



种业企业 知识产权信息分析

刘丽军 博士

中国农科院农业知识产权研究中心

2012年2月14日 北京



报告内容 contents

- 一. 知识产权信息
Intellectual Property information
- 二. 知识产权诊断
Intellectual Property audit
- 三. 知识产权提案
Invention management



开展知识产权信息分析 应对商业竞争

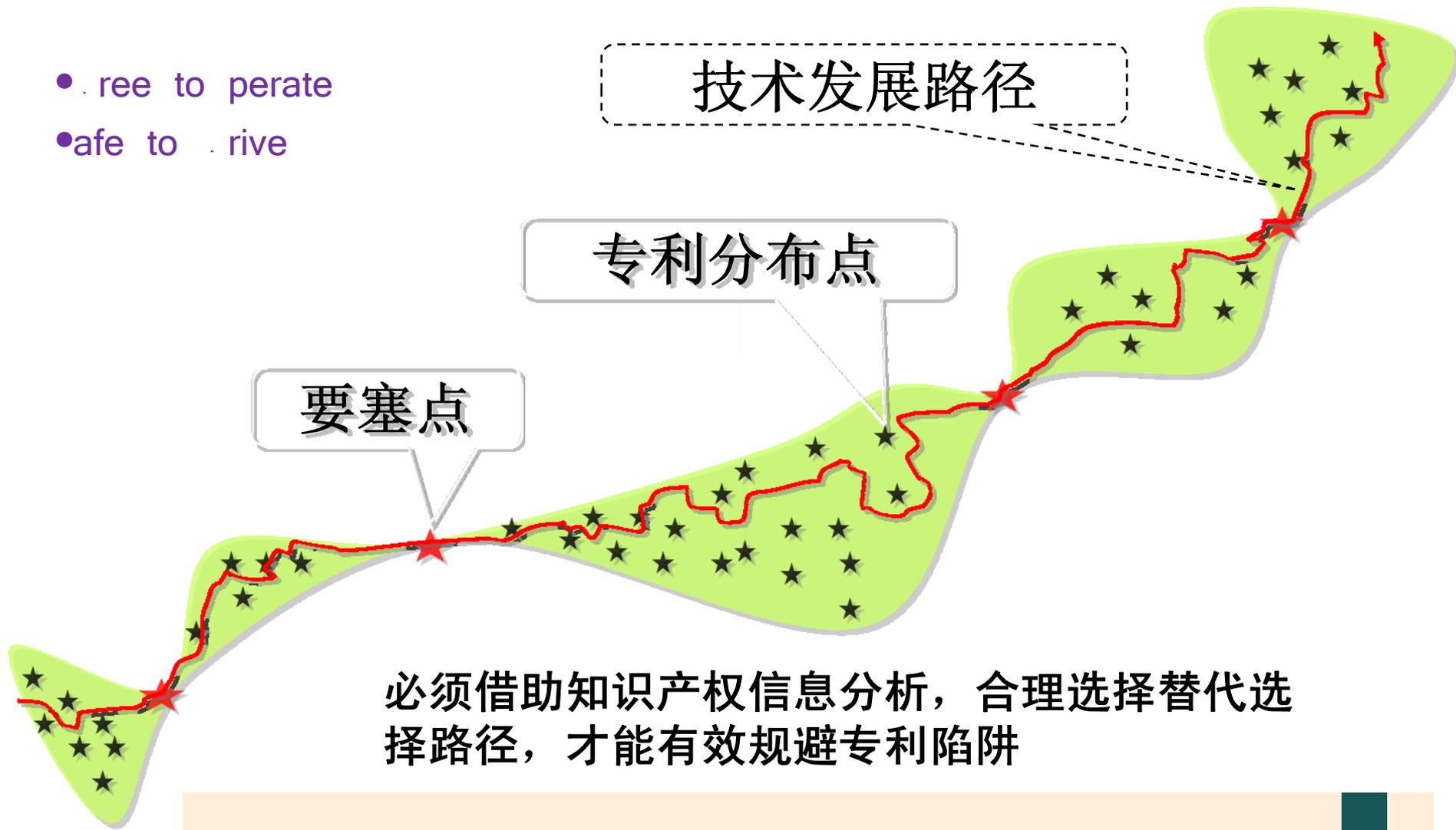
- free to perate
- safe to .rive

技术发展路径

专利分布点

要塞点

必须借助知识产权信息分析，合理选择替代选择路径，才能有效规避专利陷阱





- **提高研究效率，避免重复浪费**

缩短技术研发周期60%，节约科研经费40%--WIPO。

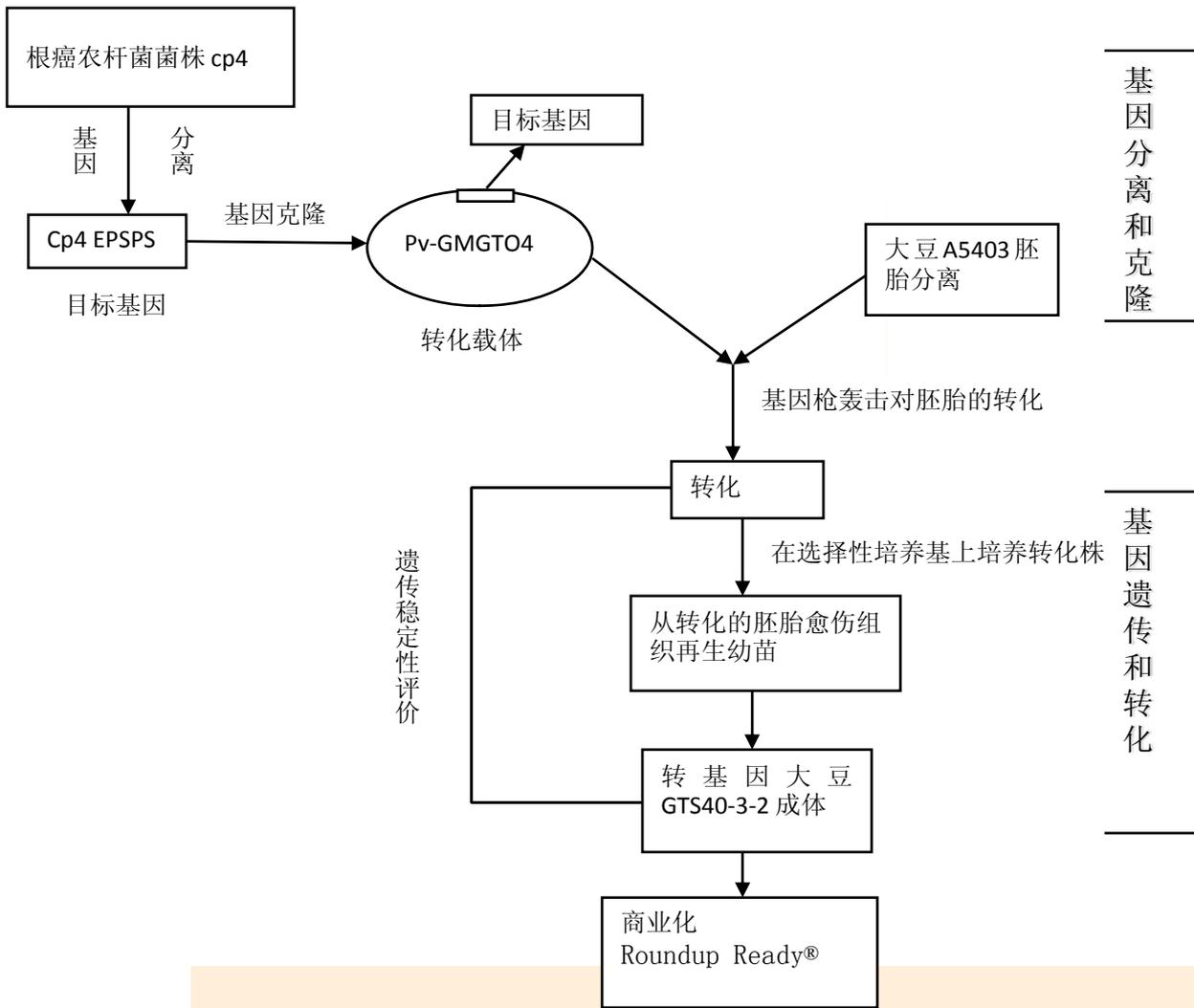
目前我国企业的专利文献利用率只有35.4%（日本企业为92%）

- **规避专利陷阱，降低侵权风险**

专利囊括了全球90%以上的最新技术情报，相比一般技术刊物所提供的信息早5-6年



知识产权信息



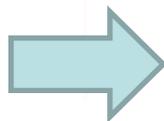
转基因大豆的Cp4 EPSPS基因来自根癌农杆菌菌株，孟山都就该菌株申请了专利保护，专利号有：
 US2008227966
 US2002007053
 US7183110 US6248876
 US5804425 US5633435
 US5627061 USRE39247

转化载体Pv-GMGTO4，被Cambia申请专利：US5432081。
 基因枪转化法由法国Biogemma公司申请专利：US7285705。
 胚胎来自A5403，该品种最早由美国的Asgrow种子所有，该公司1997被孟山都收购。
 启动子最早被加拿大的英属哥伦比亚大学申请专利：US5164316。
 1993年5月28日转让给孟山都公司。



知识产权信息

黄金大米Golden Rice的案例



涉及约70个专利和16个技术产权
分属于32个公司、大学或研究机构
构成了一个复杂的“专利丛林”



