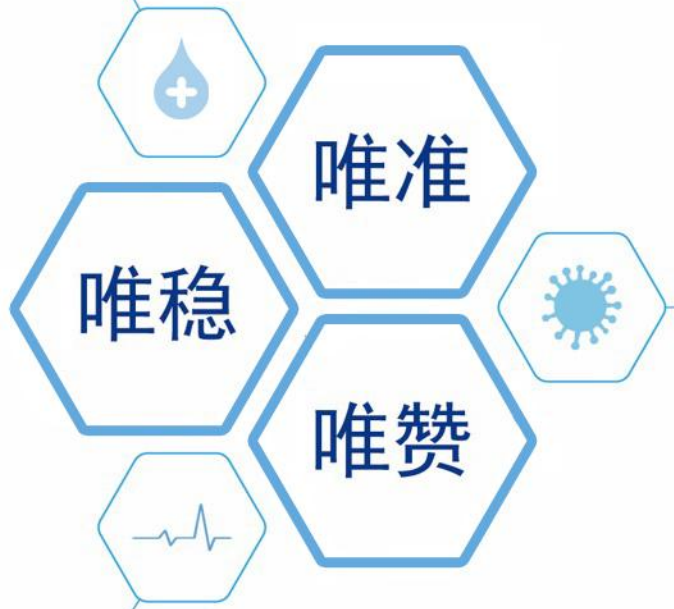
Vazyme

南京诺唯赞医疗科技有限公司

量子点精准检测技术与抗生素合理使用



南京诺唯赞医疗科技有限公司

唐波 博士

诺唯赞，从研发走向市场

- 2012年成立，年平均营收增长率100%以上，目前估值约六十亿，为南京市“**独角兽培育企业**”
- 福布斯2018非上市公司潜力企业榜，唯一IVD企业
- 由”万人计划”、”千人计划”、”双创人才” 等领导的强大人才团队，研发队伍硕士以上学历占60%以上，年研发投入45%以上
- 固定资产2.1亿，拥有GMP车间4500平米及9条诊断产品全自动生产线，自动化水平及产能国内领先

南京诺唯赞生物科技有限公司	江苏	南京	体外诊断、高通量测序建库试剂
南京甄视智能科技有限公司(小视科技)	江苏	南京	提供大数据和人工智能服务
启赟金融信息服务(上海)有限公司	上海	上海	跨境支付
秦皇岛耀华玻璃钢股份公司	河北	秦皇岛	玻璃钢制品、船舶、塑料制品
青岛易触数码科技有限公司	山东	青岛	自动售货机
陕西西大华特科技实业有限公司	陕西	西安	农药、生物类制剂生产及销售
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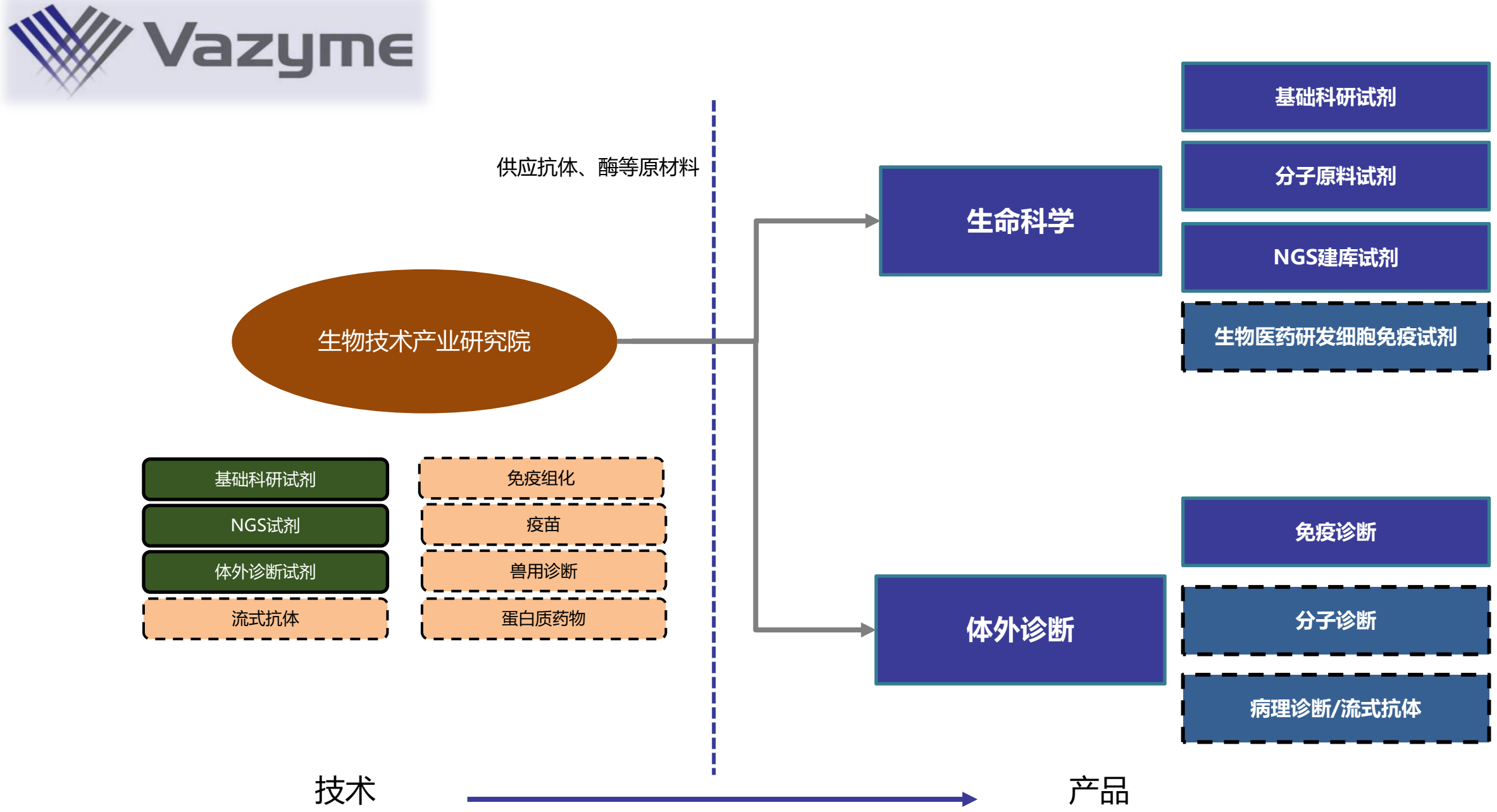
上海谋乐网络科技有限公司	上海	上海	安全产品、安全咨询、安全服务
上海益玩网络科技有限公司	上海	上海	移动游戏发行商
上海赞思餐饮管理有限公司(汤先生)	上海	上海	汤先生品牌餐厅和零售品
社宝信息科技(上海)有限公司	上海	上海	社保代缴
深圳前海大数金融服务有限公司	广东	深圳	小微大额经营性信用贷款
深圳市凡游网络科技有限公司	广东	深圳	移动游戏开发及发行

强大研发实力打造精准检测产品


供应抗体、酶等原材料
生物技术产业研究院
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蛋白质药物
生命科学
体外诊断
基础科研试剂
分子原料试剂
NGS建库试剂
生物医药研发细胞免疫试剂
免疫诊断
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分子生物学产品线	NGS建库产品线	NGS解决方案产品线	NGS临床诊断产品线
PCR产品线	DNA建库产品线	全基因组测序	NIPT产品线
qPCR产品线	RNA建库产品线	转录组测序	PGD/PGS产品线（已申报创新）
RT-PCR产品线	Tn5建库产品线	FFPE样本测序	结直肠癌早期筛查产品线（创新）
分子克隆产品线	单细胞基因组产品线	cfDNA测序	下呼吸道感染产品线
核酸纯化产品线	单细胞转录组产品线	ctDNA测序	甲状腺病变诊断产品线
细胞蛋白产品线	AmpSeq产品线	单细胞转录组测序	
	建库相关产品线	单细胞基因组测序	
		外泌体测序	
		扩增子定向测序	
		探针捕获定向测序	

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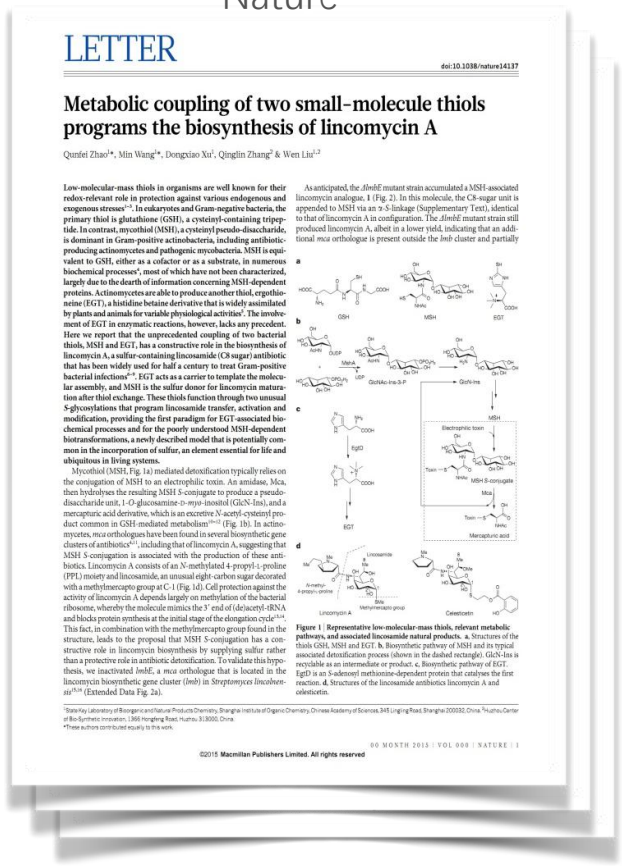
我们的优势

Nature



LETTER

doi:10.1038/nature14137

Metabolic coupling of two small-molecule thiols programs the biosynthesis of lincomycin A

Qunfei Zhao[1]*, Min Wang[1]*, Dongxiao Xu[1], Qinglin Zhang[2] & Wen Liu[1,2]

Low-molecular-mass thiols in organisms are well known for their redox-relevant role in protection against various endogenous and exogenous stresses[1–3]. In eukaryotes and Gram-negative bacteria, the primary thiol is glutathione (GSH), a cysteinyl-containing tripeptide. In contrast, mycothiol (MSH), a cysteinyl pseudo-disaccharide, is dominant in Gram-positive actinobacteria, including antibiotic-producing actinomycetes and pathogenic mycobacteria. MSH is equivalent to GSH, either as a cofactor or as a substrate, in numerous biochemical processes[4], most of which have not been characterized, largely due to the dearth of information concerning MSH-dependent proteins. Actinomycetes are able to produce another thiol, ergothioneine (EGT), a histidine betaine derivative that is widely assimilated by plants and animals for variable physiological activities[5]. The involvement of EGT in enzymatic reactions, however, lacks any precedent. Here we report that the unprecedented coupling of two bacterial thiols, MSH and EGT, has a constructive role in the biosynthesis of lincomycin A, a sulfur-containing lincosamide (C8 sugar) antibiotic that has been widely used for half a century to treat Gram-positive bacterial infections[6–8]. EGT acts as a carrier to template the molecular assembly, and MSH is the sulfur donor for lincomycin maturation after thiol exchange. These thiols function through two unusual S-glycosylations that program lincosamide transfer, activation and modification, providing the first paradigm for EGT-associated biochemical processes and for the poorly understood MSH-dependent biotransformations, a newly described model that is potentially common in the incorporation of sulfur, an element essential for life and ubiquitous in living systems.

