中国机构
CNS月报

06月报

生物探索出品

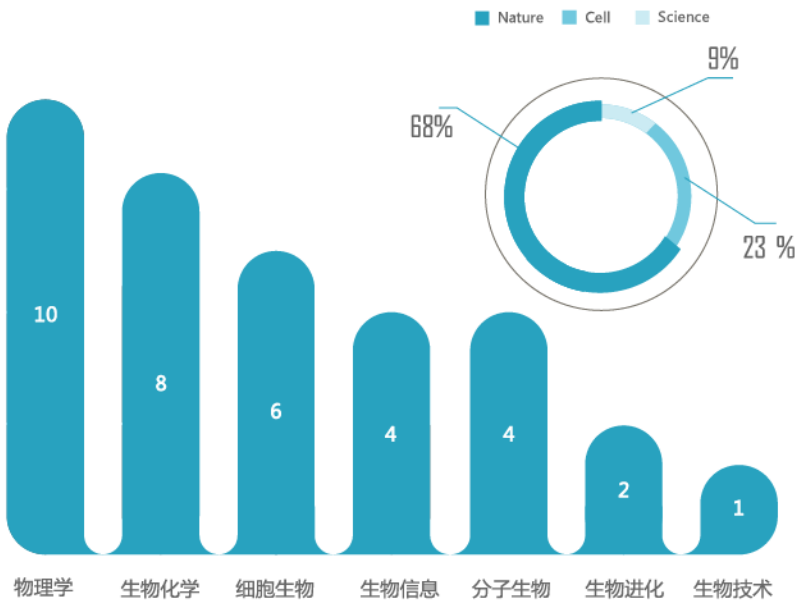
目　录

一、导语

自然系列期刊在 2012 年的论文统计显示，发文 140 篇论文的中国科学院超过日本东京大学排名亚洲机构第一位，这也是 Nature Index 统计以来中国科研机构首次排名第一，反映出中国顶尖科研机构在数量上领跑亚洲。据生物探索统计，2013 年 6 月份中国科研机构在 Nature、Cell 和 Science 三大系列期刊的总发文量是 35 篇，同比上升了 16.7%，而前 6 个月发文 181 篇，同比增长了 31.2%。

在生物学领域，三大期刊（Cell、Nature 和 Science）及其子刊，简称 CNS，倍受中国研究人员推崇，他们希望凭借 CNS 在学术界的威望将中国尖端、前沿的研究成果向全世界传达。这些研究动态可谓是中国科研机构的最高水平。作者希望对此进行统计，以便于从发文成果追踪国内科研经费动向，同时，生物医药圈内的研究人员和学生可实时了解中国顶尖研究人员从事研究的的领域和方向。

二、6 月份中国机构 CNS 发文与学术领域热度

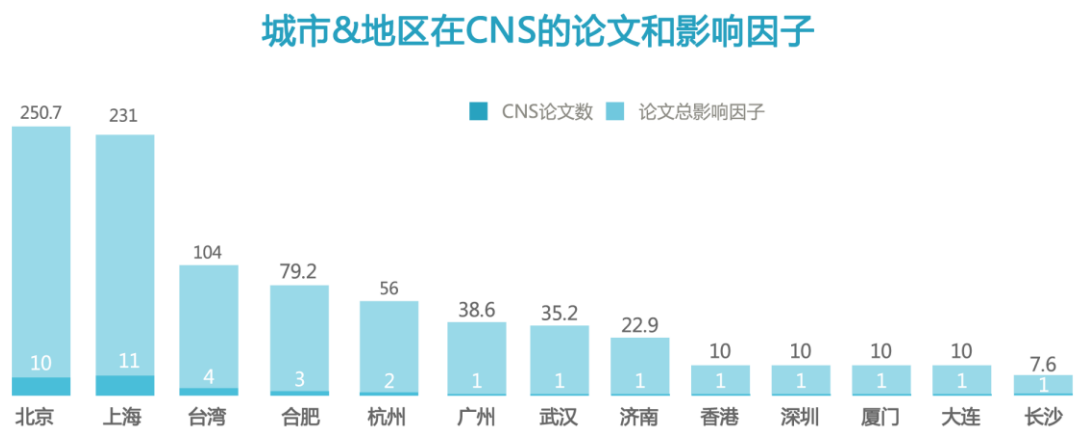


（饼状图表示期刊论文百分数）

2013 年 6 月份中国研究机构在三大系列期刊共发表 35 篇论文，包括 Nature 系列 24 篇、Cell 系列 8 篇和 Science 系列 3 篇，其中 Nature 主刊、Cell 主刊和 Science 主刊的发文量分别是 4 篇、2 篇和 2 篇。从数据上看，CNS 三大主刊中 Nature 主刊（4 篇）是发表中国机构论文的最多的，相比于 5 月份也是唯一一家发表中国机构论文略有增加的。发文中国机构论文一直处于上位的 Nature 系列期刊由 5 月份所占比例不足 50%上升到 6 月份 68%。从地区上看，6 月份发表 30 篇的大陆地区仍然是中国机构发表 CNS 论文的主体，而港台地区共发表 5 篇，这是近 5 个月内发文最多的。

6 月份 CNS 发表的中国机构研究论文中，物理学领域（10 篇）排在第 1 位，而上月排在第一的分子生物学领域下滑至第四位。生物化学领域和细胞生物学领域仍然列于第 2 位、第 3 位。从学术热度上看，以基因组学为对象的生物信息学研究持续成为热点，近 10 个月中国研究机构都有关于基因组测序的 CNS 论文发表，6 月份发表在 Nature Genetics 的 3 篇生物信息学论文和 Nat Struct Mol Biol 的 1 篇生物信息学论文分别讲到宫颈癌易感基因位点、单倍体谷子基因组变异图谱、鸭子基因组和转录组以及人类肿瘤相关的长非编码 RNAs。此外，在上图 7 个论文分类中，Cell 系列刊和 Science 系列刊同时占有 3 个，而 Nature 系列刊却包括 7 个。

三、6 月份城市&地区在 CNS 的论文和影响因子



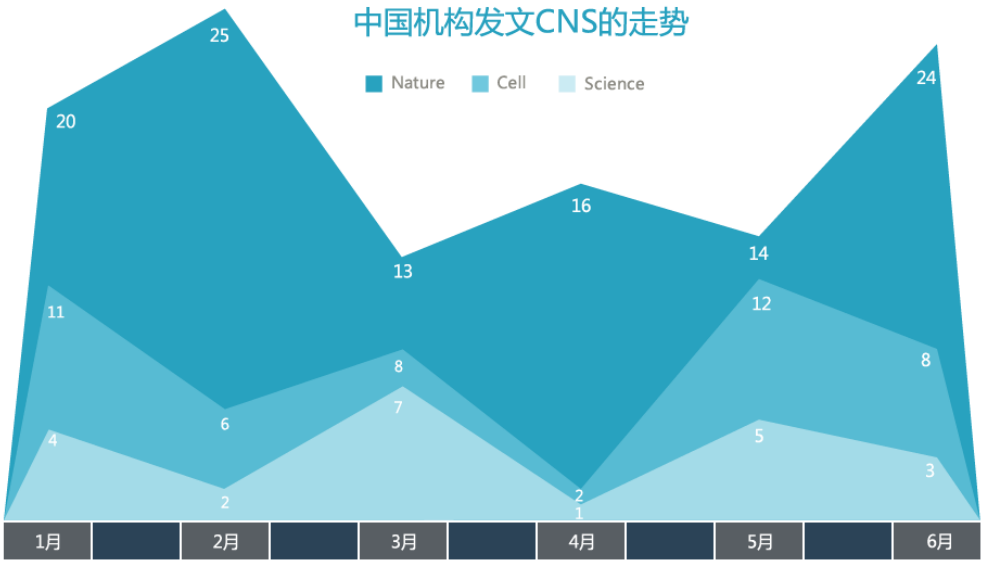
（影响因子源自 MedSci 查询系统，取小数点后一位）

从 CNS 论文影响因子看，6 月份超过 100 分的城市&地区有北京、上海和台湾，北京以 250.7 分卫冕排行榜，较上月下降了 22.4%，而发文 11 篇的上海却由 5 月份的 95.9 分飙升至 231 分。从上图可以看出，北京和上海的 CNS 论文影响因子领跑其它城市&地区。

