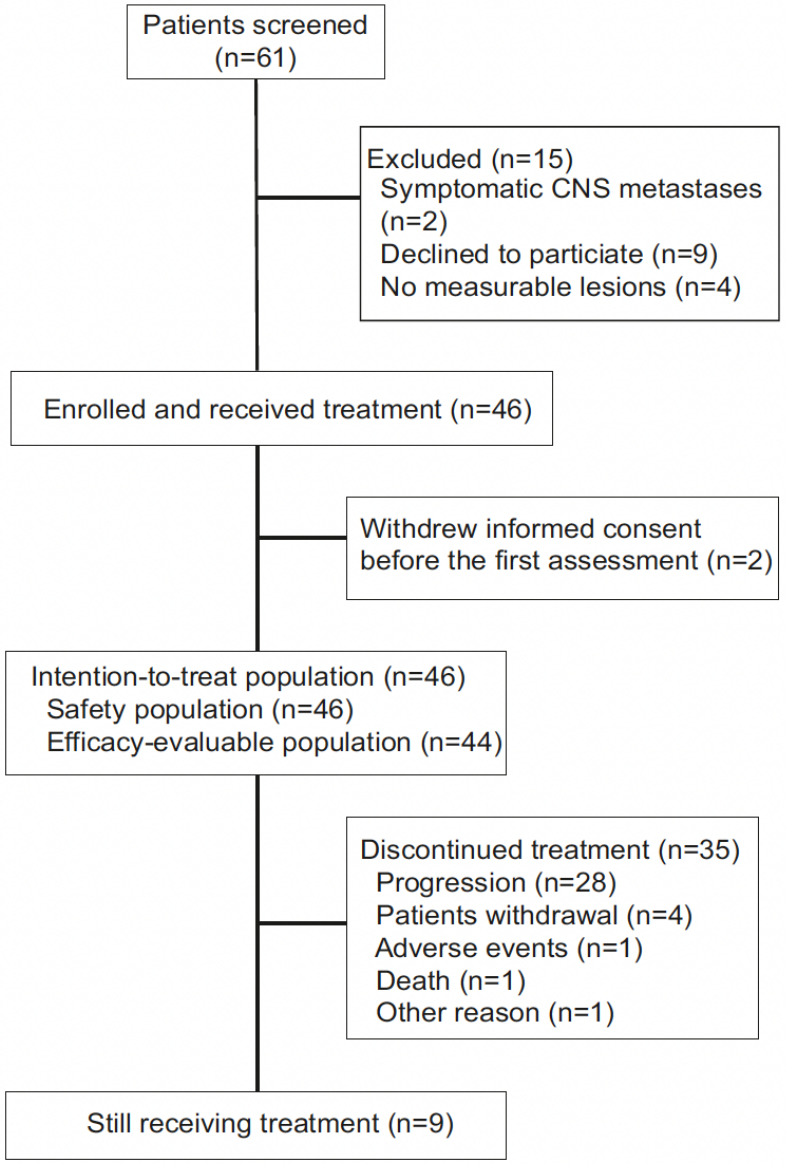


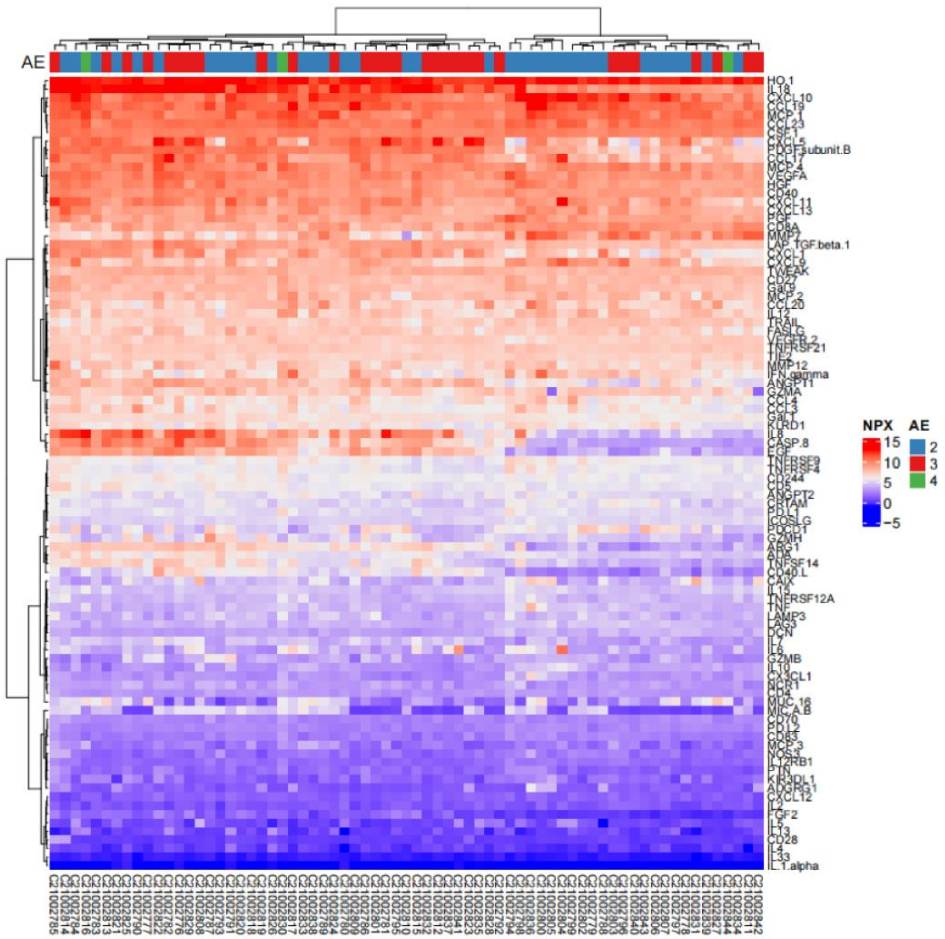
Fig. 1 Trial profile. Treatment summary and data collection of study participants. Participants were recruited from 3 hospital sites in China.