Mycothiol (MSH, Fig. 1a) mediated detoxification typically relies on the conjugation of MSH to an electrophilic toxin. An amidase, Mca, then hydrolyses the resulting MSH *S*-conjugate to produce a pseudo-disaccharide unit, 1-*O*-glucosamine-*D*-*myo*-inositol (GlcN-Ins), and a mercapturic acid derivative, which is an excretive *N*-acetyl-cysteinyl product common in GSH-mediated metabolism[9–12] (Fig. 1b). In actinomycetes, *mca* orthologues have been found in several biosynthetic gene clusters of antibiotics[9–11], including that of lincomycin A, suggesting that MSH *S*-conjugation is associated with the production of these antibiotics. Lincomycin A consists of an *N*-methylated 4-propyl-L-proline (PPL) moiety and lincosamide, an unusual eight-carbon sugar decorated with a methylmercapto group at C-1 (Fig. 1d). Cell protection against the activity of lincomycin A depends largely on methylation of the bacterial ribosome, whereby the molecule mimics the 3′ end of (de)acetyl-tRNA and blocks protein synthesis at the initial stage of the elongation cycle[13,14]. This fact, in combination with the methylmercapto group found in the structure, leads to the proposal that MSH *S*-conjugation has a constructive role in lincomycin biosynthesis by supplying sulfur rather than a protective role in antibiotic detoxification. To validate this hypothesis, we inactivated *lmbE*, a *mca* orthologue that is located in the lincomycin biosynthetic gene cluster (*lmb*) in *Streptomyces lincolnensis*[15,16] (Extended Data Fig. 2a).

As anticipated, the *ΔlmbE* mutant strain accumulated a MSH-associated lincomycin analogue, **1** (Fig. 2). In this molecule, the C8-sugar unit is appended to MSH via an α,*S*-linkage (Supplementary Text), identical to that of lincomycin A in configuration. The *ΔlmbE* mutant strain still produced lincomycin A, albeit in a lower yield, indicating that an additional *mca* orthologue is present outside the *lmb* cluster and partially

Figure 1 | Representative low-molecular-mass thiols, relevant metabolic pathways, and associated lincosamide natural products. a, Structures of the thiols GSH, MSH and EGT. **b**, Biosynthetic pathway of MSH and its typical associated detoxification process (shown in the dashed rectangle). GlcN-Ins is recyclable as an intermediate or product. **c**, Biosynthetic pathway of EGT. EgtD is an *S*-adenosyl methionine-dependent protein that catalyses the first reaction. **d**, Structures of the lincosamide antibiotics lincomycin A and celesticetin.

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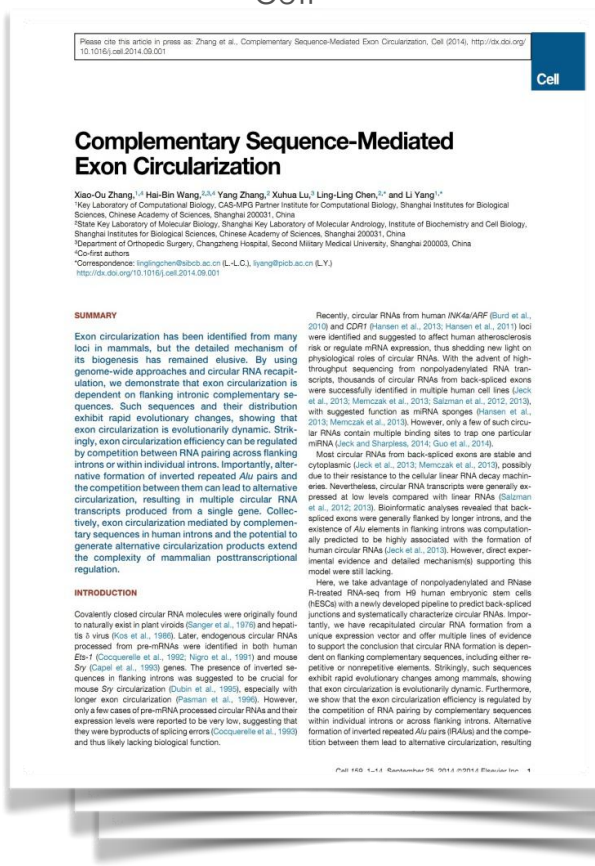
*These authors contributed equally to this work.

Cell



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Cell

Complementary Sequence-Mediated Exon Circularization

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http://dx.doi.org/10.1016/j.cell.2014.09.001

SUMMARY

Exon circularization has been identified from many loci in mammals, but the detailed mechanism of its biogenesis has remained elusive. By using genome-wide approaches and circular RNA recapitulation, we demonstrate that exon circularization is dependent on flanking intronic complementary sequences. Such sequences and their distribution exhibit rapid evolutionary changes, showing that exon circularization is evolutionarily dynamic. Strikingly, exon circularization efficiency can be regulated by competition between RNA pairing across flanking introns or within individual introns. Importantly, alternative formation of inverted repeated *Alu* pairs and the competition between them can lead to alternative circularization, resulting in multiple circular RNA transcripts produced from a single gene. Collectively, exon circularization mediated by complementary sequences in human introns and the potential to generate alternative circularization products extend the complexity of mammalian posttranscriptional regulation.

INTRODUCTION

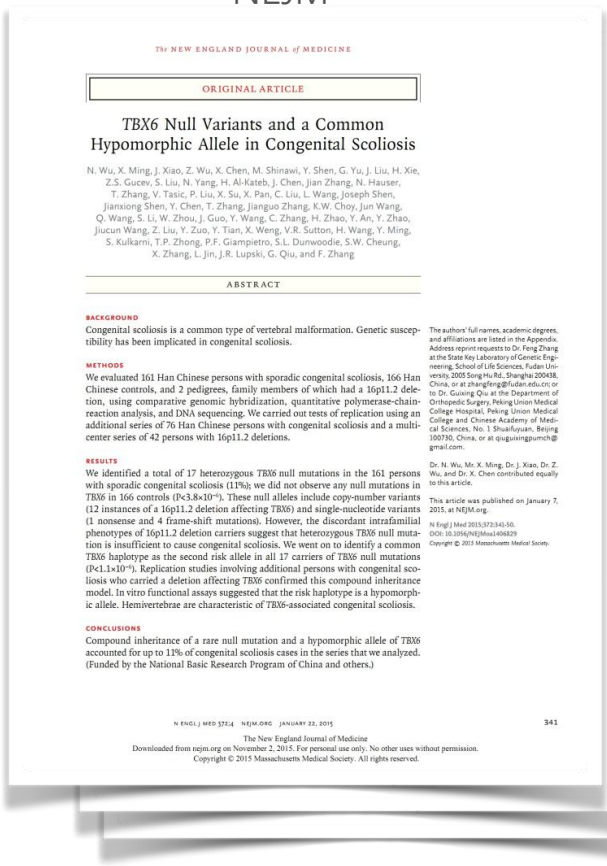
Covalently closed circular RNA molecules were originally found to naturally exist in plant viroids (Sanger et al., 1976) and hepatitis δ virus (Kos et al., 1986). Later, endogenous circular RNAs processed from pre-mRNAs were identified in both human *Ets-1* (Cocquerelle et al., 1992; Nigro et al., 1991) and mouse *Sry* (Capel et al., 1993) genes. The presence of inverted sequences in flanking introns was suggested to be crucial for mouse *Sry* circularization (Dubin et al., 1995), especially with longer exon circularization (Pasman et al., 1996). However, only a few cases of pre-mRNA processed circular RNAs and their expression levels were reported to be very low, suggesting that they were byproducts of splicing errors (Cocquerelle et al., 1993) and thus likely lacking biological function.

Recently, circular RNAs from human *INK4a/ARF* (Burd et al., 2010) and *CDR1* (Hansen et al., 2013; Hansen et al., 2011) loci were identified and suggested to affect human atherosclerosis risk or regulate mRNA expression, thus shedding new light on physiological roles of circular RNAs. With the advent of high-throughput sequencing from nonpolyadenylated RNA transcripts, thousands of circular RNAs from back-spliced exons were successfully identified in multiple human cell lines (Jeck et al., 2013; Memczak et al., 2013; Salzman et al., 2012, 2013), with suggested function as miRNA sponges (Hansen et al., 2013; Memczak et al., 2013). However, only a few of such circular RNAs contain multiple binding sites to trap one particular miRNA (Jeck and Sharpless, 2014; Guo et al., 2014).

Most circular RNAs from back-spliced exons are stable and cytoplasmic (Jeck et al., 2013; Memczak et al., 2013), possibly due to their resistance to the cellular linear RNA decay machineries. Nevertheless, circular RNA transcripts were generally expressed at low levels compared with linear RNAs (Salzman et al., 2012; 2013). Bioinformatic analyses revealed that back-spliced exons were generally flanked by longer introns, and the existence of *Alu* elements in flanking introns was computationally predicted to be highly associated with the formation of human circular RNAs (Jeck et al., 2013). However, direct experimental evidence and detailed mechanism(s) supporting this model were still lacking.

Here, we take advantage of nonpolyadenylated and RNase R-treated RNA-seq from H9 human embryonic stem cells (hESCs) with a newly developed pipeline to predict back-spliced junctions and systematically characterize circular RNAs. Importantly, we have recapitulated circular RNA formation from a unique expression vector and offer multiple lines of evidence to support the conclusion that circular RNA formation is dependent on flanking complementary sequences, including either repetitive or nonrepetitive elements. Strikingly, such sequences exhibit rapid evolutionary changes among mammals, showing that exon circularization is evolutionarily dynamic. Furthermore, we show that the exon circularization efficiency is regulated by the competition of RNA pairing by complementary sequences within individual introns or across flanking introns. Alternative formation of inverted repeated *Alu* pairs (IRAlus) and the competition between them lead to alternative circularization, resulting

NEJM



THE NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

TBX6 Null Variants and a Common Hypomorphic Allele in Congenital Scoliosis

N. Wu, X. Ming, J. Xiao, Z. Wu, X. Chen, M. Shinawi, Y. Shen, G. Yu, J. Liu, H. Xie, Z.S. Gucev, S. Liu, N. Yang, H. Al-Kateb, J. Chen, Jian Zhang, N. Hauser, T. Zhang, V. Tasic, P. Liu, X. Su, X. Pan, C. Liu, L. Wang, Joseph Shen, Jianxiong Shen, Y. Chen, T. Zhang, Jianguo Zhang, K.W. Choy, Jun Wang, Q. Wang, S. Li, W. Zhou, J. Guo, Y. Wang, C. Zhang, H. Zhao, Y. An, Y. Zhao, Jiucun Wang, Z. Liu, Y. Zuo, Y. Tian, X. Weng, V.R. Sutton, H. Wang, Y. Ming, S. Kulkarni, T.P. Zhong, P.F. Giampietro, S.L. Dunwoodie, S.W. Cheung, X. Zhang, L. Jin, J.R. Lupski, G. Qiu, and F. Zhang

ABSTRACT

BACKGROUND

Congenital scoliosis is a common type of vertebral malformation. Genetic susceptibility has been implicated in congenital scoliosis.