在 6 月份，北京（10 篇）和上海（11 篇）是发表 CNS 论文较多的，而其它城市&地区发表 CNS 论文数都不多，发表 1 篇论文以上的是台湾（4 篇）、合肥（3 篇）和杭州（2 篇），而仅发表 1 篇论文的城市&地区是广州、武汉、济南、香港、深圳、厦门、大连和长沙。

对城市&地区的 CNS 影响因子统计，生物探索网站希望向用户提供关于地区研究水平的一项指数，让科研人员在从事各自研究领域的同时选择较高的研究平台和学术氛围。此外，由于论文来自不同的经费项目，因此城市&地区的 CNS 影响因子能从一个方面反映国家经费的分配比例。

四、6 月份中国机构发文 CNS 的走势



（数据统计源自 NCBI 网站 Pubmed）

在 2013 年 1 月至 6 月之间中国机构发文 CNS 的统计结果中，数据表明：Nature 及其子刊发表的中国研究论文数量处于高位，总计 112 篇，本月排在近 6 个月的第 2 位；相反，Science 及其子刊发表的中国研究论文数量处于低位，总计 22 篇，其中 3 月最高达到 7 篇。

Nature 系列期刊的数量最多，它覆盖的学术类别和影响因子也较多，这是中国研究论文发表在 Nature 系列刊最多的原因之一；另一原因可能是，Nature 系列期刊对中国机构的研究成果认可度高，从自然出版集团在上海设立《自然-通讯》编辑部一事可以看出，它对中国机构研究成果的重视。

五、6 月份 CNS 发文机构论文量统计

研究机构	CNS 论文		
	6 月份发文量	近 5 年总数	总数
中国科学院上海生命科学研究院	4	72	100
清华大学	3	70	85
北京大学	2	44	53
复旦大学	2	37	45
中国科学院古脊椎动物与古人类研究所	2	11	41
上海交通大学	3	36	40
中国科技大学	3	28	35
香港大学	1	27	33
厦门大学	1	19	24
国立台湾大学	1	10	22
国立阳明大学	1	10	20
中国农业大学	1	13	19
浙江大学	2	15	17
国立清华大学	1	6	16
中国科学院大连化学物理研究所	1	11	15
中国科学院动物研究所	1	11	14
中国科学院上海有机化学研究所	1	9	11
中国农业科学院	1	10	10
中央研究院原子与分子科学研究所	1	6	10
华中科技大学同济医学院	1	7	9
同济大学	1	4	5
汕头大学医学院	1	2	4
中南大学	1	2	2
华南师范大学	1	1	1
南方科技大学	1	1	1
山东师范大学	1	1	1

（数据源于NCBI网站Pubmed）

从 6 月份中国机构 CNS 论文榜单上看，排名前三的分别是中国科学院上海生命科学研究院、清华大学和北京大学。在本月发文量上，超过 1 篇的研究机构是中国科学院上海生命科学研究院（4 篇）、清华大学（3 篇）、上海交通大学（3 篇）、中国科技大学（3 篇）、北京大学（2 篇）、复旦大学（2 篇）、中国科学院古脊椎动物与古人类研究所（2 篇）和浙江大学（2 篇）。其中发文 4 篇的中国科学院上海生命科学研究院是中国机构 5 月 CNS 发文最多的研究机构，而 5 月份上海交通大学以 3 篇论文量成为当月发文最多的研究机构。

在 6 月份 CNS 论文的统计数据中，除中国科学院古脊椎动物与古人类研究所、国立台湾大学和国立清华大学三家机构以外，绝大多数中国机构近 5 年发表的 CNS 论文总数不低于其 CNS 论文总数的一半，这表明近 5 年来中国机构发文 CNS 的速度和数量增加较快。6 月份，华南师范大学、南方科技大学和山东师范大学都是首次发文 CNS，除首次发文 CNS 的研究机构外，中国农业科学院和中南大学的 CNS 论文全都在近 5 年内。

六、6 月份 CNS 论文通讯作者的项目数和经费

研究机构	通讯作者	项目金额/万	项目数/个
中国科学院遗传与发育生物学研究所	李家洋	2177	16
中国科学技术大学	侯建国	2045	15
北京大学	王恩哥	2020	15
中国科学技术大学	田志刚	1909	15
中国科学院上海生命科学研究院	韩斌	1240	4
中国农业大学	李宁	985	11
中科院上海生物化学与细胞生物学研究所	徐国良	937	16
中国科学院上海生命科学研究院	罗振革	840	3
华中科技大学	马丁	734	12
清华大学	柴继杰	510	2
中国科学技术大学	吴缅	473	5
清华大学	吴嘉炜	470	3
复旦大学	夏永姚	409	5
中国科学技术大学	董振超	394	3
中国农业科学院作物科学研究所	刁现民	278	5
中国科学院上海有机化学研究所	唐功利	274	5
上海交通大学	范先群	234	5
中国科学院动物研究所	韩春生	174	4
浙江大学医学院	谢幸	150	6

厦门大学	李勇	115	2
中国科学院上海生命科学研究院	张雷	110	2
中国科学院古脊椎动物与古人类研究所	倪喜军	110	3
中国科学院上海生命科学研究院	赵允	107	2
中国科学院动物研究所	汤富酬	80	1
北京大学	李新征	80	1
吉林大学	胡继繁	70	1
中国科学技术大学	杨小鲁	40	1
复旦大学	陈东戎	30	1
同济大学	刘小乐	20	1

（数据源于 NSFC）

对于 6 月份中国机构发文 CNS 的 29 位通讯作者（统计量不完全），国家自然科学基金项目提供了详细的项目金额和数量。中国科学院遗传与发育生物学研究所的李家洋研究员以 2177 万元高举榜首，项目数为 16 个；中国科学技术大学的侯建国教授和北京大学的王恩哥教授以 2045 万和 2020 万分列第二、三名，他们的项目数都是 15 个。

排名前 10 的通讯作者分别来自北京（4 位）、上海（3 位）、合肥（2 位）和武汉（1 位）。其中，北京地区 4 位通讯作者位于项目金额榜前十位之内，这反映出北京位列 6 月份 CNS 中国机构影响因子之首的经费基础。

七、受关注的权威看法

上海生物信息技术研究中心李亦学：科研数据难共享阻碍国内生物科技发展

上海生物信息技术研究中心主任李亦学的“科研数据共享之梦”已做了 13 年。但在近日举行的首届金桥产业技术创新会议上，当记者向他问及相关进展时，听到的却是一声叹息。

13 年前，“大数据”尚未被任何字典收录，而今却被公认是全球生命科学研究的核心工具。李亦学告诉记者，科研数据难以共享已成为国内生命科学研究的一大障碍；而在大数据时代，其负面效应还可能被继续放大。

李亦学透露，国内一批院士和重量级专家正在起草一份报告，建议国家借鉴美国、欧洲、日本等的做法，建立国家级生命科学数据库，从而打破共享瓶颈。作为该调研报告的参与人，李亦学表示，在技术上，共享“不存在任何障碍”，国家应尽早落子布局。

——一辈子的难题，几个月解决

在生命科学领域引入大数据工具，将给研究带来极大便利。科学家用传统方法可能要花一辈子才能解决的难题，大数据可能只要几个月就能找到答案。

一个典型案例是“腓骨肌萎缩症（CMT）”的研究。这是一种常见的遗传性神经系统疾病，患者最初会感到四肢无力，随后逐步恶化，最终可能终身离不开轮椅。

CMT 早就被认为与基因突变有关，但全球科学家寻找致病基因花了 20 多年，始终不得要领。不过就在两三年前，美国一个小组对一位 CMT 病人连同他的 10 多位亲属进行全基因组测序，随后对所获得的数百 GB 的数据进行了“简单的比对分析”，很快就精确定位了那条致病基因和发生突变的位点。

李亦学表示，能够获得和整合数据，然后再进行快速和精准的分析，已成为生命科学研究的关键。目前，中国已成为世界领先的不断产生生物学与生物医学大数据的国家。然而，中国生命科学的数据共享却与发达国家差距巨大。他判断说，国内课题组之间的数据共享一直是一个“小概率事件”。

