# 《自然》（20241219出版）一周论文导读

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**《自然》（20241219出版）一周论文导读**。编译李言

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材料科学Material Sciences

Growth-based monolithic 3D integration of single-crystal 2D semiconductors

基于生长的单晶二维半导体单片三维集成

▲ 作者：Ki Seok Kim, Seunghwan Seo et al.

▲链接：

https://www.nature.com/articles/s41586-024-08236-9

▲摘要：

在此，我们提出了一种在非晶态和多晶表面上生长单晶通道材料的方法。这些材料特别由过渡金属二硫化物组成，在足够低的温度下进行，以保护底层的电子元件。

通过这种改良后的技术，我们展示了垂直单晶逻辑晶体管阵列的无缝单体集成。这一成果导致了由生长的单晶通道组成的前所未有的垂直互补金属氧化物半导体（CMOS）阵列的发展。最终，这一成果为以单晶形式的各种电子硬件的M3D集成提供了机会。

▲ Abstract：

Here we present a method for growing single-crystalline channel materials, specifically composed of transition metal dichalcogenides, on amorphous and polycrystalline surfaces at temperatures low enough to preserve the underlying electronic components. Building on this developed technique, we demonstrate the seamless monolithic integration of vertical single-crystalline logic transistor arrays. This accomplishment leads to the development of unprecedented vertical complementary metal oxide semiconductor (CMOS) arrays composed of grown single-crystalline channels. Ultimately, this achievement provides opportunities for M3D integration of various electronic hardware in the form of single crystals.

天文学Astronomy

Tidally driven remelting around 4.35 billion years ago indicates the Moon is old

435万年前的潮汐驱动重融显示月球非常古老

▲ 作者：Francis Nimmo, Thorsten Kleine Alessandro Morbidelli

▲链接：

https://www.nature.com/articles/s41586-024-08231-0

▲摘要：

在此，我们认为月球岩石中频繁出现的年龄4.35-Ga和锆石年龄的峰值大约同时出现，表明月球

轨道演化驱动的重熔事件，而不是月球岩浆洋（LMO）的原始结晶。

我们的结果展示了在通过拉普拉斯平面跃迁的过程中，月球经历了足够的潮汐加热和融化，导致大多数月球样品的形成年龄被重置，同时保留了早期冻结的形状和罕见的早期形成的锆石。这种模式调和了LMO结晶时间预计上存在的差异，并允许月球在太阳系形成的几千万年内形成，与类地行星形成的动力学模型一致。

月球的重熔也解释了月球撞击盆地的次数比预期的要少，并允许在月球形成后被吸积到月球上的星子中的金属被转移到月球核心，这解释了月球与地球相比明显缺乏这些物质的原因。

▲ Abstract：

Here we argue that the frequent occurrence of approximately 4.35-Ga ages among lunar rocks and a spike in zircon ages at about the same time is indicative of a remelting event driven by the Moon ’ s orbital evolution rather than the original crystallization of the LMO. We show that during passage through the Laplace plane transition, the Moon experienced sufficient tidal heating and melting to reset the formation ages of most lunar samples, while retaining an earlier frozen-in shape and rare, earlier-formed zircons. This paradigm reconciles existing discrepancies in estimates for the crystallization time of the LMO, and permits formation of the Moon within a few tens of million years of Solar System formation, consistent with dynamical models of terrestrial planet formation. Remelting of the Moon also explains the lower number of lunar impact basins than expected, and allows metal from planetesimals accreted to the Moon after its formation to be removed to the lunar core, explaining the apparent deficit of such materials in the Moon compared with Earth.

A dormant overmassive black hole in the early Universe

早期宇宙中一个休眠的超大质量黑洞

▲ 作者：Ignas Juod?balis, Roberto Maiolino et al.

▲链接：

https://www.nature.com/articles/s41586-024-08210-5

▲摘要：

在此，我们报告了JADES巡天中探测到的z=6.68星系的Hα宽发射线。该星系追踪到一个质量约为4?×?108M⊙的黑洞，其吸积速率仅为爱丁顿极限的0.02倍。黑洞与宿主星系恒星的质量比约为0.4，即约为局部关系的1000倍，而系统在宿主星系的动态质量和速度色散方面更接近局部关系。

这个天体很可能是在再电离时期周围有大量休眠黑洞的显示。它的性质与超级爱丁顿吸积的短暂爆发导致黑洞过度生长和吸积盘中大量气体排出的情况一致；在爆发之间，黑洞的大部分时间都处于休眠状态。

▲ Abstract：

Here we report the detection, from the JADES survey, of broad H α emission in a galaxy at z?=?6.68, which traces a black hole with a mass of about 4?×?108M⊙and accreting at a rate of only 0.02 times the Eddington limit. The black hole to host galaxy stellar mass ratio is about 0.4—that is, about 1,000 times above the local relation—whereas the system is closer to the local relations in terms of dynamical mass and velocity dispersion of the host galaxy. This object is most likely an indication of a much larger population of dormant black holes around the epoch of reionization. Its properties are consistent with scenarios in which short bursts of super-Eddington accretion have resulted in black hole overgrowth and massive gas expulsion from the accretion disk; in between bursts, black holes spend most of their life in a dormant state.

医学Medicine

Automated real-world data integration improves cancer outcome prediction

真实世界数据自动化集成提升癌症预后预测情况

▲ 作者：Justin Jee, Christopher Fong et al.