METHODS

We evaluated 161 Han Chinese persons with sporadic congenital scoliosis, 166 Han Chinese controls, and 2 pedigrees, family members of which had a 16p11.2 deletion, using comparative genomic hybridization, quantitative polymerase-chain-reaction analysis, and DNA sequencing. We carried out tests of replication using an additional series of 76 Han Chinese persons with congenital scoliosis and a multicenter series of 42 persons with 16p11.2 deletions.

RESULTS

We identified a total of 17 heterozygous *TBX6* null mutations in the 161 persons with sporadic congenital scoliosis (11%); we did not observe any null mutations in *TBX6* in 166 controls ($P<3.8\times10^{-5}$). These null alleles include copy-number variants (12 instances of a 16p11.2 deletion affecting *TBX6*) and single-nucleotide variants (1 nonsense and 4 frame-shift mutations). However, the discordant intrafamilial phenotypes of 16p11.2 deletion carriers suggest that heterozygous *TBX6* null mutation is insufficient to cause congenital scoliosis. We went on to identify a common *TBX6* haplotype as the second risk allele in all 17 carriers of *TBX6* null mutations ($P<1.1\times10^{-4}$). Replication studies involving additional persons with congenital scoliosis who carried a deletion affecting *TBX6* confirmed this compound inheritance model. In vitro functional assays suggested that the risk haplotype is a hypomorphic allele. Hemivertebrae are characteristic of *TBX6*-associated congenital scoliosis.

CONCLUSIONS

Compound inheritance of a rare null mutation and a hypomorphic allele of *TBX6* accounted for up to 11% of congenital scoliosis cases in the series that we analyzed. (Funded by the National Basic Research Program of China and others.)

The authors' full names, academic degrees, and affiliations are listed in the Appendix. Address reprint requests to Dr. Feng Zhang at the State Key Laboratory of Genetic Engineering, School of Life Sciences, Fudan University, 2005 Songhu Rd., Shanghai 200438, China, or at zhangfeng@fudan.edu.cn; or to Dr. Guixing Qiu at the Department of Orthopedic Surgery, Peking Union Medical College Hospital, Peking Union Medical College and Chinese Academy of Medical Sciences, No. 1 Shuaifuyuan, Beijing 100730, China, or at qiuguixingpumch@gmail.com.

Dr. N. Wu, Mr. X. Ming, Dr. J. Xiao, Dr. Z. Wu, and Dr. X. Chen contributed equally to this article.

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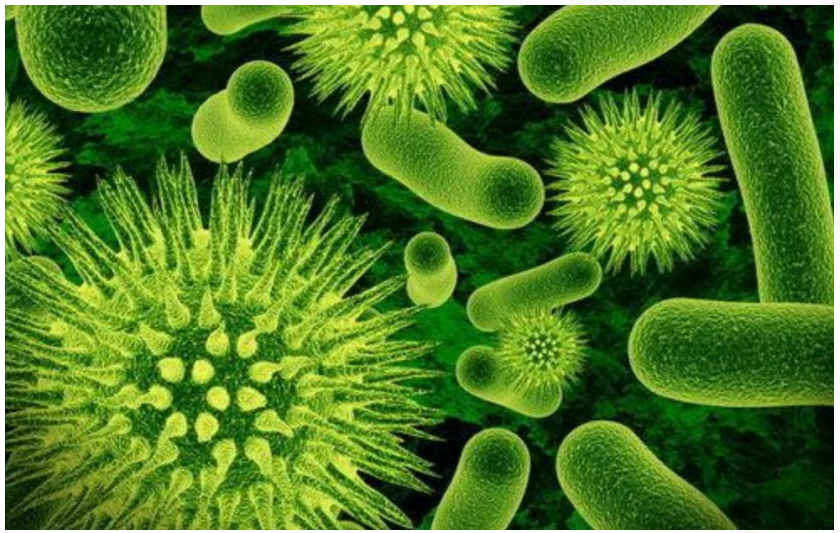
N Engl J Med 2015;372:341-50.
DOI: 10.1056/NEJMoa1406829

感染类疾病是威胁国民健康一大杀手

柳叶刀--2016全球疾病负担研究-死亡率、死因、328种疾病数据
(Lancet, Global Burden of Disease Study 2016, GBD)

- 2016年全球死亡人数为5470万，感染类疾病的死亡率为19.5%；
- 5岁以下儿童的第一大死因为下呼吸道感染；
- 在中国，发病率最高的疾病是上呼吸道感染。



常用感染鉴别手段具有局限性

检测手段		局限性
血常规	白细胞 中性粒细胞	严重感染时，由于骨髓抑制，白细胞反而不升高，不能客观的反应感染的真实情况
胸部影像	胸片	敏感度和特异度较差，可能漏诊
	胸部CT	敏感度和特异度优于胸片，但费用昂贵，辐射量大，不适用于危重患者
微生物学检查		“金标准” 耗时长，病原体检出率易受其他因素影响
CRP		升高缓慢（36h），对部分病毒感染也敏感

诊断不准确导致抗生素滥用

中国使用了全球一半的抗生素，住院患者抗生素使用率达*70%*，抗生素用药比例占据了儿童用药总体市场的 *88*%

抗生素仅仅适用于细菌引起的炎症，**对由病毒引起的炎症无效**

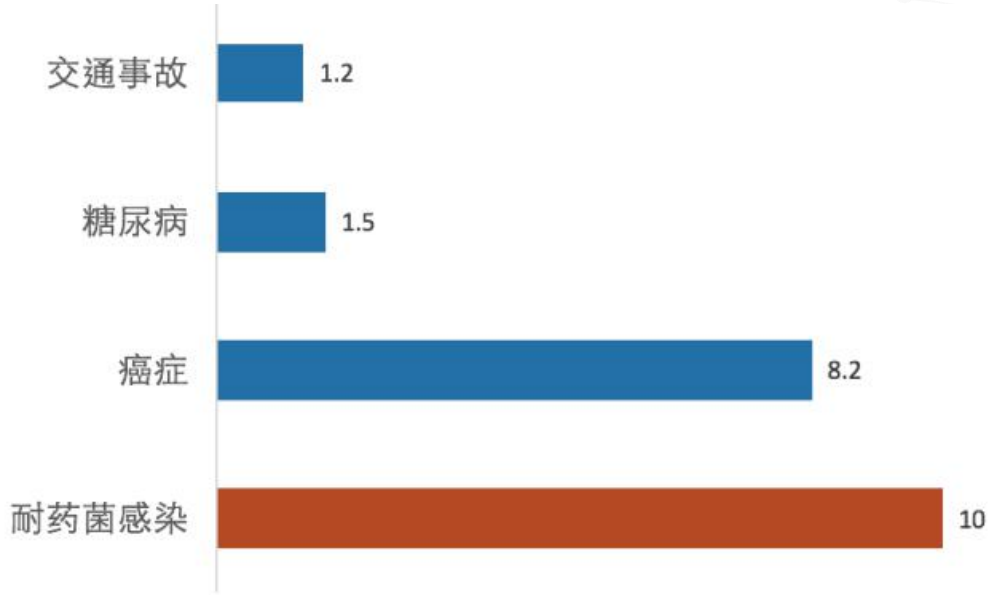
近日，**国家卫健委**再次发出《关于持续做好抗菌药物临床应用管理有关工作的通知》,强调进一步加强抗菌药物临床应用管理,**限制抗生素的使用再次升级。**

限制抗生素的使用再次升级，管控抗生素滥用！

耐药菌感染导致死亡率增加

抗生素的研究与开发速度远远跟不上细菌的耐药速度

2050年：预计全球致死因素分布（百万人）



每年全球约70万人死于耐药菌感染，23万新生儿因此不治夭折，到了2050年，每3秒就会有1人死于耐药菌

Review on Antimicrobial Resistance, 2014
CDC Antibiotic Resistance Threats,

炎症标志物提高诊断准确度和及时性

降钙素原(PCT)

——指导抗生素用药“金标准”

血清淀粉样蛋白A(SAA)

——病毒感染检测新指标

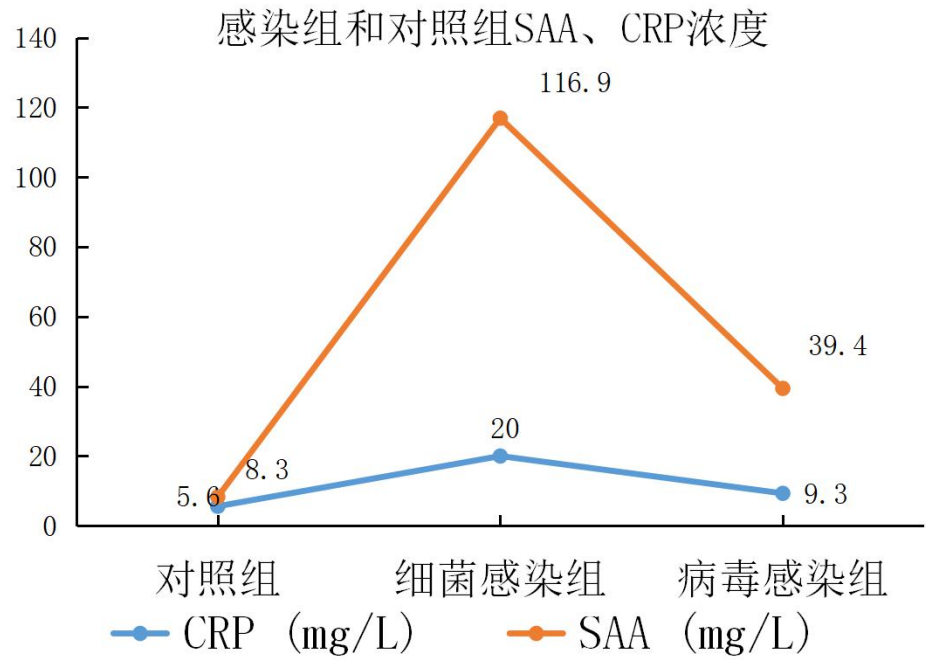
C-反应蛋白(CRP)