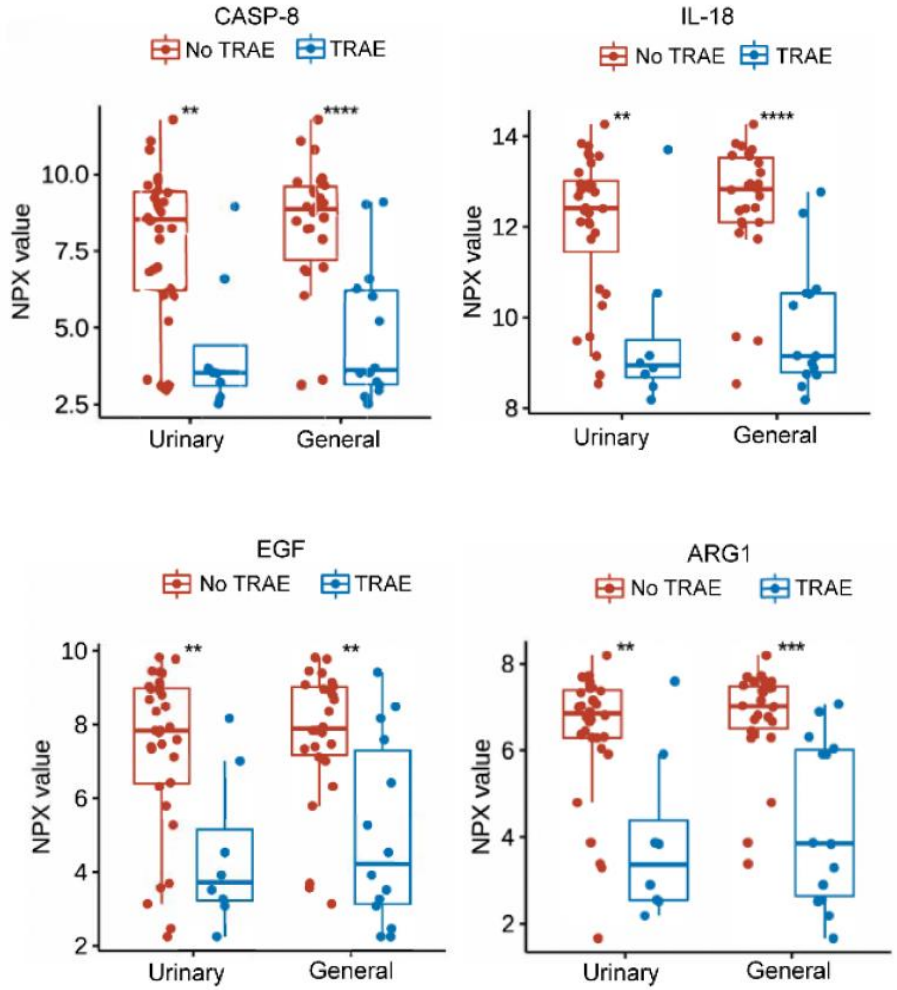
研究方案

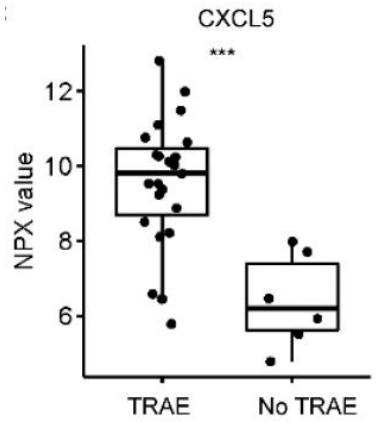
在这项研究中，研究者收集基线肿瘤组织样本、基线和治疗后3周外周血标本：

- FFPE组织切片：分别采用了免疫组化、多重免疫荧光、质谱等方法进行蛋白表达水平的检测；
- 血液样本：采用流式细胞术进行免疫细胞分群；
- 血浆样本：则采用了Olink技术（Olink Target 96 Immuno-Oncology Panel）进行血浆蛋白标志物检测和筛查；

结果







Olink血浆蛋白组检测结果主要揭示两个现象：1）在基线样本中CASP-8、IL-18、EGF或ARG1表达水平较低的患者容易发生泌尿系统或全身性不良反应；2）治疗三周后CXCL5水平较高的患者倾向于发生更多的皮肤和皮下组织相关的不良事件。

Olink Proteomics应用案例—I期临床评价安全性及有效性

Dose-dependent response

Dose selection of JAK/SYK inhibitor in AD

Icahn School of Medicine at Mount Sinai

Aim

Phase 1b study to evaluate efficacy, safety, pharmacokinetics and effects on systemic biomarkers of ASN002 (a dual JAK/SYK inhibitor) in patients with atopic dermatitis (AD).

Professor Emma Guttman-Yatsky

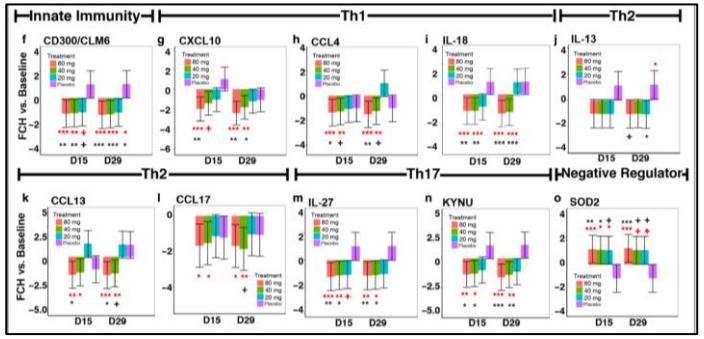
Method

AD patients randomized to ASN002 or placebo (20 mg, 40 mg and 80 mg once daily) over a 28-day period. Patient samples were analyzed by Olink (~360 proteins from Inflammation, CVD II, CVD III and Neurology panels).

Bissonnette., et al. The oral Janus kinase/spleen tyrosine kinase inhibitor ASN002 … 2019. Br J Dermatol.

Results

ASN002 significantly downregulated several serum biomarkers involved in Th1, Th2 and Th17/Th22 immunity, and decreased the atherosclerosis-associated biomarker E selectin/SELE. Both 40 and 80 mg showed good evidence of activity, but efficacy was higher for 40 mg.