▲链接：

https://www.nature.com/articles/s41586-024-08167-5

▲摘要：

在此，我们将自然语言处理注释与结构化药物、患者报告的人口统计数据、肿瘤患病登记数据、以及来自纪念斯隆—凯特琳癌症中心的24950名患者的肿瘤基因组数据结合起来，生成临床基因组上的协调肿瘤学真实数据集（MSK-CHORD）。

MSK-CHORD中的数据包括非小细胞肺癌（n=7809）、乳腺癌（n=5368）、结直肠癌（n=5543）、前列腺癌（n=3211）和胰腺癌（n=3109）的数据，并能够发现在较小数据集中不明显的临床基因组学关系。通过利用MSK-CHORD训练机器学习模型来预测总体生存率，我们发现，通过交叉验证和外部多机构数据集测试，包括自然语言处理（如疾病部位）衍生特征的模型优于基于基因组数据或单独阶段的模型。

通过注释705241份放射学报告，MSK-CHORD还发现了特定器官部位转移的预测因子，包括在独立数据集中证实的经免疫治疗的肺腺癌中SETD2突变与较低转移潜力之间的关系。

▲ Abstract：

Here we combine natural language processing annotations with structured medication, patient-reported demographic, tumour registry and tumour genomic data from 24,950 patients at Memorial Sloan Kettering Cancer Center to generate a clinicogenomic, harmonized oncologic real-world dataset (MSK-CHORD). MSK-CHORD includes data for non-small-cell lung (n?=?7,809), breast (n?=?5,368), colorectal (n?=?5,543), prostate (n?=?3,211) and pancreatic (n?=?3,109) cancers and enables discovery of clinicogenomic relationships not apparent in smaller datasets. Leveraging MSK-CHORD to train machine learning models to predict overall survival, we find that models including features derived from natural language processing, such as sites of disease, outperform those based on genomic data or stage alone as tested by cross-validation and an external, multi-institution dataset. By annotating 705,241 radiology reports, MSK-CHORD also uncovers predictors of metastasis to specific organ sites, including a relationship between SETD2 mutation and lower metastatic potential in immunotherapy-treated lung adenocarcinoma corroborated in independent datasets.

地球科学Earth Science

Atmospheric rivers cause warm winters and extreme heat events

大气层河流导致暖冬和极端高温事件

▲ 作者：Serena R. Scholz Juan M. Lora

▲链接：

https://www.nature.com/articles/s41586-024-08238-7

▲摘要：

在此，我们展示了在许多中纬度地区，大气层河流（AR）频繁发生的季节的温度也高于平均温度，并且AR事件与高于气候平均值5—10 ° C的温度异常有关。这是由于低层大气中感热和水汽的异常水平输送和辐合，增加了地表向下的感热通量和向下的长波辐射。

在小时的时间尺度上，在中纬度的大部分地区，超过70%的极端温暖温度异常发生在AR内，并且AR与全球许多地区的潮湿和复合热浪有关，这表明将AR纳入考量因素可能会提高某些极端热事件的预测能力。

▲ Abstract：

Here we show that seasons with more frequent ARs also have warmer than average temperatures in many mid-latitude regions, and that AR events are associated with temperature anomalies of 5 – 10? ° C above the climatological mean. This is due to anomalous horizontal transport and convergence of sensible heat and moisture in the lower atmosphere, which increases both downward sensible heat flux and downwelling long-wave radiation at the surface. On an hourly timescale, over 70% of extreme warm-temperature anomalies occur within ARs in large portions of the mid-latitudes, and ARs are associated with moist and compound heatwaves in many regions worldwide, suggesting that consideration of ARs may improve predictive capability for certain extreme heat events. Our results demonstrate that ARs significantly impact air temperatures on a wide array of timescales, and that they may play a wider role in global energy transport than previously recognized.

农业Agriculture

Structural variation in the pangenome of wild and domesticated barley

野生和驯化大麦泛基因组的结构变异

▲ 作者：Murukarthick Jayakodi, Qiongxian Lu et al.

▲链接：

https://www.nature.com/articles/s41586-024-08187-1

▲摘要：

在此，我们报告一个包含76个野生和驯化品种的长读序列组装和1315个基因型的短读序列数据的大麦泛基因组。作物序列变异的扩展目录包括结构复杂的位点，以及丰富的基因拷贝数变异。

为了展示泛基因组的实用性，我们重点研究了四个涉及疾病抗性、植物结构、营养释放和毛状体发育的位点。我们在白粉病抗性位点发现了新的等位基因变异，并且在调节营养分支的调控因子中发现了种群特异性的拷贝数增加。在优质麦芽中，淀粉裂解酶家族的扩展与微麦芽试验中酶活性的变化相关联。

增强子基序的缺失可能会改变大麦谷物上毛状附属物的发育轨迹。我们的发现表明，结构复杂位点的等位基因多样性可能帮助作物植物适应农业生态系统中的新选择机制。

▲ Abstract：

Here we report a pangenome of barley comprising long-read sequence assemblies of 76 wild and domesticated genomes and short-read sequence data of 1,315 genotypes. An expanded catalogue of sequence variation in the crop includes structurally complex loci that are rich in gene copy number variation. To demonstrate the utility of the pangenome, we focus on four loci involved in disease resistance, plant architecture, nutrient release and trichome development. Novel allelic variation at a powdery mildew resistance locus and population-specific copy number gains in a regulator of vegetative branching were found. Expansion of a family of starch-cleaving enzymes in elite malting barleys was linked to shifts in enzymatic activity in micro-malting trials. Deletion of an enhancer motif is likely to change the developmental trajectory of the hairy appendages on barley grains. Our findings indicate that allelic diversity at structurally complex loci may have helped crop plants to adapt to new selective regimes in agricultural ecosystems.

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