——细菌感染诊断经典指标

PCT、SAA与CRP的特点

	细菌感染	病毒感染
PCT	感染时**快速升高**，与感染严重程度相关，反映感染好转	不升高或轻微升高
SAA	感染时**快速升高**，与感染严重程度相关，反映感染好转	感染时**快速升高**，与感染严重程度相关，反映感染好转
CRP	感染后36小时升高，与感染严重程度相关，反映感染好转（特异性较差）	部分病毒感染后显著升高

SAA/CRP用于门诊感染鉴别诊断



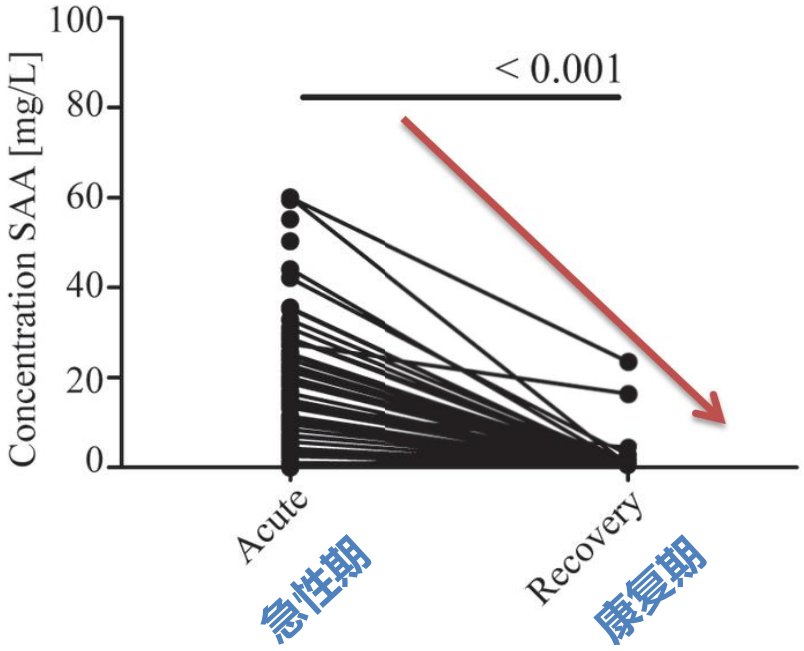
项目	病毒	细菌
SAA	明显↑	明显↑
CRP	升高幅度低	明显↑

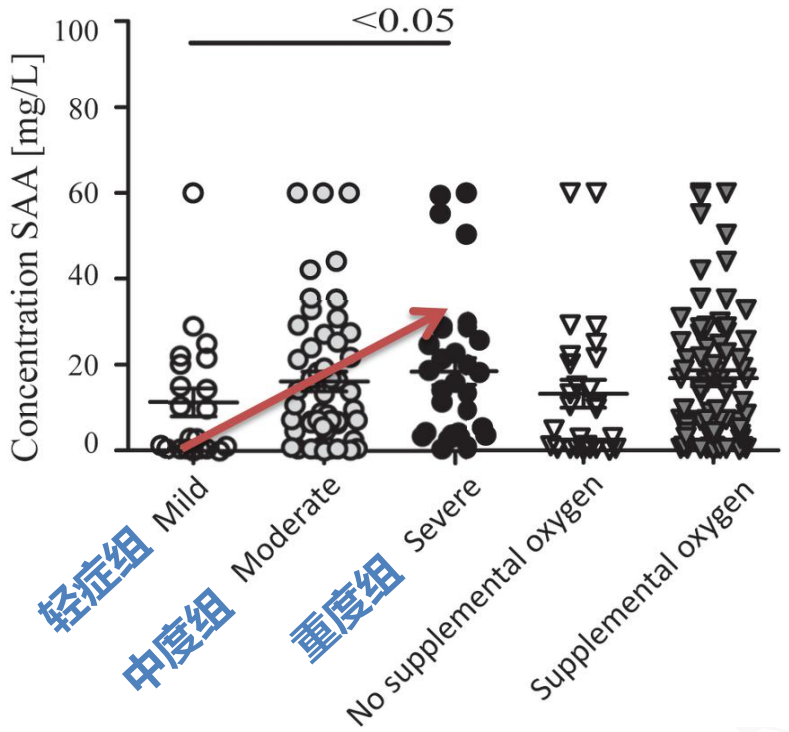
1、SAA和CRP可作为细菌感染的诊断指标。

2、联合检测SAA和CRP能更快速、准确地诊断病毒感染，为疾病的早期诊断和后续治疗提供有效的实验依据。

杨剑敏等，CRP和SAA在儿童上呼吸道感染中的鉴别诊断价值，检验医学，2016.

SAA指导抗病毒治疗





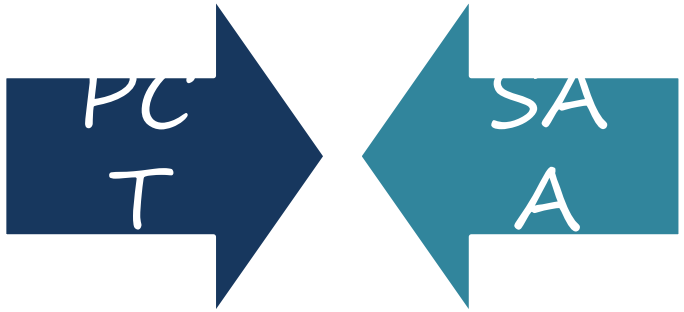
1、SAA反映儿童下呼吸道感染的好转情况。

2、SAA的浓度随着疾病轻度，中度，重度上升，反映了疾病的严重程度。

Inge M L Ahout,et al. Prospective observational study in two Dutch hospitals to assess theperformance of inflammatory plasma markers to determine disease severity of viralrespiratory tract infections in children. Bmj Open, 2017.