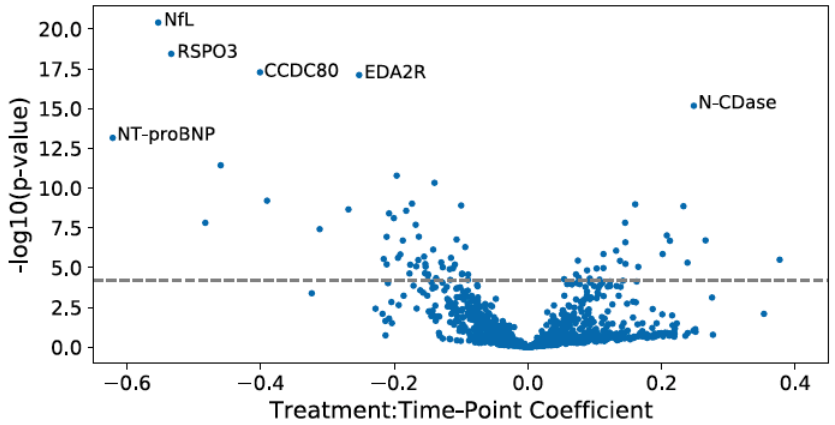
Conclusion

Enabled selection of the lower dose of 40 mg for optimal effect and decreased risk for adverse events. Protein biomarkers help dose selection in subsequent phase 2 studies. Possible to relate disease activity scores to biomarker changes – identify responders vs non-responders.

Olink Proteomics应用案例——临床药物易感人群筛选

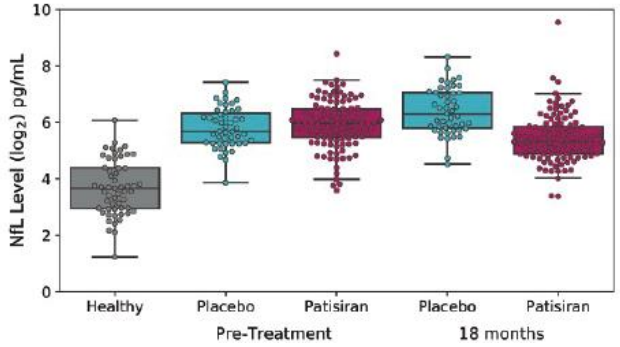
博淼生物 BIO MIAO BIOLOGICAL SINCE 2009

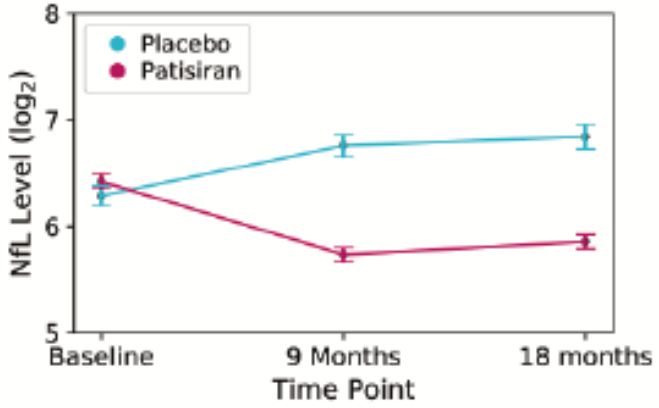
Olink delivered data on 1,161 validated proteins from 15 µL of patient plasma. A significant change in the levels of 66 proteins was observed with patisiran vs placebo.



NFL, the most significant biomarker ($p<10^{-20}$), correlated with disease severity scores over time

Ticau et al., Plasma Proteome Analysis of Patients with Hereditary Transthyretin-Mediated (hATTR) Amyloidosis Establishes Neurofilament Light Chain (NfL) as a Biomarker of Disease and Treatment Response , medRxiv preprint (2020)





Reduced NFL with patisiran and improvement in disease severity score suggests it as a biomarker of nerve damage and polyneuropathy in hATTR amyloidosis.

Enables earlier diagnosis of polyneuropathy in patients facilitating monitoring of disease progression.

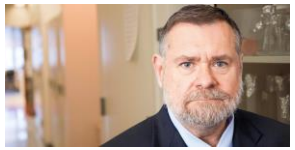
The first study proving the strong impact of NFL in hATTR and would not have been tested unless a system-wide proteomics approach with Olink was used.

Alnylam® PHARMACEUTICALS

这个临床试验项目中，采用olink蛋白组技术分析响应和不响应人群体内1161种蛋白表达的差异，进行药物（patisiran）的易感人群的发现和筛选。

Olink Proteomics应用案例——新适应症拓展

Drug post-marketing studies

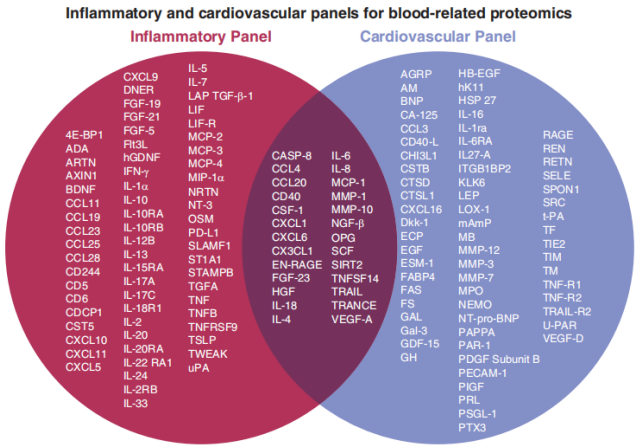


Professor James Krueger

采用olink的炎症和心血管的panel对类风湿关节炎治疗药物进行研究分析，发现可以拓展到心血管疾病领域

Aim

Psoriasis is an independent risk factor for coronary heart disease and cardiovascular mortality. How does the effect on systemic inflammation and cardiovascular risk reduction differ between drugs?



Method

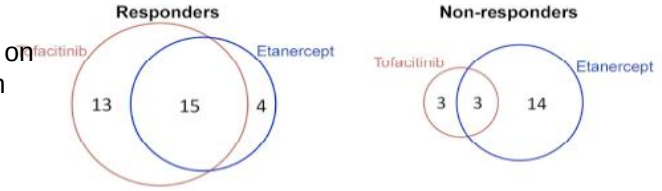
Plasma profiling of psoriasis patients at baseline and 4 weeks after treatment with Tofacitinib (pan-JAK inhibitor) and Etanercept (anti-TNF) using *Olink with ~180 inflammation and cardiovascular proteins*.

Kim et al., Reduction of inflammatory and cardiovascular proteins in the blood of psoriasis patients; differential responses ... Journal of Investigative Dermatology (2017) 138
.