李亦学 13 年前回国，曾经的理想是建立具有国家权威的公益性的生命科学数据中心，推动国内的生命科学研究数据共享。但迄今进展不大，这让他无比遗憾。

——只给看论文，无法看数据

美国是生命科学大数据产出和应用的领先者，不仅数据量和分析技术领先，而且在数据共享方面也是如此。

李亦学告诉记者，美国国立生物技术信息中心（NCBI）存储了分子生物学、生物化学、遗传学领域的海量数据，一大批计算机专家和生物学家维护着这个庞大的数据库和自动分析系统。这个平台对支撑起美国在生命科学领域的地位至关重要。NCBI 的数据是科学家无偿提供的。根据规定，美国科学家要想拿到政府经费，必须在申请课题时就承诺在课题完成后，将详细的研究数据提供给 NCBI；如果违背承诺，这名研究者将被列入黑名单，可能再也无法得到资助。这是 NCBI 获得大量数据的根本保证。

李亦学说，国内的政府科研项目一直没有强制性的数据公开和共享要求。生命科学的数据零散地掌握在各个科研单位和研究小组内部，对国家的科研投入来说，这是一种巨大的浪费。

据了解，在我国，这样的现象时有发生：国家向某个重大研究课题投入巨资，支持其从基因组层面研究若干重要的遗传疾病。最终，虽然该研究发表了一系列高水平论文，但却从未将详细数据公开。

李亦学认为，这样的研究本可以整体提升中国相关领域学术水平，但“只给看论文、无法看数据”的做法，极大限制了国家级课题的带动效应。

——科研数据要当成战略资源

最近，国内一批院士和重量级专家正联名起草一份调研报告，希望能在国内也建立一个类似 NCBI 的国家级生命科学数据库。这份报告将在今年完成并提交。

最让专家们揪心的，不仅是数据不共享将给国家创新体系带来损失，更在于“如果有一天，NCBI 不再与中国科学家共享数据，我们怎么办？”

NCBI 向全球免费提供数据。李亦学说，目前，所有的访问量中，来自中国科学家的占了相当大的份额。一旦 NCBI 向中国关上大门，一些院士的判断是：“中国生命科学研究可能倒退 20 年。”

在大数据时代，数据就如石油一般，是国家的战略资源。李亦学认为，正因为如此，必须由国家出面，建立科研数据共享的机制和环境。而目前，哪怕政府对所资助的课题提出数据共享的强制性要求，科学家也不知道该去哪儿共享。

在生命科学领域，国际学术界有一个不成文的规定：要想在顶级刊物发表论文，科学家必须共享其实验数据，而且大都必须将数据递交到 NCBI 的数据库体系。李亦学说，因此，在 NCBI 的数据库，由中国科学家提供的数据占了不小比例。这种“国内数据、国外整合”的做法不合理，但也表明在国内推动数据共享存在可操作性。

根据调研，在我国建立国家级的公益性生命科学数据平台也许需要数亿元的年度预算，以建

立一个海量科学数据存储和计算服务的软硬件架构，以及维持一支高水平的研发和服务团队。但一旦建立起来，这个平台的回报以及潜在的社会经济效益，“无论怎样估计都不会过分”。

饶毅：我不认为郎咸平是“学术骗子”

学术圈媒体近日讨论过多的是郎咸平的学历和工作经历真假性，大家都在不停地扔出各种论据来证明郎咸平到底是不是学术界的骗子，而北京大学终身讲席教授、前任生命科学学院院长饶毅对此却有自己的看法。

有良知的媒体在介入有关科学和技术的问题、并特意激起公开讨论以前，也不妨核实事实，而且媒体和媒体人的基本底线应该是不反复播散已经证明是骗子的观点。

需要说明的是，我不认为郎咸平是“学术骗子”。以前，“说话大帅”郎咸平在电视上公开宣称广西大学生精子下降与转基因应用有关。在转基因和相关的分子生物学方面，郎咸平毫无学术背景，而且发表言论的时候显示在这方面他不学无术，不可能与“学术”有关，我不认为郎咸平在此问题上是“学术”骗子，因为这样称呼他是涂黑“学术”两字，所以必需省略。

“电视说话大帅”郎咸平对转基因的说法，绝大多数是简单的造谣，少数是稍微绕了圈的谣言。

对于其他一些人，包括方舟子提到的人反转基因的人，包括极端的人，只要他们确实相信他们所说的，也就不是骗子，只能说是偏执、或者不懂，或者其他。

对于一般有疑问的人，需要更多了解，包括请做转基因的科学家出来说明实情。

在此问题上，我愿起的作用是为辛辛苦苦在中国做转基因的科学家做外围工作，稍微弱化像郎咸平一样的造谣或无理智者的滥炸。

不能因为一些没有原则、没有标准 、不能区分言论自由和低级趣味的电视台继续用造谣的“电视说话大帅”，就不敢反击他们歪曲转基因的科学、技术及其相关的科学家、技术人员。

八、专家精选

TAp73 enhances the pentose phosphate pathway and supports cell proliferation.

中国科技大学的吴缅教授（左图）等在癌症代谢机制研究中取得一项突破性发现，证实 TAp73 促进了癌细胞中的戊糖磷酸途径以支持细胞增殖。相关论文发表在 6 月 30 日的《自然细胞生物学》（Nature Cell Biology）杂志上。

在这项研究中，研究人员证实 TAp73 支持了人类和小鼠肿瘤细胞的增殖。TAp73 激活了戊糖磷酸途径（PPP）的限速酶——6-磷酸葡糖脱氢酶（glucose-6-phosphate dehydrogenase ，G6PD)的表达。通过刺激 G6PD，TAp73 提高了戊糖磷酸途径的效率，促进了 NADPH 和核糖生成，从而推动了大分子合成及活性氧簇（ROS）解毒。此外，研究人员证实通过增强 G6PD 表达，或是利用核苷结合一种 ROS 清除剂处理 TAp73 缺陷细胞，可使这种细胞的生长缺陷得以修复。

研究人员发现，这项研究揭示了 TAp73 在调控代谢中的重要作用，将 TAp73 和戊糖磷酸途径与致癌细胞生长联系起来。从而为药物研究人员提供了防治癌症的新潜在药物靶点。

A haplotype map of genomic variations and genome-wide association studies of agronomic traits in foxtail millet (Setaria italica).

中国农业科学院作物科学研究所的刁现民研究员（左图）和中科院遗传与发育生物学研究所和中科院上海生命科学研究院的研究人员，一起绘制出了谷子(foxtail millet)的基因组单体型图谱，并对其农艺性状进行了全基因组关联研究。相关成果公布在 6 月 23 日的《自然遗传学》（Nature Genetics）杂志上。

在这项研究中，研究人员对于 916 个不同的谷子品种进行测序，鉴别出了 258 万个 SNPs，并利用 80 万个常见 SNPs 构建出了一个谷子基因组单体型图谱。研究人员将谷子的品种按照与早晚期开花时间分为两个分化群体。此外，他们对五种不同环境下的 916 个不同的谷子品种进行了基因分型，通过全基因组关联研究确定了与 47 种农艺性状相关的 512 个基因座。研究人员将一种狗尾草与一种谷子的深度测序基因进行了从头组装（de novo assembly），鉴别出了复杂的种间（interspecies）和种内（intraspecies）变异体。研究人员还鉴别出了 36 个似乎发生在现代育种过程中的选择性清除（selective sweep）。

这些研究结果为谷子的遗传研究打下了基础，对于遗传改良谷子性状提供了基础资源，对于谷子品种选育具有重要的意义。

The duck genome and transcriptome provide insight into an avian influenza virus reservoir species.