PCT/SAA用于急诊、住院感染鉴别诊断

细菌感染特异性高



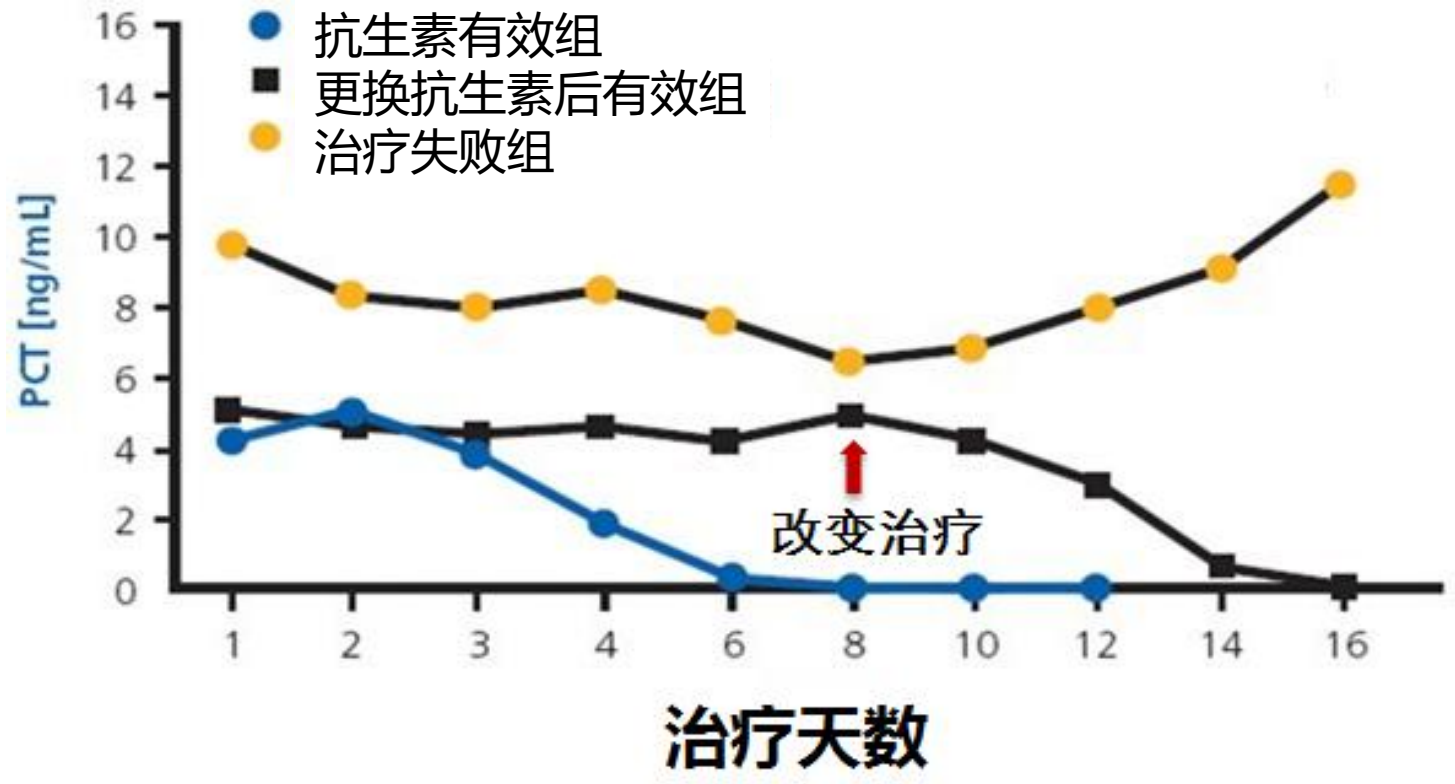
对感染灵敏度高

升高	**升高**
不升高	**升高**

细菌感染

病毒感染

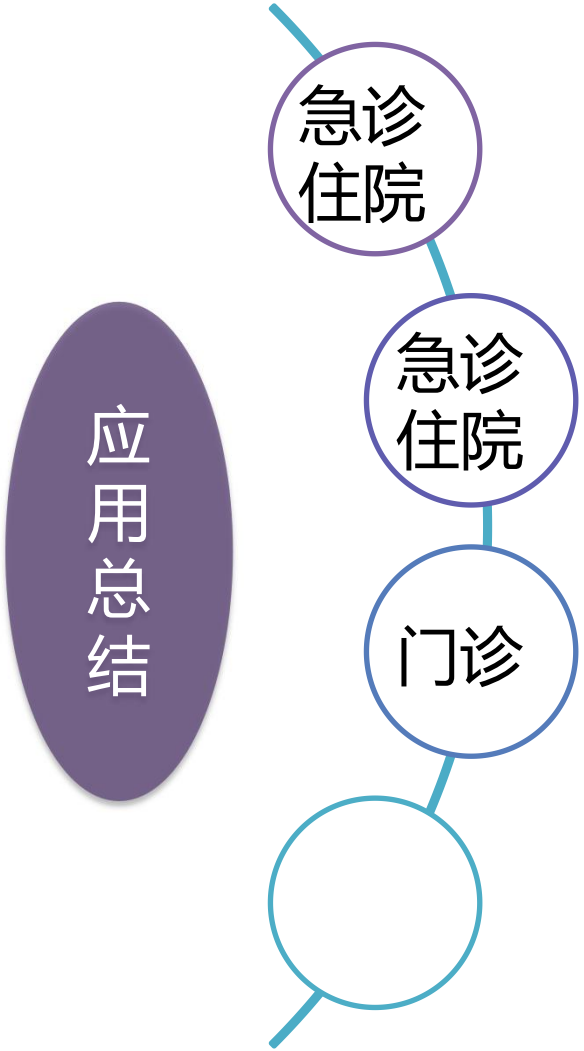
PCT用于急诊、住院抗生素指导



2016《降钙素原(PCT)急诊临床应用的专家共识》指出：

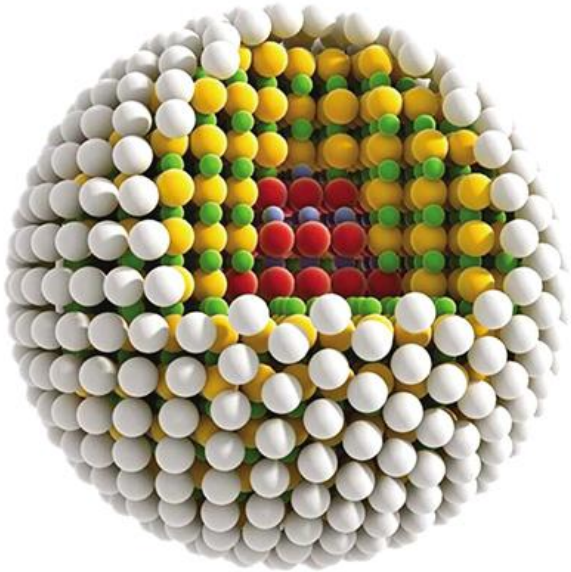
- 疗效判断标准：PCT浓度在治疗开始三天内每天下降30%。
- 确定抗生素疗程：PCT浓度下降80%建议停用抗生素，下降90%强烈建议停用抗生素。

PCT/SAA/CRP适用于不同诊断场景



什么是量子点

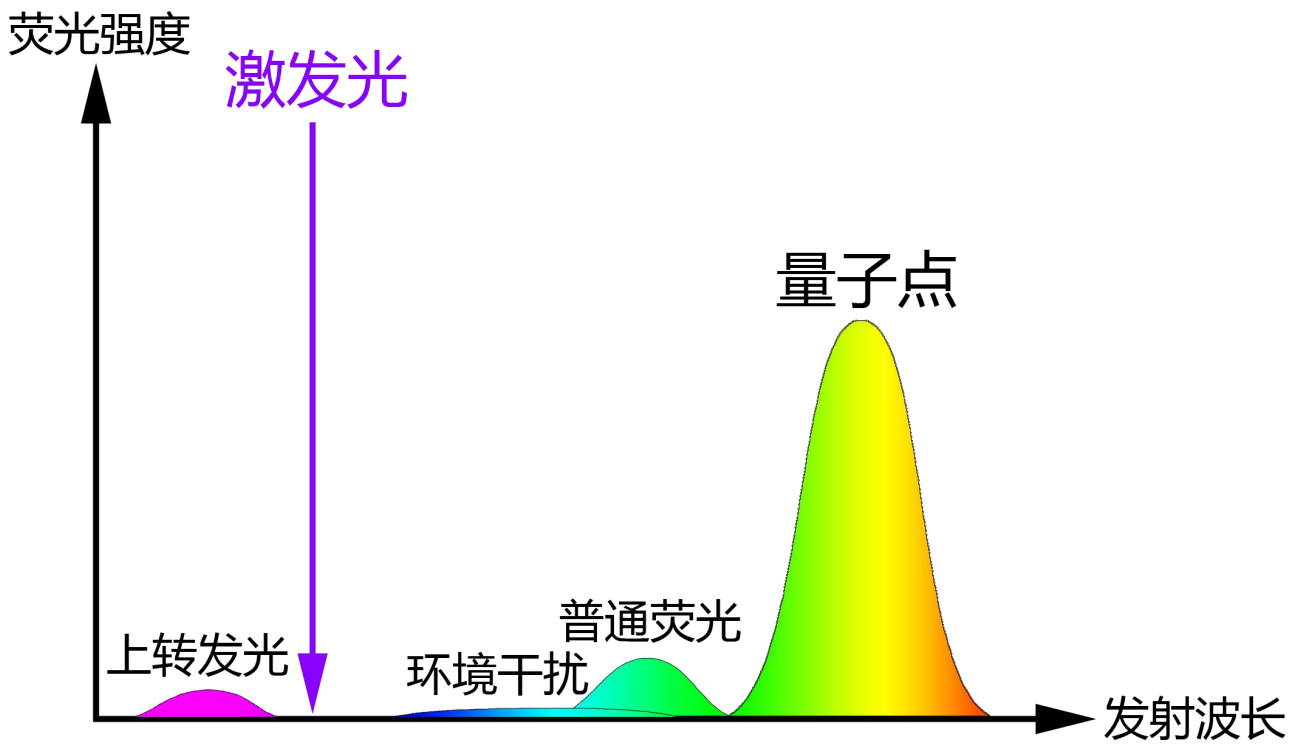
Quantum Dots，量子点



- 是指空间三个维度上存在量子限域效应的半导体纳米晶材料，粒径介于1-10nm，具有独特的光学特性，是新一代荧光标记探针的最佳选择。

- 2003年被《SCIENCE》评为**“十大科学突破”**
- 《国家中长期科学和技术发展规划》中将量子调控研究作为**重大科学研究计划**之一

量子点的优势



新一代荧光材料

✓荧光产率是普通荧光素的60倍

——高灵敏度

✓斯托克位移大，不受环境荧光干扰

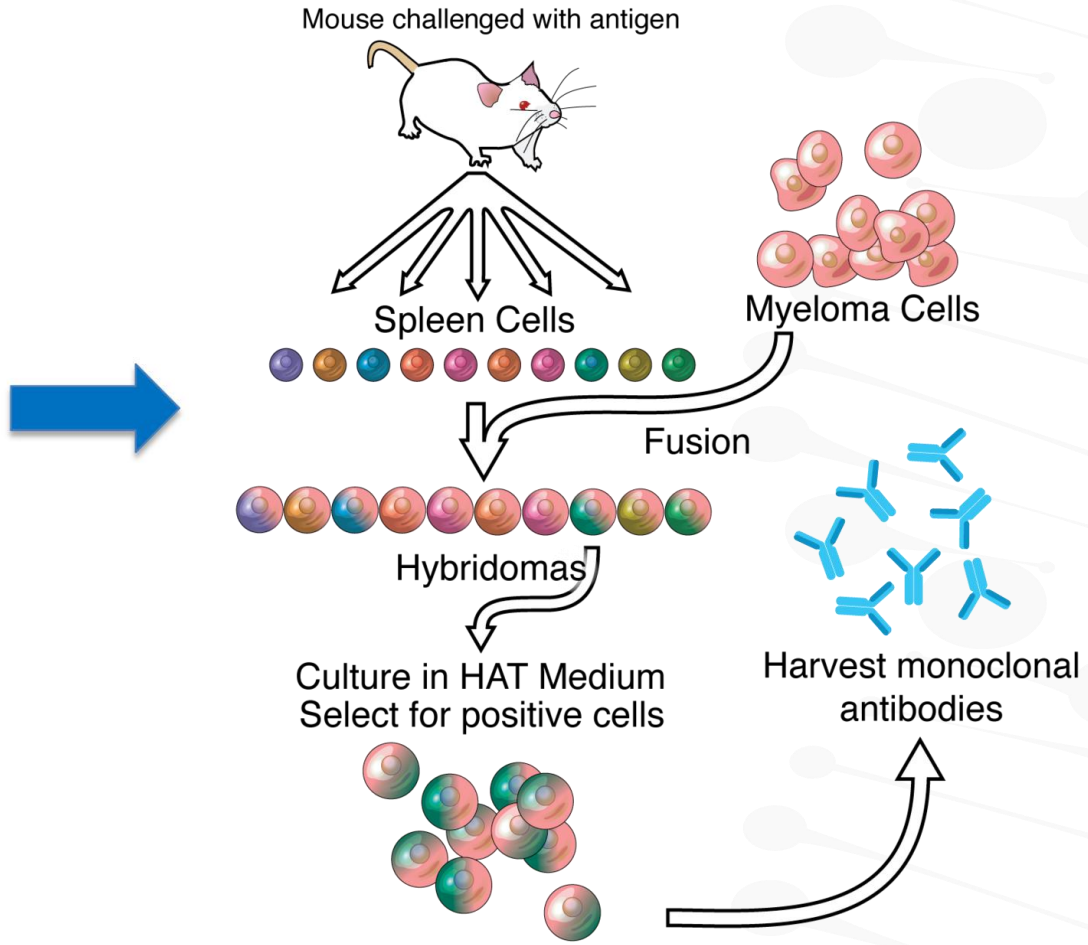
——高特异性

✓“永不淬灭”，持续激发6个月荧光损失< 5%

——高稳定性

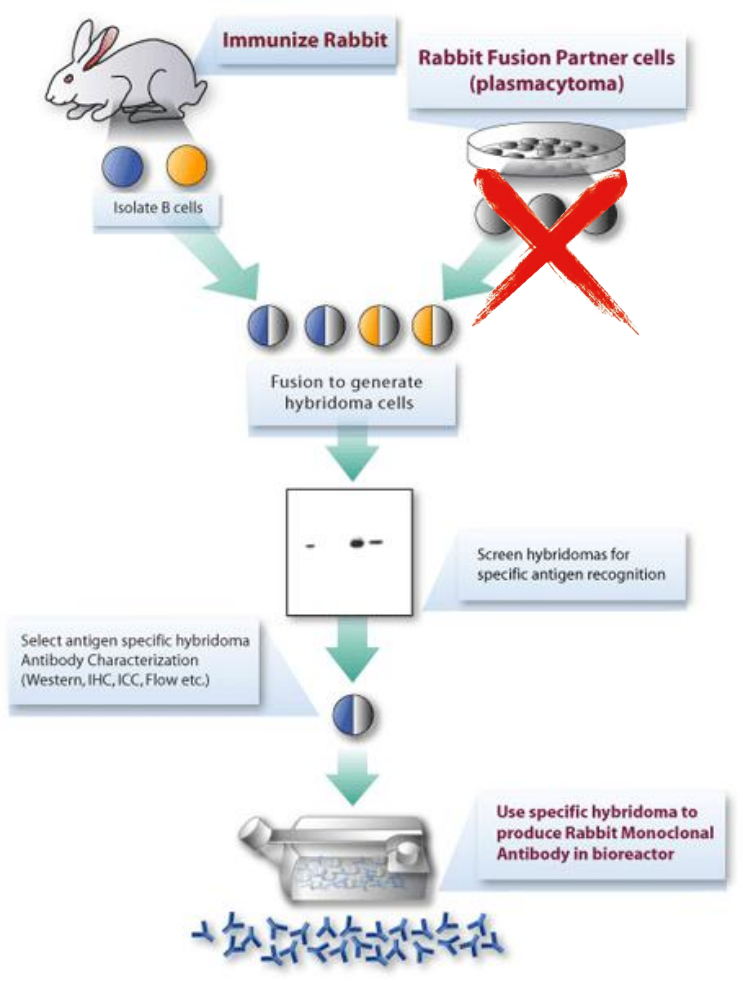
诺唯赞拥有国内领先诊断抗体开发技术

- 凋亡基因敲除和促融合基因整合染色体的改造后骨髓瘤融合细胞，融合效率提升**100**倍，抗体筛选成功率大幅度提高；
- 单次免疫可获得大量可用单抗，更容易筛选到**高亲和力高特异性**抗体，时间为传统方法的1/5
- 融合后**无血清表达**即可获得极高产量，可达**2-8 g/L**