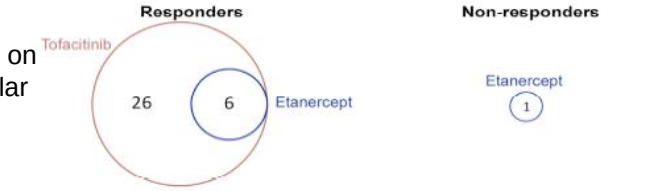
Results

A wider spectrum of cardiovascular blood protein reduction effects was seen with Tofacitinib compared with Etanercept in responders.

Drug effects on inflammation proteins



Drug effects on cardiovascular risk proteins



Conclusion

Potential for 托法替布Tofacitinib post-marketing studies to claim benefits on systemic inflammation and reduced CVD risk. Proof of concept on drug differentiation strategy that can influence design of phase 2/3.

蛋白标志物组应用于抗血管药物治疗NSCLC疗效预测研究

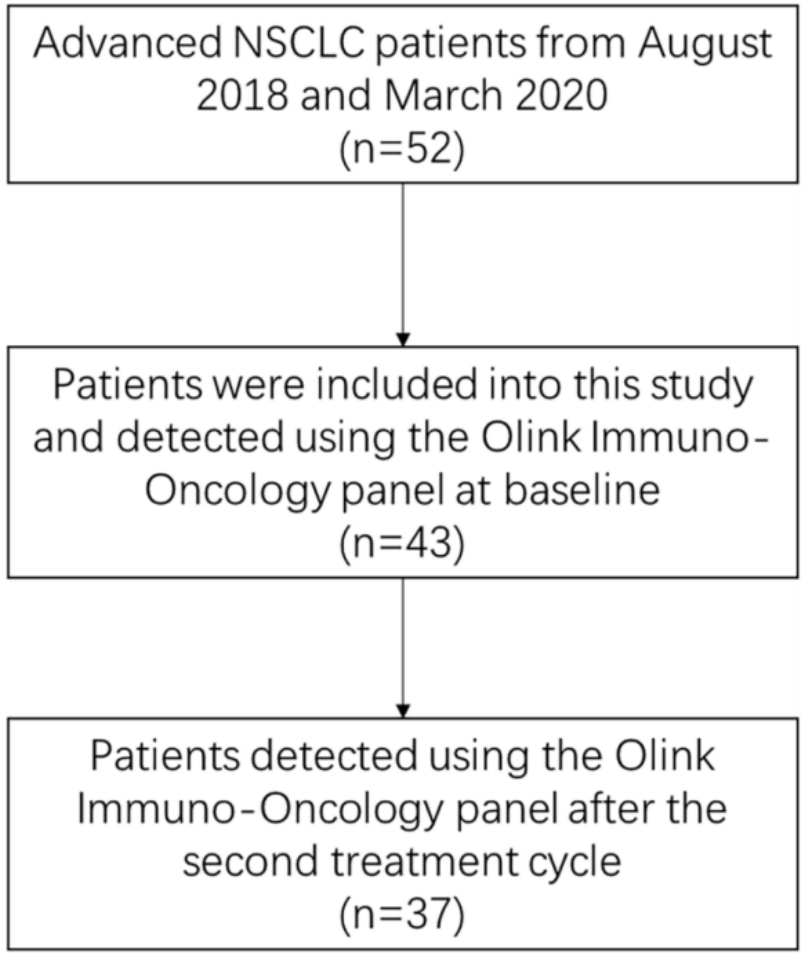
frontiers in Oncology

Front Oncol. 2021; 11: 756902.
Published online 2022 Jan 7. doi: 10.3389/fonc.2021.756902
PMCID: PMC8777128
PMID: 35070967

A Linear Discriminant Analysis Model Based on the Changes of 7 Proteins in Plasma Predicts Response to Anlotinib Therapy in Advanced Non-Small Cell Lung Cancer Patients

Fei Xu, [1,†] Haiyan Xu, [2,†] Zhiyi Wan, [3,†] Guangjian Yang, [1] Lu Yang, [1] Xueying Wu, [3] Jin Song, [4,*] and Yan Wang [1,*]

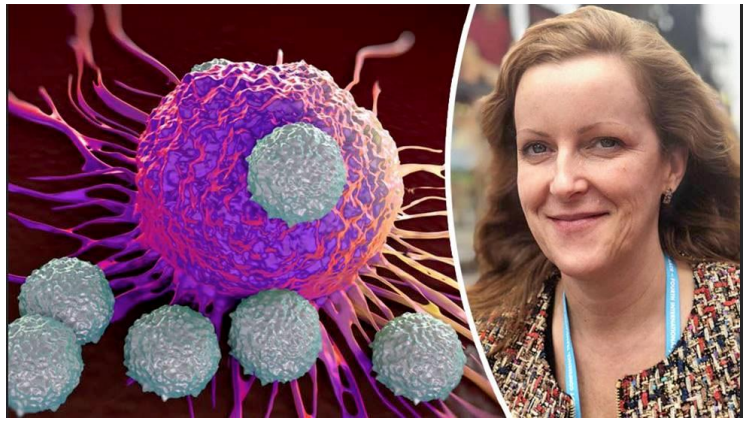
- 晚期 NSCLC患者入组，采用安罗替尼作为二线治疗或二线后治疗，在治疗前和第一次治疗评估时收集血浆，并采用Olink Immuno-Oncology panel进行检测。
- 炎症反应是肿瘤发生的重要因素，炎症因子被认为是预测药物疗效的潜在生物标志物，可以开发出一种更广泛的生物标志物，应用于具有不同遗传背景的患者;
- 患者血浆中蛋白标志物的变化，可以很好的预测安罗替尼的疗效，这些结果对晚期NSCLC的治疗具有非常重要的临床意义。



免疫水平丨对CAR T细胞治疗的安全性和有效性进行评估

Aim

First clinical phase I/IIa trial using third generation CAR T cells targeting CD19 to evaluate treatment safety and efficacy.