中国农业大学的李宁教授（左图）联合其它研究机构合作完成北京鸭基因组的测序和分析，鉴定了鸭子对禽流感产生免疫反应的相关遗传基因，将有助于进一步了解鸟类的免疫机制，同时为深入解析禽流感病毒与其宿主之间的相互作用奠定了重要的遗传学基础。研究成果发表在在《自然 • 遗传学》（Nature Genetics）杂志上。

研究人员对北京鸭肺部组织进行了转录组测序，以确定其基因表达状况。通过对高致病性及低致病性 H5N1 病毒感染后的鸭子和对照组间的对比分析，研究人员发现鸭子肺部组织的基

因表达情况因病毒感染而有所变化，并且对比鉴定出一批对禽流感病毒响应的新基因。β-防御素在流感病毒感染后被诱导产生，而 BTNL 基因在哺乳动物中参与 T 细胞的激活和浸润。

目前众多研究已证实β-防御素和 BTNL 在哺乳动物的免疫反应中起到重要作用，但二者在鸟类中对于禽流感免疫反应的作用至今还未明确。在本研究中，科研人员进一步证实了β-防御素和 BTNL 在使鸭子成为禽流感病毒天然宿主的过程中发挥了重要作用。

Genetic and Neural Mechanisms that Inhibit Drosophila from Mating with Other Species.

浙江大学的应颂敏博士（左图）以第一作者身份发表的论文中，发现核酸酶 MUS81－EME1 促进了普通脆性位点（common fragile site）的表达，并证实 CFS 断裂实际上是一个有助于基因组稳定的主动过程。研究成果发表在 6 月 30 日的《自然细胞生物学》（Nature Cell Biology）杂志上。

在这篇文章中，研究人员证实在有丝分裂早期细胞中，DNA 结构特异性核酸酶 MUS81－EME1 定位到了普通脆性位点上，促进了中期染色体普通脆性位点上出现特征性的缺口或断裂。这表明普通脆性位点断裂是一种主动的、依赖 MUS81－EME1 的过程，而非染色体凝缩过程中偶然性的染色单体断裂的结果。并且研究人员发现，MUS81－EME1 导致的普通脆性位点断裂，实际上促进了正确的姐妹染色体单体分离

这项研究发现对于当前普遍的学术观点“普通脆性位点断裂是有害于细胞的非特异性被动过程”提出了挑战。脆性位点在体细胞中是稳定的，但它们在许多癌细胞和某些神经性疾病细胞中经常发生缺失或重排。因此，了解脆性位点的生物学特性对多种重大疾病研究，如癌症研究和神经退行性疾病研究有深远意义。

九、6 月份论文列表

A genome-wide association study identifies two new cervical cancer susceptibility loci at 4q12 and 17q12.

通讯作者：马丁、师咏勇、谢幸(华中科技大学同济医学院&上海交通大学&浙江大学医学院)Nat Genet. 2013 Jun 30. doi: 10.1038/ng.2687.

To identify new genetic risk factors for cervical cancer, we conducted a genome-wide association study in the Han Chinese population. The initial discovery set included 1,364 individuals with cervical cancer (cases) and 3,028 female controls, and we selected a 'stringently matched samples' subset (829 cases and 990 controls) from the discovery set on the basis of principal component analysis; the follow-up stages included two independent sample sets (1,824 cases and 3,808 controls for follow-up 1 and 2,343 cases and 3,388 controls for follow-up 2). We identified strong evidence of associations between cervical cancer and two new loci: 4q12 (rs13117307, $P_{combined,\ stringently\ matched} = 9.69 \times 10^{-9}$, per-allele odds ratio $(OR)_{stringently\ matched} = 1.26$) and 17q12 (rs8067378, $P_{combined,\ stringently\ matched} = 2.00 \times 10^{-8}$, per-allele $OR_{stringently\ matched} = 1.18$). We additionally replicated an association between HLA-DPB1 and HLA-DPB2 (HLA-DPB1/2) at 6p21.32 and cervical cancer (rs4282438, $P_{combined,\ stringently\ matched} = 4.52 \times 10^{-27}$, per-allele $OR_{stringently\ matched} = 0.75$). Our findings provide new insights into the genetic etiology of cervical cancer.

Liver receptor homolog-1 is essential for pregnancy.

通讯作者: Bruce D Murphy (山东师范大学)Nat Med. 2013 Jun 30. doi: 10.1038/nm.3192

Successful pregnancy requires coordination of an array of signals and factors from multiple tissues. One such element, liver receptor homolog-1 (Lrh-1), is an orphan nuclear receptor that regulates metabolism and hormone synthesis. It is strongly expressed in granulosa cells of ovarian follicles and in the corpus luteum of rodents and humans. Germline ablation of Nr5a2 (also called Lrh-1), the gene coding for Lrh-1, in mice is embryonically lethal at gastrulation. Depletion of Lrh-1 in the ovarian follicle shows that it regulates genes required for both steroid synthesis and ovulation. To study the effects of Lrh-1 on mouse gestation, we genetically disrupted its expression in the corpus luteum, resulting in luteal insufficiency. Hormone replacement permitted embryo implantation but was followed by gestational failure with impaired endometrial decidualization, compromised placental formation, fetal growth retardation and fetal death. Lrh-1 is also expressed in the mouse and human endometrium, and in a primary culture of human endometrial stromal cells, reduction of NR5A2 transcript abundance by RNA interference abrogated decidualization. These findings show that Lrh-1 is necessary for maintenance of the corpus luteum, for promotion of decidualization and for formation of the placenta. It therefore has multiple, indispensible roles in establishing and sustaining pregnancy.

Observation of room-temperature ballistic thermal conduction persisting over 8.3 μm in SiGe nanowires.

通讯作者: Chih-Wei Chang(国立台湾大学)Nat Nanotechnol. 2013 Jul;8(7):534-8. doi: 10.1038/nnano.2013.121. Epub 2013 Jun 30.

In ballistic thermal conduction, the wave characteristics of phonons allow the transmission of energy without dissipation. However, the observation of ballistic heat transport at room temperature is challenging because of the short phonon mean free path. Here we show that ballistic thermal conduction persisting over 8.3 μm can be observed in SiGe nanowires with low thermal conductivity for a wide range of structural variations and alloy concentrations. We find that an unexpectedly low percentage (~0.04%) of phonons carry out the heat conduction process

in SiGe nanowires, and that the ballistic phonons display properties including non-additive thermal resistances in series, unconventional contact thermal resistance, and unusual robustness against external perturbations. These results, obtained in a model semiconductor, could enable wave-engineering of phonons and help to realize heat waveguides, terahertz phononic crystals and quantum phononic/thermoelectric devices ready to be integrated into existing silicon-based electronics.

Histology and postural change during the growth of the ceratopsian dinosaur Psittacosaurus lujiatunensis.

通讯作者：Qi Zhao (中国科学院古脊椎动物与古人类研究所)Nat Commun. 2013 Jun 28;4:2079. doi: 10.1038/ncomms3079.

A few dinosaurs are inferred to have undergone an ontogenetic shift from quadrupedal-to-bipedal posture, or vice versa, based on skeletal allometry. The basal ceratopsian Psittacosaurus lujiatunensis is considered to have been mainly bipedal as an adult. Here we infer a postural shift in this species based on a novel combination of limb measurements and histological data. The forelimb is strongly negatively allometric relative to the hindlimb, and patterns of vascular canal orientation provide evidence that growth of the hindlimb was particularly rapid during the middle part of ontogeny. Histology also makes it possible to determine the ontogenetic ages of individual specimens, showing that the forelimb-to-hindlimb ratio changed rapidly during the first or second year of life and thereafter decreased gradually. Occurrence of an ontogenetic shift from quadrupedality to bipedality was evidently widespread in dinosaurs, and may even represent the ancestral condition for the entire group.

TAp73 enhances the pentose phosphate pathway and supports cell proliferation.

通讯作者：吴缅、杨小鲁(中国科学技术大学)Nat Cell Biol. 2013 Jun 30. doi: 10.1038/ncb2789.

TAp73 is a structural homologue of the pre-eminent tumour suppressor p53. However, unlike p53, TAp73 is rarely mutated, and instead is frequently overexpressed in human tumours. It remains unclear whether TAp73 affords an advantage to tumour cells and if so, what the underlying mechanism is. Here we show that TAp73 supports the proliferation of human and mouse tumour cells. TAp73 activates the expression of glucose-6-phosphate dehydrogenase (G6PD), the rate-limiting enzyme of the pentose phosphate pathway (PPP). By stimulating G6PD, TAp73 increases PPP flux and directs glucose to the production of NADPH and ribose, for the synthesis of macromolecules and detoxification of reactive oxygen species (ROS). The growth defect of TAp73-deficient cells can be rescued by either enforced G6PD expression or the presence of nucleosides plus an ROS scavenger. These findings establish a critical role for TAp73 in regulating metabolism, and connect TAp73 and the PPP to oncogenic cell growth.