该平台目前已经成功筛选60余种靶抗原的配对抗体，细胞库保存杂交瘤细胞2万多株。

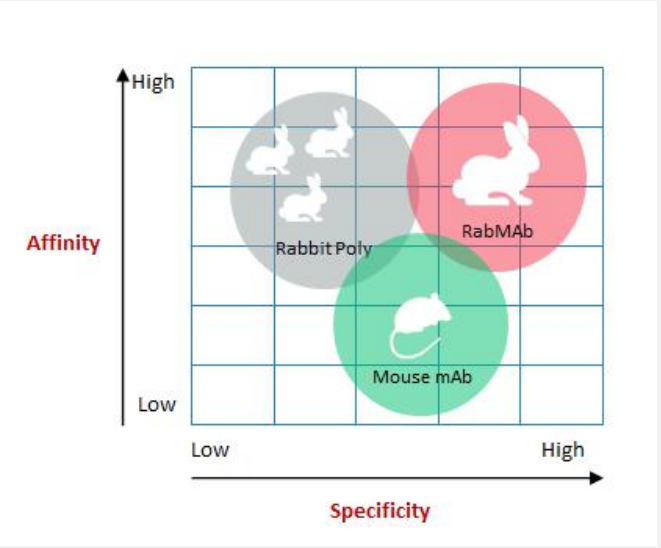
单细胞测序兔单克隆抗体筛选



无需细胞融合，单个B细胞基因测序直接获得抗体DNA序列

改造的高表达载体克隆

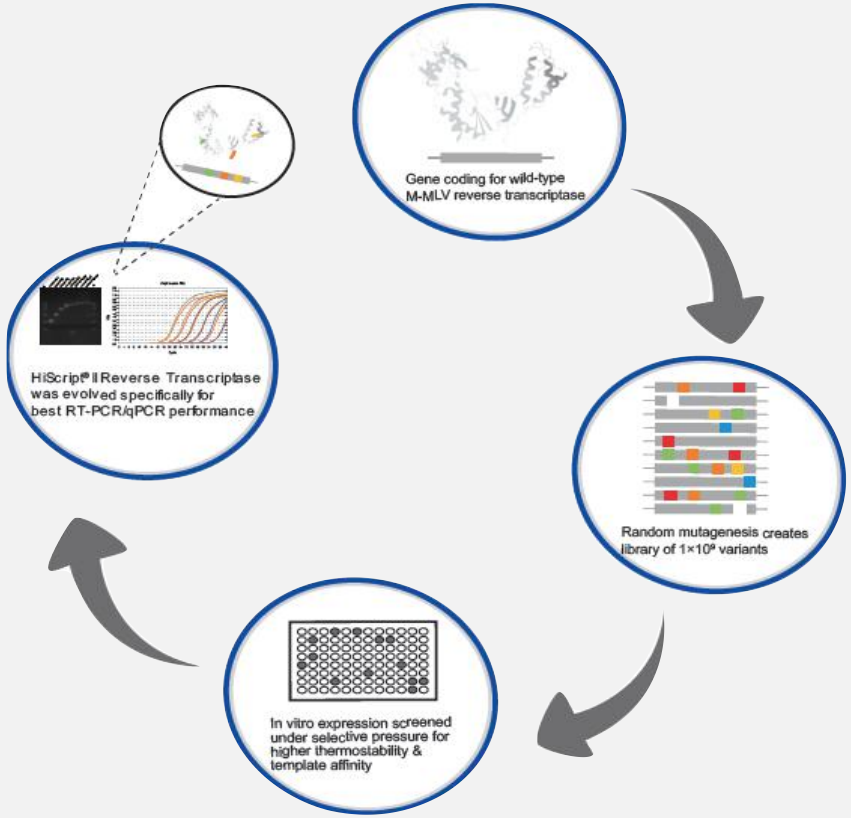
改造的高产细胞系无血清发酵生产



兔单抗亲和力是小鼠的**100-1000**倍

完成**8种**靶抗原抗体制备

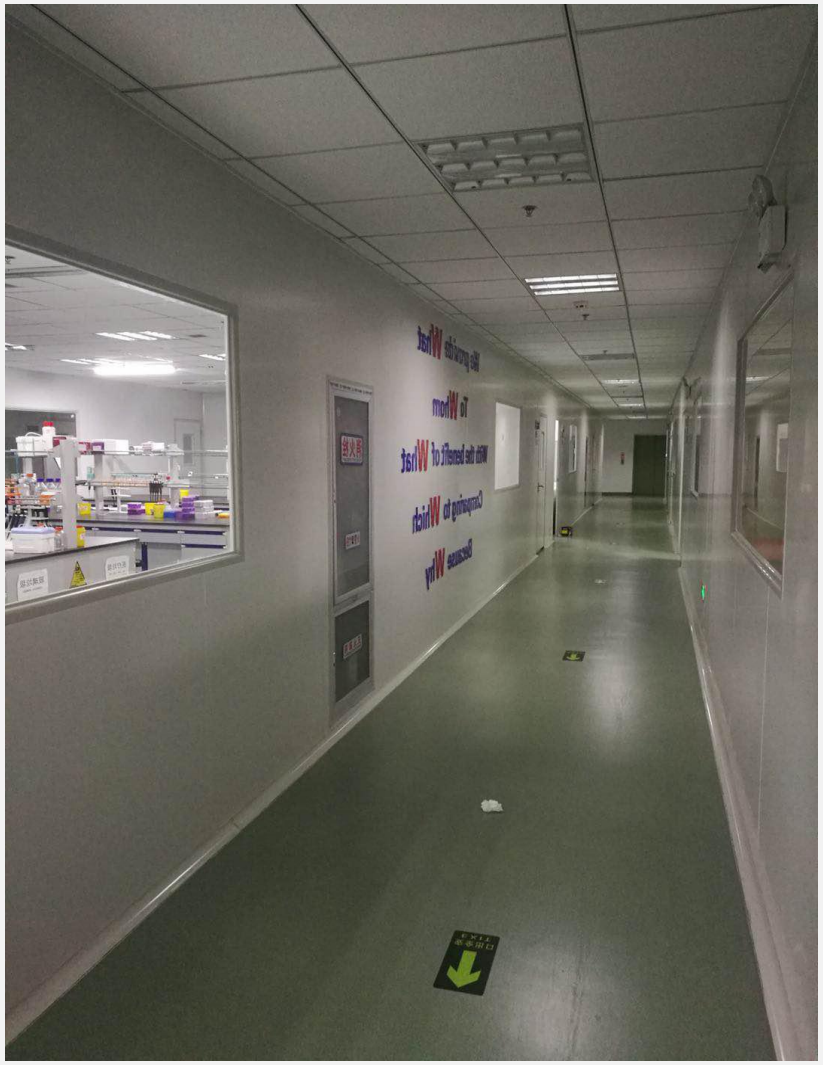
重组抗原哺乳动物细胞表达技术

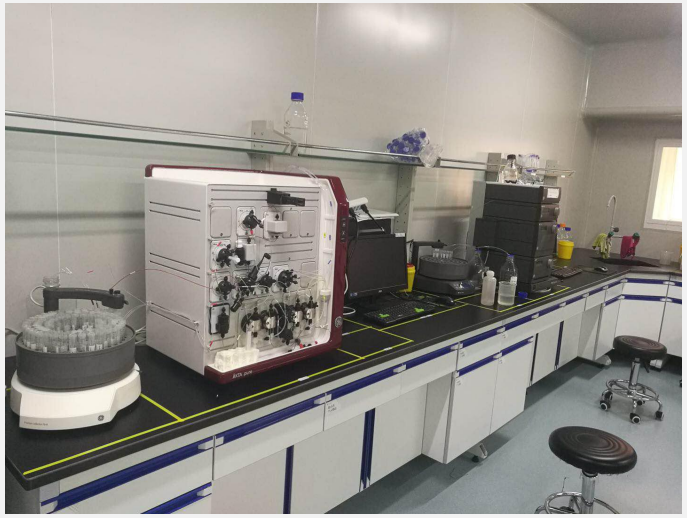


哺乳动物表达——保证复杂蛋白天然性

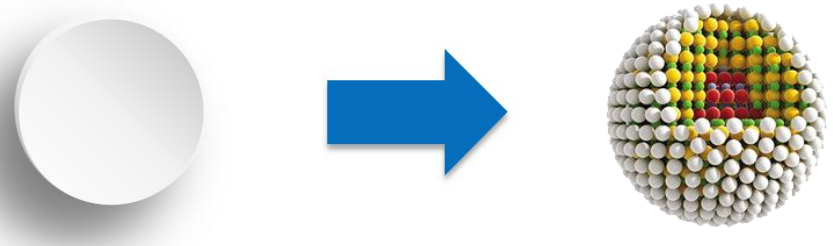
- 哺乳动物表达系统，mRNA翻译系统、翻译后修饰、蛋白质构象最接近人细胞，所得抗原最接近天然蛋白
- 掌握10+诊断原料相关发明专利、**一套自主知识产权的顺式原件表达调控载体**（满足膜蛋白、毒蛋白、高糖基化修饰等多种蛋白表达需求）
- 基于自研原料开发出Lp-PLA2、AMH、anti-PLA2R等多种新产品
- 受中检院委托研发5种国家标准物质（LP-PLA2、PCT、SAA、MYO、NT-proBNP）