Professor Angelica Loskog, Uppsala Unviersity

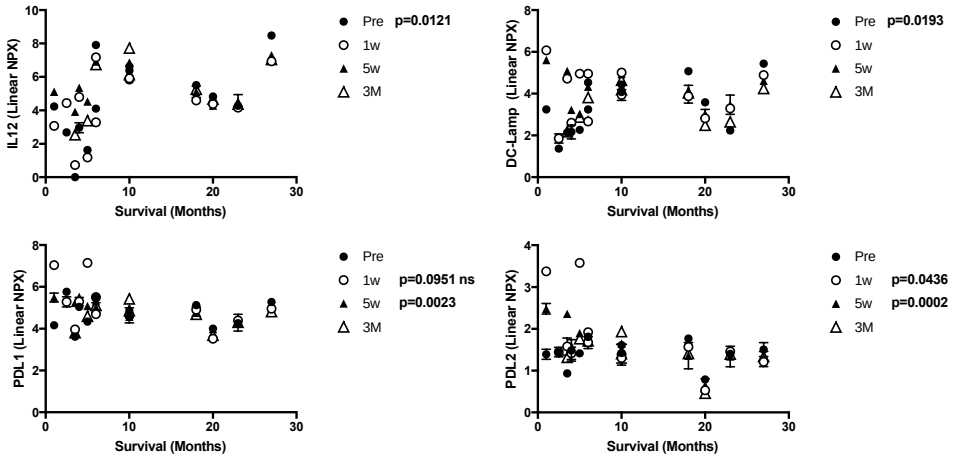
Method

Fifteen patients with B cell lymphoma or leukemia were treated with CAR T cells. Peripheral blood was sampled before and at multiple time points post CAR infusion to evaluate both the persistence of CAR T cells and for immune profiling using **Olink's Immuno Oncology panel (92 proteins).**

Enbladh., et al. A phase I/IIa trial using CD19-targeted third generation CAR T cells for lymphoma and leukemia. 2018. Clinical Cancer Research.

Results

Best predictor of response was a good immune status prior to CAR infusion with high IL12, DC-Lamp, Fas ligand and TRAIL. Responding patients had low monocytic MDSCs (CD14+CD33+HLA-DR-) and low levels of IL6, IL8, NAP3, sPDL1 and sPDL2.



Protein profile (pre/post CAR infusion) correlation to overall survival

Conclusion

Patient prior immune status is important for response to CAR T cells and this finding may contribute to the design of future studies and development of CAR T cell therapy.

博淼生物
BIO MIAO BIOLOGICAL
SINCE 2009

应用4
人群疾病和健康大队列研究

案例：CKB队列血浆蛋白标志物与肥胖及心脏代谢风险的相关性

JAMA Cardiology | Original Investigation

Associations of Adiposity, Circulating Protein Biomarkers, and Risk of Major Vascular Diseases

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IMPORTANCE Obesity is associated with a higher risk of cardiovascular disease (CVD), but little is known about the role that circulating protein biomarkers play in this association.

OBJECTIVE To examine the observational and genetic associations of adiposity with circulating protein biomarkers and the observational associations of proteins with incident CVD.

DESIGN, SETTING, AND PARTICIPANTS This subcohort study included 628 participants from the prospective China Kadoorie Biobank who did not have a history of cancer at baseline. The Olink platform measured 92 protein markers in baseline plasma samples. Data were collected from June 2004 to January 2016 and analyzed from January 2019 to June 2020.

研究结果表明：肥胖指标BMI与27种血浆蛋白生物标志物呈正相关，与3种蛋白呈负相关。尤其是白介素6，白介素18，单核细胞趋化蛋白-1，单核细胞趋化蛋白-3，TNF相关凋亡诱导配体和肝细胞生长因子。

此外，多种蛋白标志物还与心血管疾病风险相关，很好的解释了肥胖与心血管疾病之间的关系。

案例：健康人群队列多组学研究中的应用

Check for updates

Multiomic blood correlates of genetic risk identify presymptomatic disease alterations

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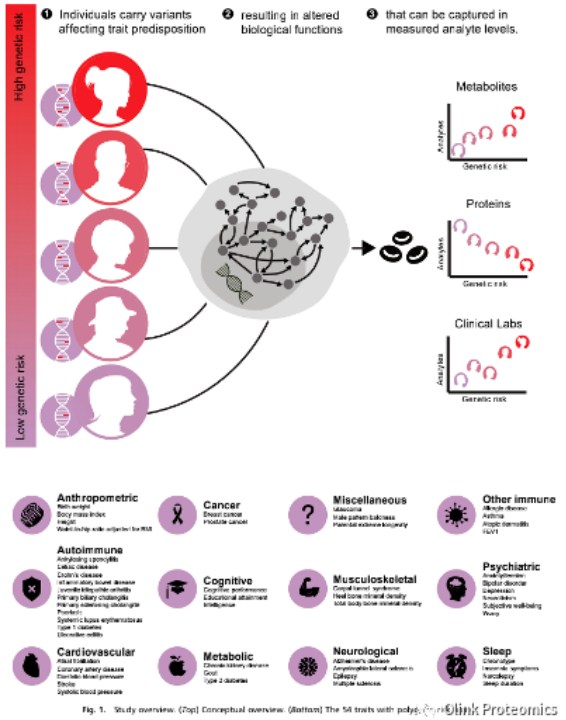
Contributed by Leroy Hood, July 9, 2020 (sent for review March 9, 2020; reviewed by Ali Torkamani and Sheng Zhong)



- Leroy Hood教授团队招募了108位健康人参与了一个著名的先锋100健康计划即P00项目，该项目使用多组学大数据来做健康研究的可能性；
- 作者将54种疾病的PRSs分数和基于血浆的蛋白质组，代谢组学和常规临床实验室检测之间的关系进行分析；
- 采用了Olink的INF，CVD2和CVD3三个 Panel，研究表明疾病易感PRSs分数较高的个人，其相关蛋白质标志物和代谢标志物有着一致性的变化，这些蛋白质等生物标志物可以进行疾病的预测和预防。