MUS81 promotes common fragile site expression.

第一作者：应颂敏(浙江大学)Nat Cell Biol. 2013 Jun 30. doi: 10.1038/ncb2773.

Fragile sites are chromosomal loci with a propensity to form gaps or breaks during early mitosis, and their instability is implicated as being causative in certain neurological disorders and cancers. Recent work has demonstrated that the so-called common fragile sites (CFSs) often impair the faithful disjunction of sister chromatids in mitosis. However, the mechanisms by which CFSs express their fragility, and the cellular factors required to suppress CFS instability, remain largely undefined. Here, we report that the DNA structure-specific nuclease MUS81-EME1 localizes to CFS loci in early mitotic cells, and promotes the cytological appearance of characteristic gaps or breaks observed at CFSs in metaphase chromosomes. These data indicate that CFS breakage is an active, MUS81-EME1-dependent process, and not a result of inadvertent chromatid rupturing during chromosome condensation. Moreover, CFS cleavage by MUS81-EME1 promotes faithful sister chromatid disjunction. Our findings challenge the prevailing view that CFS breakage is a nonspecific process that is detrimental to cells, and indicate that CFS cleavage actually promotes genome stability.

Genetic and Neural Mechanisms that Inhibit Drosophila from Mating with Other Species.

通讯作者：Nirao M. Shah（北京大学）Cell. 2013 Jul 3;154(1):89-102. doi: 10.1016/j.cell.2013.06.008. Epub 2013 Jun 27.

Genetically hard-wired neural mechanisms must enforce behavioral reproductive isolation because interspecies courtship is rare even in sexually naïve animals of most species. We find that the chemoreceptor Gr32a inhibits male D. melanogaster from courting diverse fruit fly species. Gr32a recognizes nonvolatile aversive cues present on these reproductively dead-end targets, and activity of Gr32a neurons is necessary and sufficient to inhibit interspecies courtship. Male-specific Fruitless (Fru(M)), a master regulator of courtship, also inhibits interspecies courtship. Gr32a and Fru(M) are not coexpressed, but Fru(M) neurons contact Gr32a neurons, suggesting that these genes influence a shared neural circuit that inhibits interspecies courtship. Gr32a and Fru(M) also suppress within-species intermale courtship, but we show that distinct mechanisms preclude sexual displays toward conspecific males and other species. Although this chemosensory pathway does not inhibit interspecies mating in D. melanogaster females, similar mechanisms appear to inhibit this behavior in many other male drosophilids.

Omega-3 Fatty Acids Prevent Inflammation and Metabolic Disorder through Inhibition of NLRP3 Inflammasome Activation.

通讯作者：田志刚 (中国科学技术大学) Immunity. 2013 Jun 27;38(6):1154-63. doi: 10.1016/j.immuni.2013.05.015.

Omega-3 fatty acids (ω-3 FAs) have potential anti-inflammatory activity in a variety of inflammatory human diseases, but the mechanisms remain poorly understood. Here we show that stimulation of macrophages with ω-3 FAs, including eicosapentaenoic acid (EPA), docosahexaenoic acid (DHA), and other family members, abolished NLRP3 inflammasome activation and inhibited subsequent caspase-1 activation and IL-1β secretion. In addition, G protein-coupled receptor 120 (GPR120) and GPR40 and their downstream scaffold protein β-arrestin-2 were shown to be involved in inflammasome inhibition induced by ω-3 FAs.

Importantly, ω-3 FAs also prevented NLRP3 inflammasome-dependent inflammation and metabolic disorder in a high-fat-diet-induced type 2 diabetes model. Our results reveal a mechanism through which ω-3 FAs repress inflammation and prevent inflammation-driven diseases and suggest the potential clinical use of ω-3 FAs in gout, autoinflammatory syndromes, or other NLRP3 inflammasome-driven inflammatory diseases.

Quantum simulation of low-temperature metallic liquid hydrogen.

通讯作者：李新征、王恩哥(北京大学)Nat Commun. 2013 Jun 28;4:2064. doi: 10.1038/ncomms3064.

The melting temperature of solid hydrogen drops with pressure above ~65 GPa, suggesting that a liquid state might exist at low temperatures. It has also been suggested that this low-temperature liquid state might be non-molecular and metallic, although evidence for such behaviour is lacking. Here we report results for hydrogen at high pressures using ab initio methods, which include a description of the quantum motion of the protons. We determine the melting temperature as a function of pressure and find an atomic solid phase from 500 to 800 GPa, which melts at <200 K. Beyond this and up to 1,200 GPa, a metallic atomic liquid is stable at temperatures as low as 50 K. The quantum motion of the protons is critical to the low melting temperature reported, as simulations with classical nuclei lead to considerably higher melting temperatures of ~300 K across the entire pressure range considered.

Applied physics: cloaking of heat.

通讯作者：Ulf Leonhardt（华南师范大学）Nature. 2013 Jun 27;498(7455):440-1. doi: 10.1038/498440a.

For time immemorial, clothes have been used for thermal insulation. Cloaking devices have now been demonstrated that insulate from heat while maintaining its flow, thus hiding objects from heat sensors.

Molecular adsorption induces the transformation of rhombohedral- to Bernal-stacking order in trilayer graphene.

通讯作者: Zexiang Shen、Lain-Jong Li (中央研究院原子与分子科学研究所) Nat Commun. 2013 Jun 25;4:2074. doi: 10.1038/ncomms3074.

The Bernal (ABA)-stacked graphene trilayer is presumed to be thermodynamically more stable than the rhombohedral (ABC) counterpart. However, the thermal transformation from ABC to ABA domains does not occur at a temperature lower than 1,000 °C. Here we report that ABC-stacked trilayers are transformed to ABA-stacked layers after an organic molecule triazine is evaporated onto graphene surfaces at 150 °C. The transformation is found to always initiate at the ABA-ABC domain boundaries. Simulations based on density function theory considering the van der Waals interaction suggest that after triazine decoration the energy difference between ABA and ABC domains is larger, providing a driving force for stacking transformation. The molecular

dynamics simulation results further suggest that the triazine decoration on the wrinkles at the ABC-ABA domain boundary activates the wrinkle sliding toward the ABC domains, leading to the stacking transformation from ABC to ABA.

A haplotype map of genomic variations and genome-wide association studies of agronomic traits in foxtail millet (Setaria italica).

通讯作者: 刁现民、韩斌、李家洋(中国农业科学院&中国科学院上海生命科学研究院&中国科学院遗传与发育生物学研究所)Nat Genet. 2013 Jun 23. doi: 10.1038/ng.2673.

Foxtail millet (Setaria italica) is an important grain crop that is grown in arid regions. Here we sequenced 916 diverse foxtail millet varieties, identified 2.58 million SNPs and used 0.8 million common SNPs to construct a haplotype map of the foxtail millet genome. We classified the foxtail millet varieties into two divergent groups that are strongly correlated with early and late flowering times. We phenotyped the 916 varieties under five different environments and identified 512 loci associated with 47 agronomic traits by genome-wide association studies. We performed a de novo assembly of deeply sequenced genomes of a Setaria viridis accession (the wild progenitor of S. italica) and an S. italica variety and identified complex interspecies and intraspecies variants. We also identified 36 selective sweeps that seem to have occurred during modern breeding. This study provides fundamental resources for genetics research and genetic improvement in foxtail millet.

Unconventional origin and hybrid system for construction of pyrrolopyrrole moiety in kosinostatin biosynthesis.