无血清蛋白质生产平台



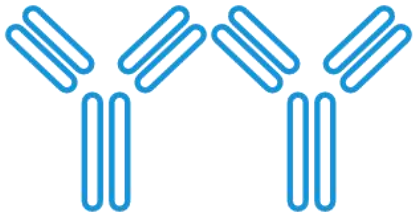


诺唯赞量子点精准检测技术



水溶性量子点修饰技术

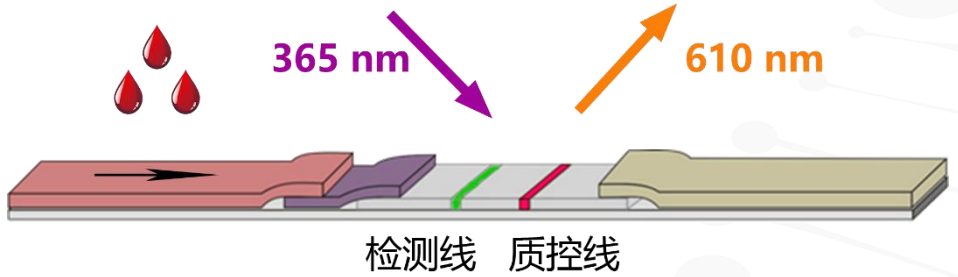
产品稳定性好，耐受非特异性干扰



高特异性、高亲和力单克隆抗体

检测灵敏度和特异性高

量子点技术与“优选”单抗有机结合

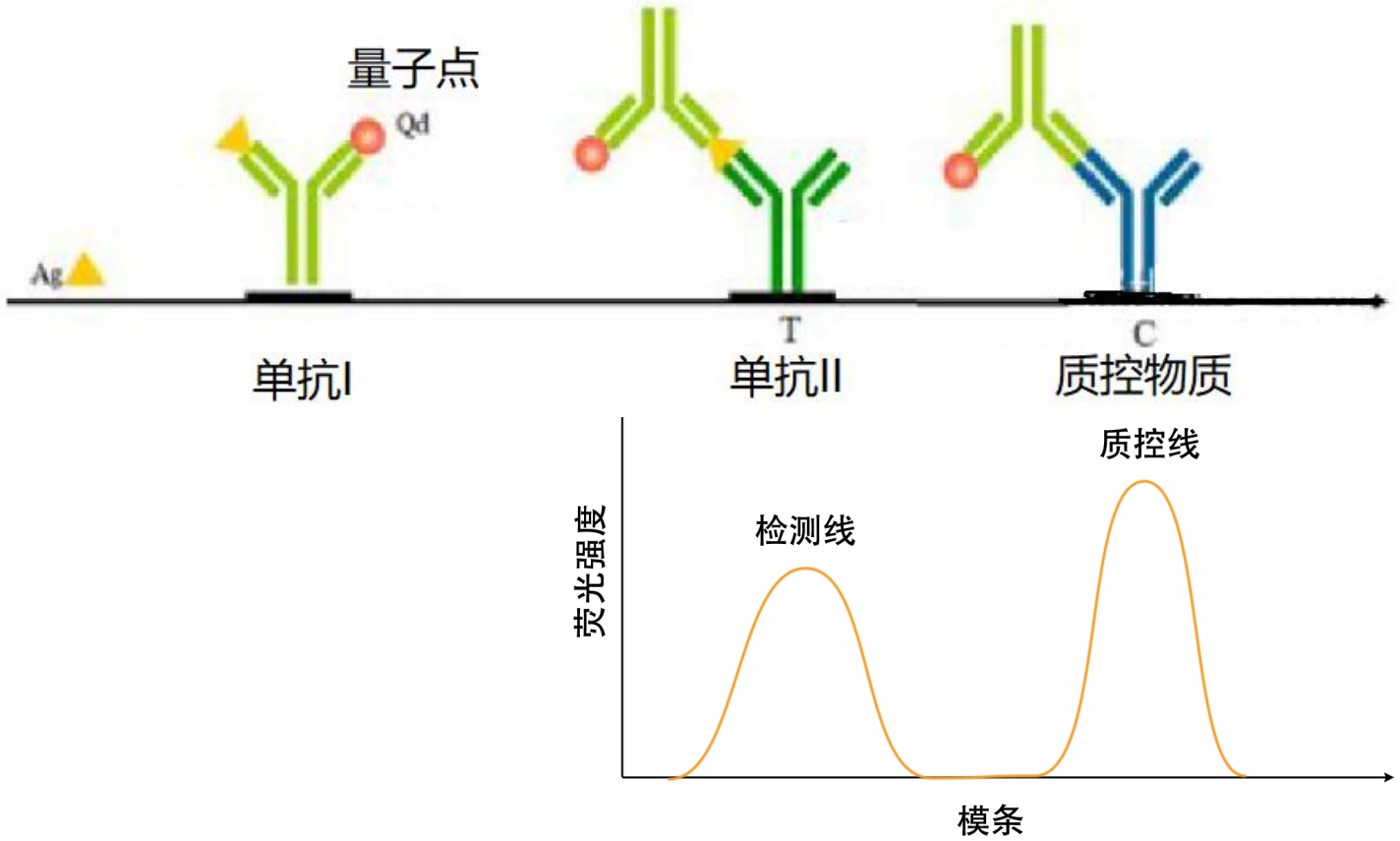


兼容全血检测

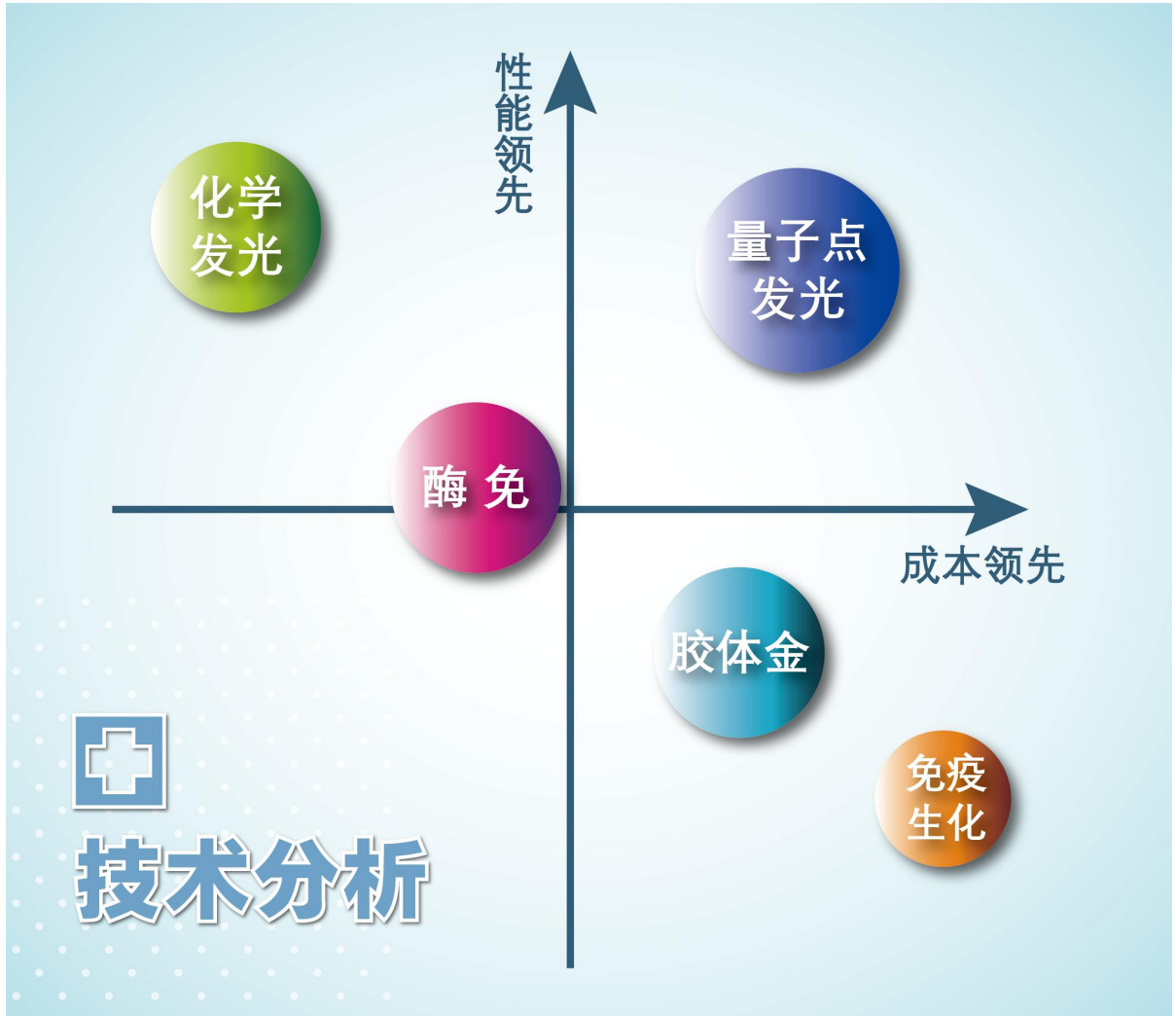
PCT功能灵敏度

0.02 ng/ml

量子点荧光免疫检测原理

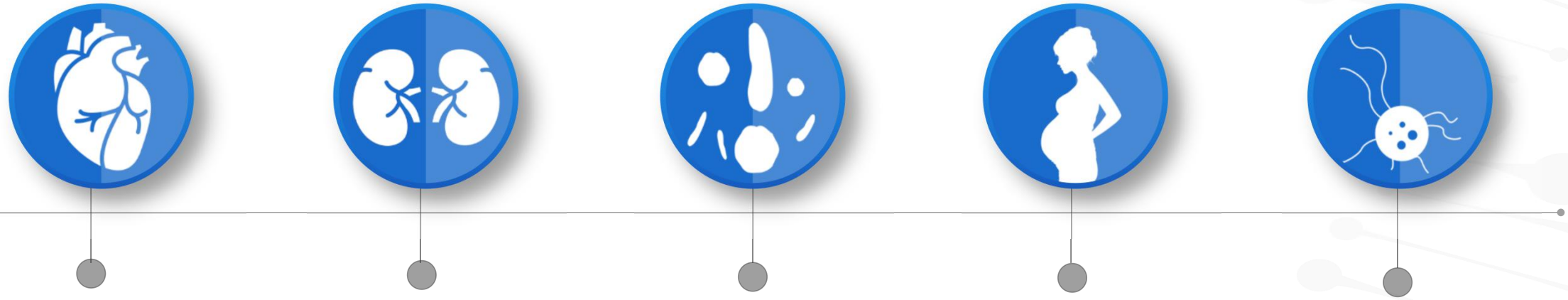


标志物浓度 = T线荧光值/C线荧光值
（内部质控体系，避免hook效应）



量子点检测技术具有
最佳的性价比

诺唯赞量子点技术产品线



心肌标志物	肾脏疾病	炎症（**末梢血**）	优生优育	肿瘤标志物
Lp-PLA2 NT-proBNP cTnI，MYO, CK-MB H-FABP, **hs-cTnI**, D-D	**NGAL** CYS-C RBP **anti-PLAR**	**PCT** **SAA** **CRP** IL-6	**AMH** β-HCG INHB	**PGI** **PGII** **G-17**

特点：产品性能领先

	PCT	CRP	SAA
样本类型	全血/血清/血浆/末梢血		
样本量	80 μL	10 μL	10 μL
检测范围	0.02 - 200 ng/mL	0.5 - 300 mg/L	5 - 300 mg/L
检测时间	15 min	5 min	5 min
精密度	≤ 10%		