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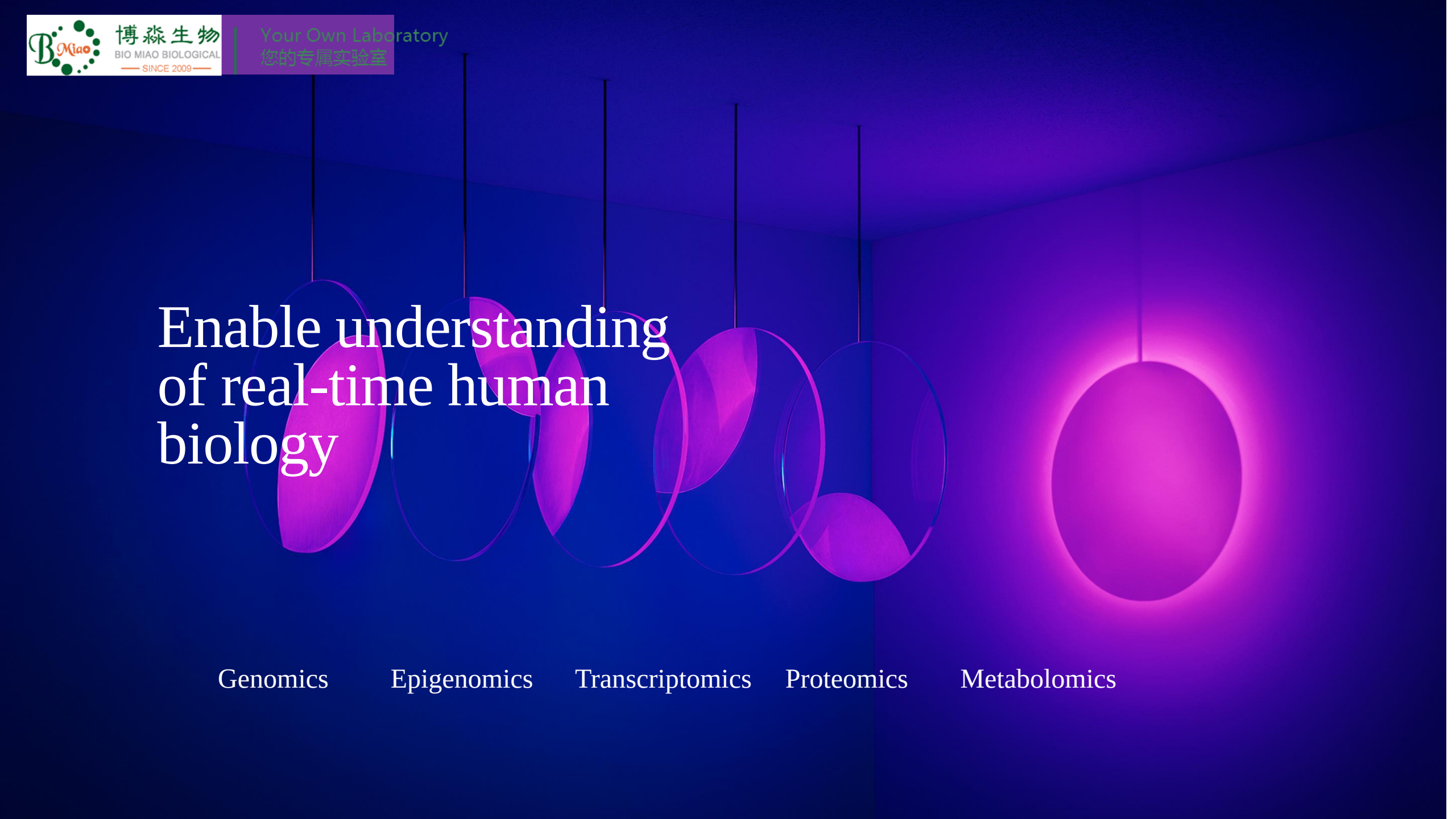


Enable understanding of real-time human biology

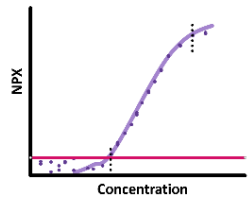
Genomics Epigenomics Transcriptomics Proteomics Metabolomics

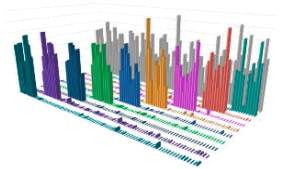
数据质量可靠可信赖

基于邻位延伸分析技术（PEA）

关键免疫分析指标验证

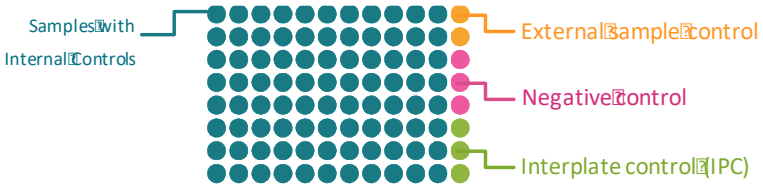
- 灵敏度，特异性，精密度，可扩展性，动态范围，干扰，分析前因素等



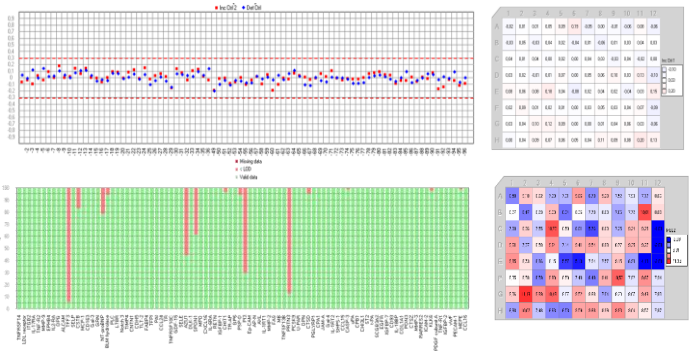


严格的内置质量控制

- 四个内部对照和八个外部对照



质控、标准化、可视化



Olink 蛋白质组学适用样本类型（标准）

Serum collection 收集血清

- 收集全血到血清采集试管中;
- 血液在室温下凝固，这通常需要 15-30 分钟。在放置超过 60 分钟的样品中，凝结的细胞有可能开始溶血;
- 在制冷离心机（2-8℃）中以 1000-2000 x g 离心 10 分钟，以去除血块;
- 立即将血清转移到干净的管中;
- 储存在 -80℃

Plasma collection 收集血浆

- 收集全血到市售的抗凝剂处理采集管内(经 EDTA，柠檬酸或肝素处理);
- 在制冷离心机（2-8℃）中以 1000-2000 x g 离心 10 分钟，以去除血浆中的细胞; （4℃的话也需要在8小时内完成离心）
- 立即将血浆转移到干净的管中;
- 储存在 -80 ℃

采集管种类及尺寸

任何指定用于采集血清或血浆的市售采集管均可。请确保所有样本的采集方式和采集管种类相一致（同一品牌、同一规格等）

实验室建议送样要求

寄样试管及尺寸

样品应以耐温、非结合蛋白的塑料制品寄送，例如 96 孔 PCR 板，最好是带完整裙边的平板， 并使用耐-80 °C 低温且质量有保证的封膜 (e.g. Sarstedt #72.1980.202 with seal from Life Technologies #4306311 or the biobanking system from Matrix, Thermo Fischer). Olink 实验室也可以将样品从 PCR 8 联冠或 Eppendorf 管转移至 96 孔板，请联系实验室提前确认。