通讯作者: 唐功利(中国科学院上海有机化学研究所) Chem Biol. 2013 Jun 20;20(6):796-805. doi: 10.1016/j.chembiol.2013.04.013.
Kosinostatin (KST), an antitumor antibiotic, features a pyrrolopyrrole moiety spirally jointed to a five-membered ring of an anthraquinone framework glycosylated with a γ-branched octose. By a combination of in silico analysis, genetic characterization, biochemical assay, and precursor feeding experiments, a biosynthetic pathway for KST was proposed, which revealed (1) the pyrrolopyrrole moiety originates from nicotinic acid and ribose, (2) the bicyclic amidine is constructed by a process similar to the tryptophan biosynthetic pathway, and (3) a discrete adenylation enzyme and a peptidyl carrier protein (PCP) are responsible for producing a PCP-tethered building block parallel to type II polyketide synthase (PKS) rather than for the PKS priming step by providing the starter unit. These findings provide an opportunity to further explore the inexplicable enzymatic logic that governs the formation of pyrrolopyrrole moiety and the spirocyclic skeleton.

Riboswitch Regulation of Aminoglycoside Resistance Acetyl and Adenyl Transferases.

通讯作者：陈东戎(复旦大学) Cell. 2013 Jun 20;153(7):1419-1420. doi: 10.1016/j.cell.2013.05.050. Epub 2013 Jun 20. No abstract available.

n our recent paper, we reported an aminoglycoside-sensing RNA in the leader RNA of the aminoglycoside acetyl transferase (AAC) and aminoglycoside adenyl transferase (AAD), enzymes

that confer resistance to aminoglycoside antibiotics through modification of the drugs. Our study explains a well-known phenomenon: the induction of expression levels of the AAC/AAD proteins on addition of aminoglycosides. In this paper, we presented data that showed: (1) aminoglycoside-specific induction of reporter genes mediated by the leader RNA of the AAC in *Pseudomonas fluorescens*; (2) aminoglycoside binding to the leader RNA by surface plasmon resonance spectroscopy (SPR); (3) that binding induces a structural transition in the leader RNA that can be detected by changes in gel electrophoretic mobility and chemical probing; (4) the identification of a specific aminoglycoside-RNA crosslink; (5) confirmation, via mutational analysis, of the main features of the RNA secondary structure and the importance of structural elements within it for drug binding.

Magnetoelectric effects and valley-controlled spin quantum gates in transition metal dichalcogenide bilayers.

通讯作者: Wang Yao (香港大学)Nat Commun. 2013 Jun 19;4:2053. doi: 10.1038/ncomms3053.

In monolayer group-VI transition metal dichalcogenides, charge carriers have spin and valley degrees of freedom, both associated with magnetic moments. On the other hand, the layer degree of freedom in multilayers is associated with electrical polarization. Here we show that transition metal dichalcogenide bilayers offer an unprecedented platform to realize a strong coupling between the spin, valley and layer pseudospin of holes. Such coupling gives rise to the spin Hall effect and spin-dependent selection rule for optical transitions in inversion symmetric bilayer and leads to a variety of magnetoelectric effects permitting quantum manipulation of these electronic degrees of freedom. Oscillating electric and magnetic fields can both drive the hole spin resonance where the two fields have valley-dependent interference, making an interplay between the spin and valley as information carriers possible for potential valley-spintronic applications. We show how to realize quantum gates on the spin qubit controlled by the valley bit.

Myosin Vb controls biogenesis of post-Golgi Rab10 carriers during axon development.

通讯作者: 罗振革(中国科学院上海生命科学研究院)Nat Commun. 2013 Jun 17;4:2005. doi: 10.1038/ncomms3005.

Polarized membrane addition is crucial for axon development and elongation during neuronal morphogenesis. This process is believed to be regulated by directed membrane trafficking of Rab10-containing post-Golgi carriers. However, the mechanisms underlying the biogenesis of these carriers remain unclear. Here, we report that Rab10 interaction with myosin Vb (MYO5B) determines the formation of Rab10 carriers and is important for axon development. Rab10 interacts with the exon D-encoded domain of MYO5B. Downregulating the expression of MYO5B (+D) or blocking its interaction with Rab10 impairs the fission of Rab10 vesicles from trans-Golgi membranes, causes a decrease in the number of Rab10 transport carriers and inhibits axon development in cultured hippocampal neurons. Furthermore, the MYO5B-Rab10 system is required for axon development of vertebrate neocortical neurons or zebrafish retinal ganglion cells in vivo. Thus, specific interaction between Rab10 and MYO5B controls the formation of Rab10 vesicles, which is required for axon development.

Tet1 Regulates Adult Hippocampal Neurogenesis and Cognition.

通讯作者: 徐国良(中科院上海生物化学与细胞生物学研究所)Cell Stem Cell. 2013 Jun 12. doi:pii: S1934-5909(13)00199-9. 10.1016/j.stem.2013.05.006.

DNA hydroxylation catalyzed by Tet dioxygenases occurs abundantly in embryonic stem cells and neurons in mammals. However, its biological function in vivo is largely unknown. Here, we demonstrate that Tet1 plays an important role in regulating neural progenitor cell proliferation in adult mouse brain. Mice lacking Tet1 exhibit impaired hippocampal neurogenesis accompanied by poor learning and memory. In adult neural progenitor cells deficient in Tet1, a cohort of genes involved in progenitor proliferation were hypermethylated and downregulated. Our results indicate that Tet1 is positively involved in the epigenetic regulation of neural progenitor cell proliferation in the adult brain.

TRIB2 Acts Downstream of Wnt/TCF in Liver Cancer Cells to Regulate YAP and C/EBPα Function.

通讯作者: Junhao Mao (上海交通大学)Mol Cell. 2013 Jun 12. doi:pii: S1097-2765(13)00376-6. 10.1016/j.molcel.2013.05.013.

Dysregulation of Wnt signaling is closely associated with human liver tumorigenesis. However, liver cancer-specific Wnt transcriptional programs and downstream effectors remain poorly understood. Here, we identify tribbles homolog 2 (TRIB2) as a direct target of Wnt/TCF in liver cancer and demonstrate that transcription of Wnt target genes, including TRIB2, is coordinated by the TCF and FoxA transcription factors in liver cancer cells. We show that Wnt-TRIB2 activation is critical for cancer cell survival and transformation. Mechanistically, TRIB2 promotes protein stabilization of the YAP transcription coactivator through interaction with the βTrCP ubiquitin ligase. Furthermore, we find that TRIB2 relieves the liver tumor suppressor protein C/EBPα-mediated inhibition of YAP/TEAD transcriptional activation in liver cancer cells. Altogether, our study uncovers a regulatory mechanism underlying liver cancer-specific Wnt transcriptional output, and suggests that TRIB2 functions as a signaling nexus to integrate the Wnt/β-catenin, Hippo/YAP, and C/EBPα pathways in cancer cells.

Parallel neural pathways mediate CO2 avoidance responses in Drosophila.

通讯作者: Ann-Shyn Chiang (国立清华大学)Science. 2013 Jun 14;340(6138):1338-41. doi: 10.1126/science.1236693.

Different stimulus intensities elicit distinct perceptions, implying that input signals are either conveyed through an overlapping but distinct subpopulation of sensory neurons or channeled into divergent brain circuits according to intensity. In Drosophila, carbon dioxide (CO2) is detected by a single type of olfactory sensory neuron, but information is conveyed to higher brain centers through second-order projection neurons (PNs). Two distinct pathways, PN(v)-1 and PN(v)-2, are necessary and sufficient for avoidance responses to low and high CO2 concentrations, respectively. Whereas low concentrations activate PN(v)-1, high concentrations activate both PN(v)s and

GABAergic PN(v)-3, which may inhibit PN(v)-1 pathway-mediated avoidance behavior. Channeling a sensory input into distinct neural pathways allows the perception of an odor to be further modulated by both stimulus intensity and context.

Conserved regulatory elements in AMPK.

通讯作者: 吴嘉炜(清华大学)Nature. 2013 Jun 13;498(7453):E8-10. doi: 10.1038/nature12189.

The AMP-activated protein kinase (AMPK), an αβγ heterotrimeric enzyme, has a central role in regulating cellular metabolism and energy homeostasis. The α-subunit of AMPK possesses the catalytic kinase domain, followed by a regulatory region comprising the autoinhibitory domain (AID) and α-linker. Structural and biochemical studies suggested that AID is central to mammalian AMPK regulation; however, this notion has been challenged recently by Xiao *et al*. on the basis of their active AMPK structure (Protein Data Bank accession 2Y94). On close inspection, however, we found that the α-subunit regulatory region was incorrectly built in their model, and our rebuilt model suggests a universal occurrence of the AID domain in AMPKs; we have also identified a novel regulatory motif that is essential for AMPK regulation.