兼容更多样本类型，操作更简便！

精密度≤10%，结果更准确！

PCT高敏检测，准确检测感染状态！

SAA/CRP快速检测，减少医生等待时间！

特点：检测操作便捷

单通道检测仪器

——随到随测，无需等待

12通道检测仪器

——12通道自由组合项目

全自动检测仪器即将推出

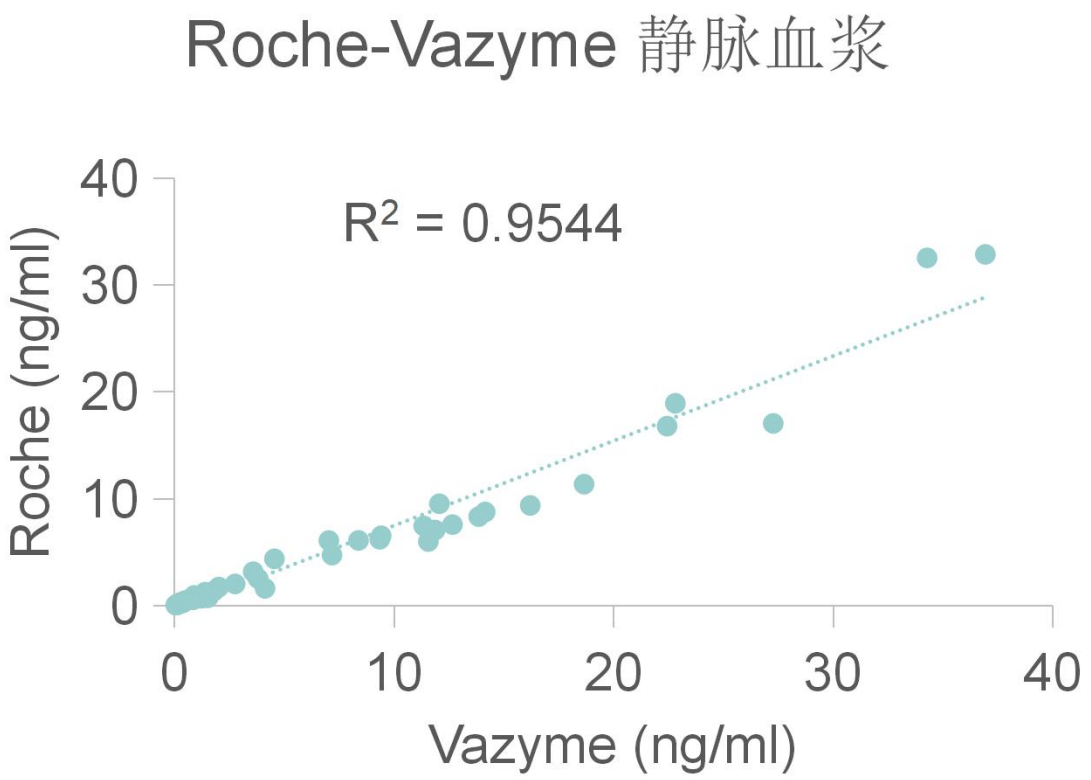
- ✓ 加样后单击屏幕，仪器自动完成检测；
- ✓ 可连接扫码枪及LIS系统，无需手动录入信息；
- ✓ 彩色触摸屏，反应灵敏，无需连接电脑；
- ✓ 自带热敏打印机，也可连接外部打印机；
- ✓ 兼容诺唯赞所有量子点检测试剂

诺唯赞PCT试剂性能评价

与江苏某三甲医院合作
研究PCT测定指尖血样本和静脉血样本的量值差异

序号	检测项目	检验标准	检验结果	是否合格
1	精密度	分析内变异系数（CV）不大于 10.0%	质控水平 1 CV=8.3% 质控水平 2 CV=6.1%	合格
2	线性范围验证	符合回归方程 Y= bX+m （相关系数大于 95%，0.95 ≤ b ≤ 1.05）	线性回归方程 Y= 1.0401X+0.0164 相关系数为 0.996	合格
3	与对比试剂的量值一致性	符合回归方程 Y= bX+m （相关系数大于 95%，0.95 ≤ b ≤ 1.05）	线性回归方程 Y=0.9852X+0.0712 相关系数为 0.9658	合格

诺唯赞PCT试剂临床评价

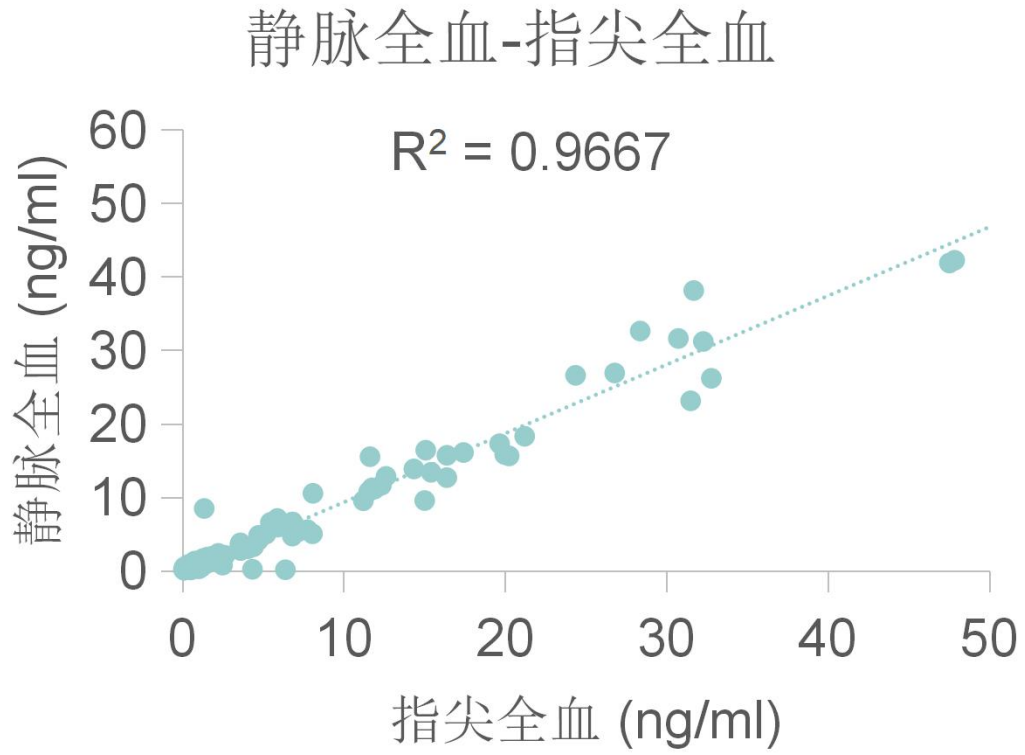


		Roche	
		阳性	阴性
Vazyme	阳性	35	0
	阴性	0	15

阳性符合率	100%	cut-off值	0.5 ng/ml
阴性符合率	100%		

在测定**静脉血浆**样本时，Vazyme PCT量子点荧光免疫试剂与Roche PCT化学发光试剂的**量值和临床诊断结果具有非常好的一致性**

诺唯赞PCT试剂指尖血临床评价



		Roche	
		阳性	阴性
Vazyme	阳性	98	8
	阴性	4	41

阳性符合率	**92%**	cut-off值	0.5 ng/ml
阴性符合率	**91%**		

指尖血检测PCT时某些干扰因素会在一定程度上影响检测结果准确性

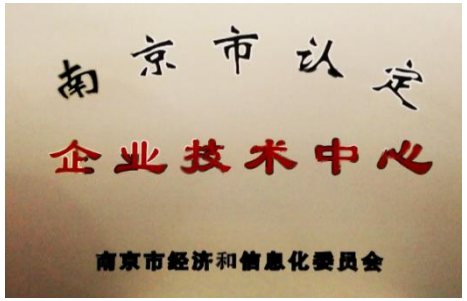
诺唯赞PCT指尖血检测试剂**经过临床验证及针对性研发，**准确度有保证

客户列表

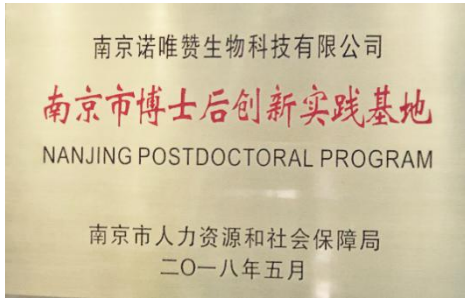
中国人民解放军第302医院（三甲）
中国人民解放军第307医院（三甲）
中国人民解放军第211医院（三甲）
宜兴市人民医院（三甲）
广州市第一人民医院（三甲）
湖南省人民医院马王堆分院（三甲）
湘雅医院（三甲）
增城人民医院（三甲）
惠州市中医院（三甲）
惠州第三人民医院（三甲）
中国医科大学第二附属医院（三甲）

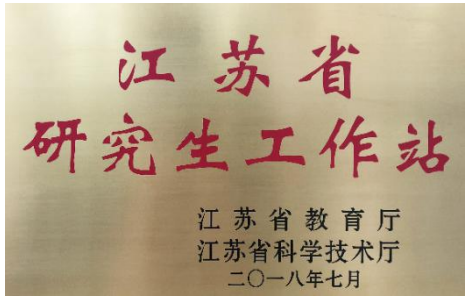
包头医学院第一附属医院（三甲）
吉林省人民医院（三甲）
吉林省妇幼保健院（三甲）
包头市第三医院（三级）
山西省儿童医院（三级）
航天中心医院（三级）
中国人民解放军国防大学医院（二级）
肇庆市第二人民医院（二甲）
北京市建宫医院（二甲）
华兆益生健康体检机构　　5A级体检中心

部分主要科技成果


南京市认定
企业技术中心
南京市经济和信息化委员会


授予
南京诺唯赞生物科技有限公司
2017年度江苏省
最具成长性高科技企业
100强


南京诺唯赞生物科技有限公司
南京市博士后创新实践基地
NANJING POSTDOCTORAL PROGRAM
南京市人力资源和社会保障局
二〇一八年五月


江苏省
研究生工作站
江苏省教育厅
江苏省科学技术厅
二〇一八年七月


南京市工程技术研究中心
南京市科学技术委员会
二〇一七年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二〇一七年


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生物医药行业总决赛成长组十二强。
中国创新创业大赛组委会
二〇一七年


证书
南京诺唯赞生物科技有限公司 曹林：
入选为创新人才推进计划科技创新创业人才，
特发此证。
第 2016RA3178 号
2017年6月15日


第二届江苏省科协青年会员创新创业大赛
生命科学领域（创新组）
一等奖
江苏省科学技术协会
二〇一七年十月


2017年南京市科技创新创业大赛
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特颁此证，以资鼓励！


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2017年8月


高新技术企业
证书


SGS
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ISO 9001:2015


CERTIFICATE

灵敏

特异

唯准

唯稳

快速

简便

感谢聆听

THANK YOU FOR LISTENING

唯稳 • 唯准 • 唯赞