样品体积

请提供 ≥40 微升 (µL) 的每个样品

建议体积

96 孔板：50 微升/样品

Eppendorf 试管：100 -500 微升/样品

注意：如果是需要做explore 检测，则建议至少送80ul样品

样品数量

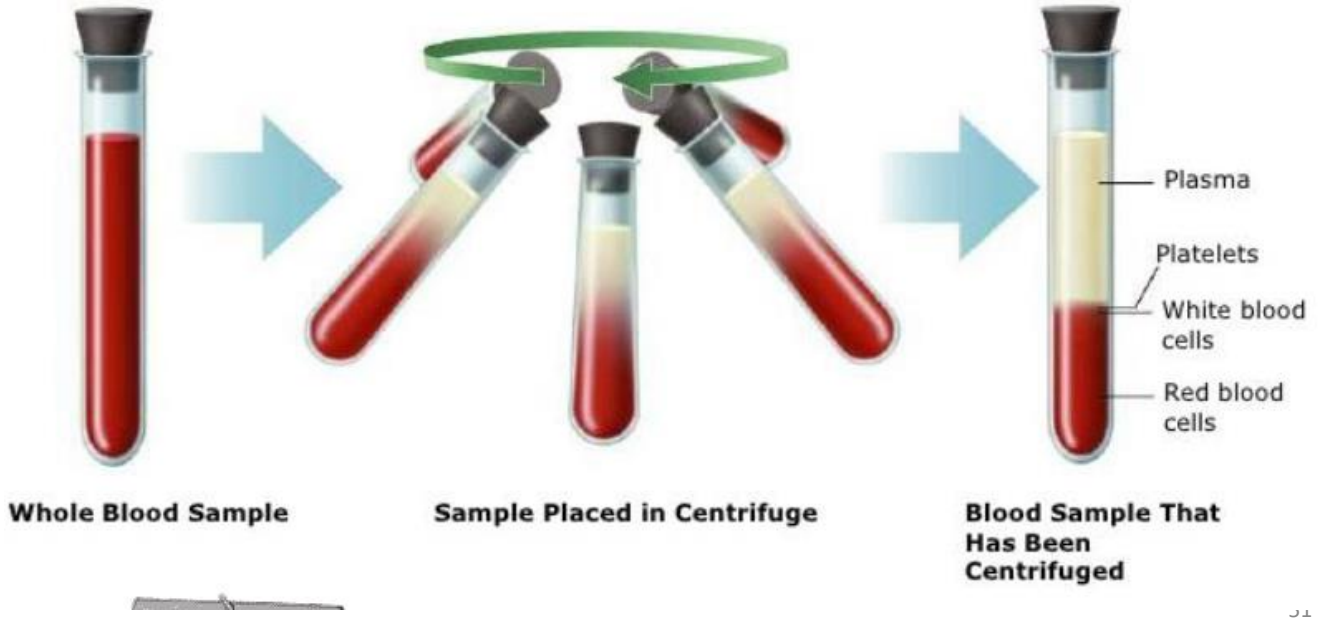
对于 Olink 进行的分析，每个受试者/患者只需要一管血浆或血清即可。

血清，血浆，以及全血的区别

PLASMA: ~55% of total blood Normal plasma = 90-92% water Contains: Electrolytes, antibodies, metabolites, hormones, enzymes and blood plasma proteins (fibrinogen/albumin/globulin). Function: Transport medium for blood cells, along with nutrients, wastes, chemical messengers, antibodies

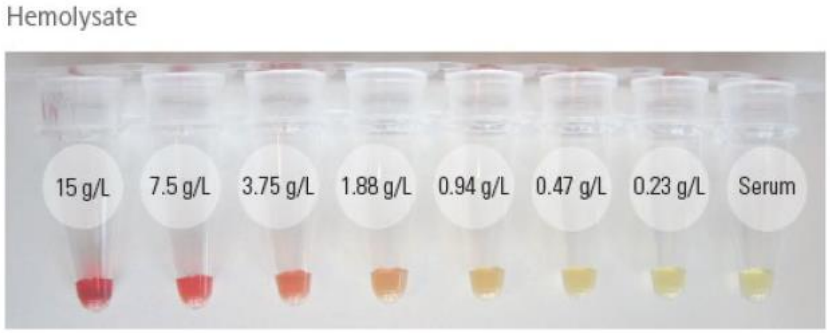
SERUM: Plasma minus fibrinogen (blood clotting protein). Contains all other plasma elements: antibodies, electrolytes, metabolites, hormones, enzymes, albumin, globulin