Crystal Structure of NLRC4 Reveals Its Autoinhibition Mechanism.

通讯作者: 柴继杰(清华大学)Science. 2013 Jun 13. doi: 10.1126/science.1236381. Epub 2013 Jun 13.

NOD-like receptor (NLR) proteins oligomerize into multiprotein complexes termed "inflammasomes" when activated. Their autoinhibition mechanism remains poorly defined. Here, we report the crystal structure of the mouse NLRC4 in a closed form. The ADP-mediated interaction between the central nucleotide-binding domain (NBD) and the winged-helix domain (WHD) was critical for stabilizing the closed conformation of NLRC4. The helical domain (HD2) repressively contacted a conserved and functionally important α-helix of the NBD. The C-terminal leucine-rich repeat (LRR) domain is positioned to sterically occlude one side of the NBD domain and consequently sequester NLRC4 in a monomeric state. Disruption of ADP-mediated NBD-WHD or NBD-HD2/NBD-LRR interactions resulted in constitutive activation of NLRC4. Together, our data reveal the NBD-organized cooperative autoinhibition mechanism of NLRC4 and provide insight into its activation.

Dynamics of 5-hydroxymethylcytosine during mouse spermatogenesis.

通讯作者: 韩春生、汤富酬(中国科学院动物研究所)Nat Commun. 2013 Jun 13;4:1995. doi: 10.1038/ncomms2995.

Little is known about how patterns of DNA methylation change during mammalian spermatogenesis. 5hmC has been recognized as a stable intermediate of DNA demethylation with potential regulatory functions in the mammalian genome. However, its global pattern in germ cells has yet to be addressed. Here, we first conducted absolute quantification of 5hmC in eight consecutive types of mouse spermatogenic cells using liquid chromatography-tandem mass

spectrometry, and then mapped its distributions in various genomic regions using our chemical labeling and enrichment method coupled with deep sequencing. We found that 5hmC mapped differentially to and changed dynamically in genomic regions related to expression regulation of protein-coding genes, piRNA precursor genes and repetitive elements. Moreover, 5hmC content correlated with the levels of various transcripts quantified by RNA-seq. These results suggest that the highly ordered alterations of 5hmC in the mouse genome are potentially crucial for the differentiation of spermatogenic cells.

Patent portfolios for biotech inventions.

通讯作者: Shyh-Jen Wang (国立阳明大学)Nat Biotechnol. 2013 Jun;31(6):501-3. doi: 10.1038/nbt.2598. No abstract available.

Choosing the right patent portfolio strategy will aid in protecting your valuable biotech intellectual property.

The duck genome and transcriptome provide insight into an avian influenza virus reservoir species.

通讯作者: 李宁(中国农业大学)Nat Genet. 2013 Jun 9;45(7):776-83. doi: 10.1038/ng.2657. Epub 2013 Jun 9.

The duck (Anas platyrhynchos) is one of the principal natural hosts of influenza A viruses. We present the duck genome sequence and perform deep transcriptome analyses to investigate immune-related genes. Our data indicate that the duck possesses a contractive immune gene repertoire, as in chicken and zebra finch, and this repertoire has been shaped through lineage-specific duplications. We identify genes that are responsive to influenza A viruses using the lung transcriptomes of control ducks and ones that were infected with either a highly pathogenic (A/duck/Hubei/49/05) or a weakly pathogenic (A/goose/Hubei/65/05) H5N1 virus. Further, we show how the duck's defense mechanisms against influenza infection have been optimized through the diversification of its β-defensin and butyrophilin-like repertoires. These analyses, in combination with the genomic and transcriptomic data, provide a resource for characterizing the interaction between host and influenza viruses.

Intrachromosomal Looping Is Required for Activation of Endogenous Pluripotency Genes during Reprogramming.

通讯作者: 范先群、胡继繁(上海交通大学&吉林大学)Cell Stem Cell. 2013 Jul 3;13(1):30-5. doi: 10.1016/j.stem.2013.05.012. Epub 2013 Jun 6.

Generation of induced pluripotent stem cells (iPSCs) by defined factors is an extremely inefficient process, because there is a strong epigenetic block preventing cells from achieving pluripotency. Here we report that virally expressed factors bound to the promoters of their target genes to the same extent in both iPSCs and unreprogrammed cells (URCs). However, expression of endogenous pluripotentcy genes was observed only in iPSCs. Comparison of local chromatin

structure of the OCT4 locus revealed that there was a cohesin-complex-mediated intrachromosomal loop that juxtaposes a downstream enhancer to the gene's promoter, enabling activation of endogenous stemness genes. None of these long-range interactions were observed in URCs. Knockdown of the cohesin-complex gene SMC1 by RNAi abolished the intrachromosomal interaction and affected pluripotency. These findings highlight the importance of the SMC1-orchestrated intrachromosomal loop as a critical epigenetic barrier to the induction of pluripotency.

Ter94 ATPase complex targets k11-linked ubiquitinated ci to proteasomes for partial degradation.

通讯作者: 赵允、张雷(中国科学院上海生命科学研究院)Dev Cell. 2013 Jun 24;25(6):636-44. doi: 10.1016/j.devcel.2013.05.006. Epub 2013 Jun 6.

The Cubitus interruptus (Ci)/Gli family of transcription factors can be degraded either completely or partially from a full-length form (Ci155/Gli(FL)) to a truncated repressor (Ci75/Gli(R)) by proteasomes to mediate Hedgehog (Hh) signaling. The mechanism by which proteasomes distinguish ubiquitinated Ci/Gli to carry out complete versus partial degradation is not known. Here, we show that Ter94 ATPase and its mammalian counterpart, p97, are involved in processing Ci and Gli3 into Ci75 and Gli3(R), respectively. Ter94 regulates the partial degradation of ubiquitinated Ci by Cul1-Slimb-based E3 ligase through its adaptors Ufd1-like and dNpl4. We demonstrate that Cul1-Slimb-based E3 ligase, but not Cul3-Rdx-based E3 ligase, modifies Ci by efficient addition of K11-linked ubiquitin chains. Ter94(Ufd1-like/dNpl4) complex interacts directly with Cul1-Slimb, and, intriguingly, it prefers K11-linked ubiquitinated Ci. Thus, Ter94 ATPase and K11-linked ubiquitination in Ci contribute to the selectivity by proteasomes for partial degradation.

Chemical mapping of a single molecule by plasmon-enhanced Raman scattering.

通讯作者: 侯建国、董振超(中国科学技术大学)Nature. 2013 Jun 6;498(7452):82-6. doi: 10.1038/nature12151.

Visualizing individual molecules with chemical recognition is a longstanding target in catalysis, molecular nanotechnology and biotechnology. Molecular vibrations provide a valuable 'fingerprint' for such identification. Vibrational spectroscopy based on tip-enhanced Raman scattering allows us to access the spectral signals of molecular species very efficiently via the strong localized plasmonic fields produced at the tip apex. However, the best spatial resolution of the tip-enhanced Raman scattering imaging is still limited to 3-15 nanometres, which is not adequate for resolving a single molecule chemically. Here we demonstrate Raman spectral imaging with spatial resolution below one nanometre, resolving the inner structure and surface configuration of a single molecule. This is achieved by spectrally matching the resonance of the nanocavity plasmon to the molecular vibronic transitions, particularly the downward transition responsible for the emission of Raman photons. This matching is made possible by the extremely precise tuning capability provided by scanning tunnelling microscopy. Experimental evidence suggests that the highly confined and broadband nature of the nanocavity plasmon field in the tunnelling gap is essential for ultrahigh-resolution imaging through the generation of an efficient

double-resonance enhancement for both Raman excitation and Raman emission. Our technique not only allows for chemical imaging at the single-molecule level, but also offers a new way to study the optical processes and photochemistry of a single molecule.

The oldest known primate skeleton and early haplorhine evolution.

通讯作者：倪喜军(中国科学院古脊椎动物与古人类研究所) Nature. 2013 Jun 6;498(7452):60-4. doi: 10.1038/nature12200.

Reconstructing the earliest phases of primate evolution has been impeded by gaps in the fossil record, so that disagreements persist regarding the palaeobiology and phylogenetic relationships of the earliest primates. Here we report the discovery of a nearly complete and partly articulated skeleton of a primitive haplorhine primate from the early Eocene of China, about 55 million years ago, the oldest fossil primate of this quality ever recovered. Coupled with detailed morphological examination using propagation phase contrast X-ray synchrotron microtomography, our phylogenetic analysis based on total available evidence indicates that this fossil is the most basal known member of the tarsiiform clade. In addition to providing further support for an early dichotomy between the strepsirrhine and haplorhine clades, this new primate further constrains the age of divergence between tarsiiforms and anthropoids. It also strengthens the hypothesis that the earliest primates were probably diurnal, arboreal and primarily insectivorous mammals the size of modern pygmy mouse lemurs.

Acetylation of Ets-1 Is the Key to Chromatin Remodeling for miR-192 Expression.

通讯作者：Zheng Dong (中南大学)Sci Signal. 2013 Jun 4;6(278):pe21. doi: 10.1126/scisignal.2004299.

By regulating gene expression, microRNAs (miRNAs) play pivotal roles in physiological and pathological processes. However, the regulation of miRNAs is elusive. miR-192 is a key regulator of renal fibrosis and hypertrophy in diabetic nephropathy. Natarajan et al. showed that the miR-192 gene contains an upstream region with Ets-1 and Smad3 binding sites. In control cells, all Ets-1 sites were occupied, resulting in a locked chromatin structure that kept miR-192 expression low. In response to transforming growth factor-β (TGF-β) stimulation, Smad3 and Akt were activated, and the latter further activated p300 to induce partial acetylation and dissociation of Ets-1 and the recruitment of Smad3 to the miR-192 gene, inducing transient miR-192 expression. During prolonged TGF-β treatment, p300 acetylated histone and Ets-1, resulting in complete dissociation of Ets-1 and the opening of the chromatin for sustained miR-192 expression. Thus, transcription factors and chromatin remodeling control microRNA gene expression in a dynamic, coordinated fashion.

All-solution processed polymer light-emitting diode displays.

通讯作者：Jian Wang (南方科技大学)Nat Commun. 2013 Jun 5;4:1971. doi: 10.1038/ncomms2971.

Adopting the emerging technology of printed electronics in manufacturing novel ultrathin flat panel displays attracts both academic and industrial interests because of the challenge in the device physics and the potential of reducing production costs. Here we produce all-solution processed polymer light-emitting diode displays by solution-depositing the cathode and utilizing a multifunctional buffer layer between the cathode and the organic layers. The use of ink-jetted conducting nanoparticles as the cathode yields high-resolution cathode patterns without any mechanical stress on the organic layers. The buffer layer, which offers the functions of solvent-proof electron injection and proper affinity, is fabricated by mixing the water/alcohol-soluble polymer and a curable epoxy adhesive. Our 1.5-inch polymer light-emitting diode displays are fabricated without any dead pixels or dead lines. The all-solution process eliminates the need for high vacuum for thermal evaporation of the cathode, which paves the way to industrial roll-to-roll manufacturing of flat panel displays.

Stable Li-ion battery anodes by in-situ polymerization of conducting hydrogel to conformally coat silicon nanoparticles.

通讯作者：崔毅、包哲南(清华大学)Nat Commun. 2013 Jun 4;4:1943. doi: 10.1038/ncomms2941.

Silicon has a high-specific capacity as an anode material for Li-ion batteries, and much research has been focused on overcoming the poor cycling stability issue associated with its large volume changes during charging and discharging processes, mostly through nanostructured material design. Here we report incorporation of a conducting polymer hydrogel into Si-based anodes: the hydrogel is polymerized in-situ, resulting in a well-connected three-dimensional network structure consisting of Si nanoparticles conformally coated by the conducting polymer. Such a hierarchical hydrogel framework combines multiple advantageous features, including a continuous electrically conductive polyaniline network, binding with the Si surface through either the crosslinker hydrogen bonding with phytic acid or electrostatic interaction with the positively charged polymer, and porous space for volume expansion of Si particles. With this anode, we demonstrate a cycle life of 5,000 cycles with over 90% capacity retention at current density of 6.0 A g(-1).

The antiparasitic drug ivermectin is a novel FXR ligand that regulates metabolism.

通讯作者: 李勇(厦门大学)Nat Commun. 2013 Jun 3;4:1937. doi: 10.1038/ncomms2924.

Farnesoid X receptor (FXR) has important roles in maintaining bile acid and cholesterol homeostasis. Here we report that the antiparasitic drug ivermectin is a ligand for nuclear FXR. We identify ivermectin using a high-throughput compound library screening and show that it induces the transcriptional activity of the FXR with distinctive properties in modulating coregulator recruitment. The crystal structure of ivermectin complexed with the ligand-binding domain of FXR reveals a unique binding mode of ivermectin in the FXR ligand-binding pocket, including the highly dynamic AF-2 helix and an expanded ligand-binding pocket. Treatment of wild-type mice, but not of FXR-null mice, with ivermectin decreases serum glucose and cholesterol levels, suggesting that ivermectin regulates metabolism through FXR. Our results establish FXR as the first mammalian protein targeted by ivermectin with high selectivity. Considering that ivermectin

is a widely used clinical drug, our findings reveal a safe template for the design of novel FXR ligands.

Integrative genomic analyses reveal clinically relevant long noncoding RNAs in human cancer.

通讯作者：刘小乐(同济大学)Nat Struct Mol Biol. 2013 Jul;20(7):908-13. doi: 10.1038/nsmb.2591. Epub 2013 Jun 2.

Despite growing appreciation of the importance of long noncoding RNAs (lncRNAs) in normal physiology and disease, our knowledge of cancer-related lncRNAs remains limited. By repurposing microarray probes, we constructed expression profiles of 10,207 lncRNA genes in approximately 1,300 tumors over four different cancer types. Through integrative analysis of the lncRNA expression profiles with clinical outcome and somatic copy-number alterations, we identified lncRNAs that are associated with cancer subtypes and clinical prognosis and predicted those that are potential drivers of cancer progression. We validated our predictions by experimentally confirming prostate cancer cell growth dependence on two newly identified lncRNAs. Our analysis provides a resource of clinically relevant lncRNAs for the development of lncRNA biomarkers and the identification of lncRNA therapeutic targets. It also demonstrates the power of integrating publically available genomic data sets and clinical information for discovering disease-associated lncRNAs.

Capture and conversion of CO2 at ambient conditions by a conjugated microporous polymer.

通讯作者: Wei-Qiao Deng (中国科学院大连化学物理研究所)Nat Commun. 2013 Jun 3;4:1960. doi: 10.1038/ncomms2960.

Conjugated microporous polymers are a new class of porous materials with an extended π-conjugation in an amorphous organic framework. Owing to the wide-ranging flexibility in the choice and design of components and the available control of pore parameters, these polymers can be tailored for use in various applications, such as gas storage, electronics and catalysis. Here we report a class of cobalt/aluminium-coordinated conjugated microporous polymers that exhibit outstanding CO2 capture and conversion performance at atmospheric pressure and room temperature. These polymers can store CO2 with adsorption capacities comparable to metal-organic frameworks. The cobalt-coordinated conjugated microporous polymers can also simultaneously function as heterogeneous catalysts for the reaction of CO2 and propylene oxide at atmospheric pressure and room temperature, wherein the polymers demonstrate better efficiency than a homogeneous salen-cobalt catalyst. By combining the functions of gas storage and catalysts, this strategy provides a direction for cost-effective CO2 reduction processes.

Li-O2 batteries: An agent for change.

通讯作者：夏永姚(复旦大学)Nat Chem. 2013 Jun;5(6):445-7. doi: 10.1038/nchem.1658.

The rechargeable Li–O_2 battery has low energy efficiency, which is mainly due to kinetic difficulties in the electrochemical oxidation of the insulating discharge product, Li_2O_2. Now a

redox mediator, acting as an electron–hole transfer agent, has been used to promote this oxidation reaction.