Whole blood=Plasma+blood cell

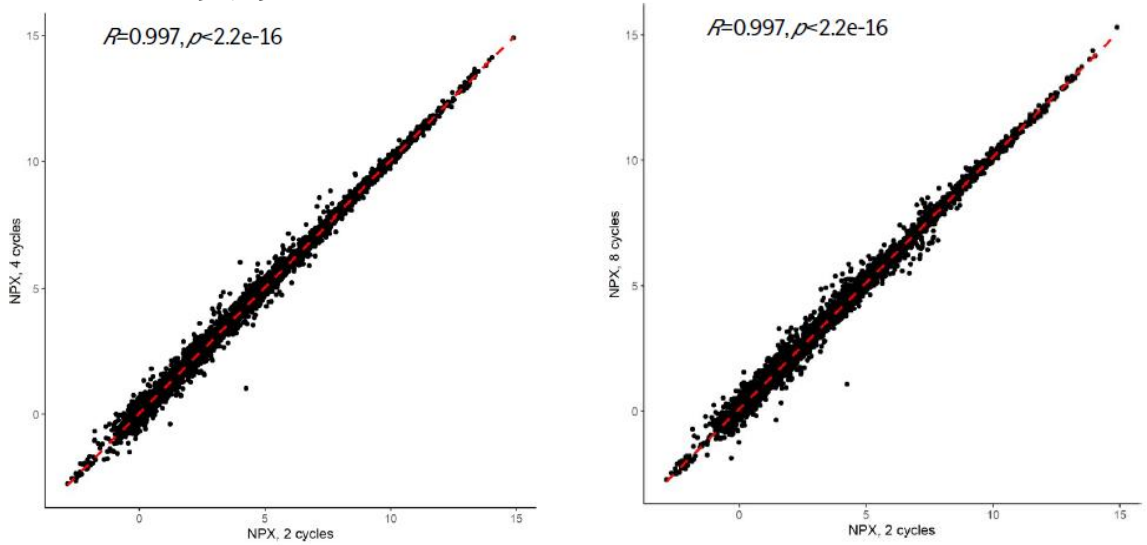


样品收集及储存对蛋白质生物标志物检测的前影响因素

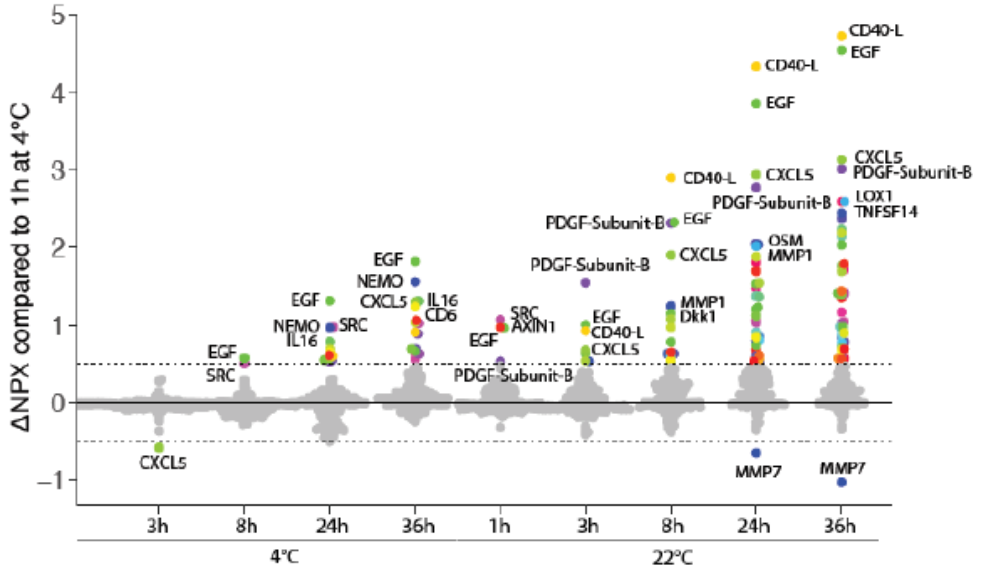
❖ 溶血影响，不同浓度血红蛋白测定其干扰



❖ 反复冻融影响



❖ 延迟离心影响，4度8小时内，室温1小时内进行离心



❖ 保存时间影响

最长测试-80度测试30年的样本

❖ 温度影响

长期保存，-80度或者更低温度，干冰运输

其他注意事项

- 对于其他非标样本，请参考非标样品处理指南或联系厂家
- 组织或者细胞裂解液，由于组织以及细胞的异质性，建议提前与厂家进行实验沟通：总蛋白浓度要求，稀释倍数，样本数目
- 关于Panel选择以及需要的样本数量，各个panel相关检出率进一步联系厂家，具体项目具体分析

- Olink样本指南-干血斑Dried Blood Samples-v2.pdf
- Olink样本指南-泪液Tear_v1.pdf
- Olink样本指南-尿液Urine.pdf
- Olink样本指南-唾液Saliva_v2.pdf
- Olink样本指南-指尖血(Mitra微量取样装置)_VAMS.pdf
- Olink样品指南-鼻吸附条SAM.pdf
- Olink样品指南-腹水Ascites_v2.pdf
- Olink样品指南-脑脊液CSF_v1.pdf
- Olink样品指南-皮肤胶带Tape strips_v1.pdf
- Olink样品指南-乳汁Breast milk.pdf
- Olink样品指南-痰液Sputum.pdf
- Olink样品指南-外泌体Extracellular Vesicles_v2.pdf
- Olink样品指南-细胞裂解物Cell Lysates_v2.pdf
- Olink样品指南-细胞培养上...lture Supernatants_v2.pdf
- Olink样品指南-羊水Amniotic fluid.pdf
- Olink样品指南-组织裂解物Tissue Lysates_v2.pdf

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Olink pilot study:

Alternative matrices

Aiming to apply the unique features of the PEA technology on a matrix other than serum or plasma? We would like to share some previous knowledge to guide you to the optimal results.

Olink assays are optimized and thoroughly validated for analysis of serum and plasma, meaning that the dynamic range of the assay has been adjusted to protein concentrations expected in serum and plasma. In addition, both cerebrospinal fluid (CSF) and urine have been thoroughly evaluated with set analysis recommendations. Whilst a wide range of additional sample types are compatible with the technology, it is important to determine the performance of each specific matrix in order to obtain accurate and reliable results.

In this document, we have summarized information and examples of study layouts to help answer different types of questions that may be important prior to running a larger study. Please do not hesitate to contact support@olink.com for a discussion on your specific study.

Why run a pilot study?

First of all, the relative composition of proteins can be very different between sample types. Plasma and serum have a protein concentration range spanning 12 orders of magnitude with a few high abundant proteins making up the largest percentage. Other matrices, such as cell and tissue lysates, span a lower order of magnitude but may instead be more divergent than serum/plasma due to e.g. differences in sample preparation methods, cell line characteristics and differences between tissue types.

Therefore, running a pilot study will ensure that you run your samples under the optimal conditions, guiding the sample dilution to confirm that the data is in the dynamic, linear range of the assay and whether any assays are at risk of hook[1]. The recommendation from Olink is to evaluate a smaller subset of samples prior to running the whole sample set, but the optimal pilot study design for your specific study will depend on the questions you would like to answer.

Sample preparation recommendations

Guidelines for sample preparation, including buffer recommendations, are available for a selected number of matrices. Please contact support@olink.com for more information.

Standardizing samples: determining protein concentration or cell density

The read out from the Olink platform is in relative abundances. To make accurate comparisons between samples, it is therefore important to standardize samples before running the assay. Most standard total protein measurement assays (e.g. Lowry, Bradford, BCA, Nanodrop etc) can be used to measure your protein concentrations.

Protein concentrations are expected to vary for different tissues (e.g. heart, brain, muscle), cell lines (e.g. stable cell line, primary cultures, culture conditions) and sample preparation methods. The general recommendation by Olink is a standardized total protein concentration of 0.5-1 mg/mL. Cell supernatants are preferably normalized to starting cell density due to difficulties in accurately measuring total protein concentration.

[1] https://www.olink.com/question/what-is-the-high-dose-hook-effect/

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