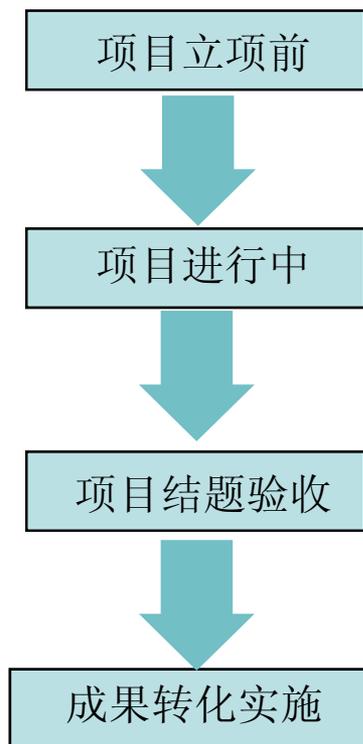
如何开展知识产权信息分析

科研过程

用户需求

信息分析

信息分析贯穿整个创新过程

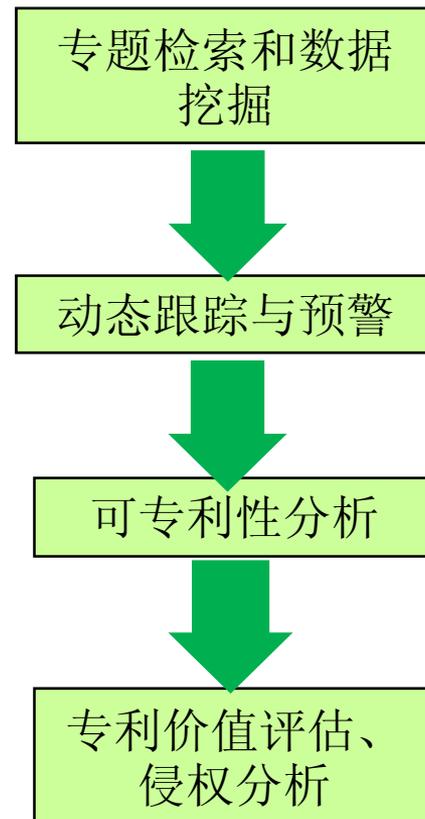


谁在做类似的研究?
我的创新思路是否可行?

竞争对手在做什么?

成果符合专利申请的要求吗?

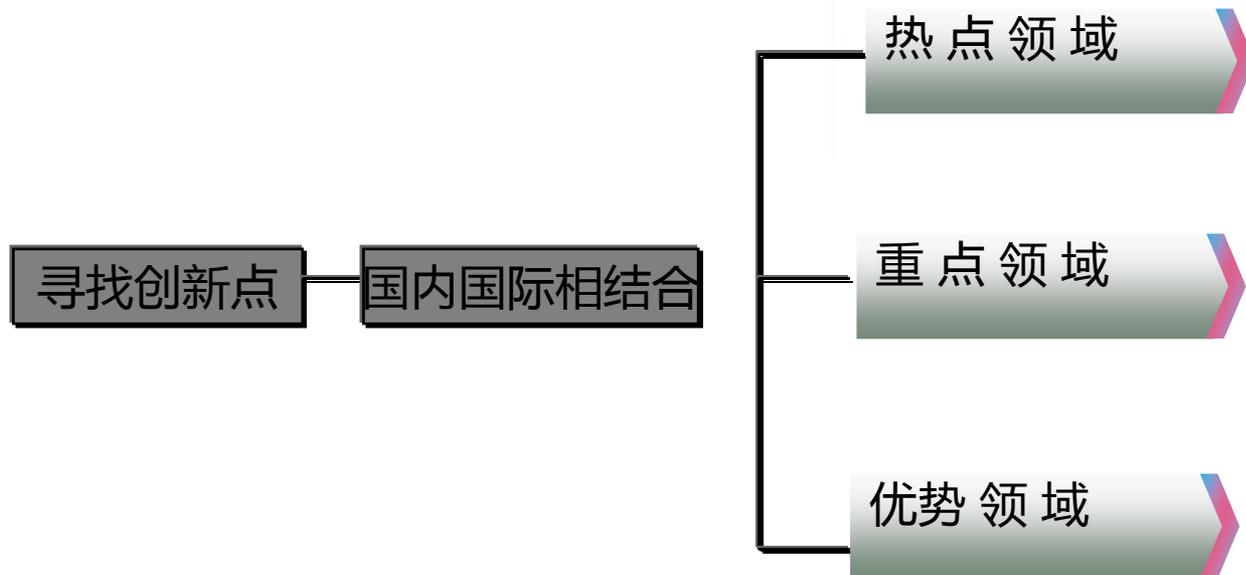
技术的价值如何?
是否有人侵犯我的知识产权?





知识产权信息

信息分析的主要任务：
知识产权诊断、知识产权提案



如生物技术

如常规水稻育种



知识产权诊断

知识产权诊断的主要目标：

确保 *free to operate*

技术风险

- 技术功效矩阵、技术发展路径、专利地图

经济风险

- 生命周期、竞争对手分析、价值评估、市场评估

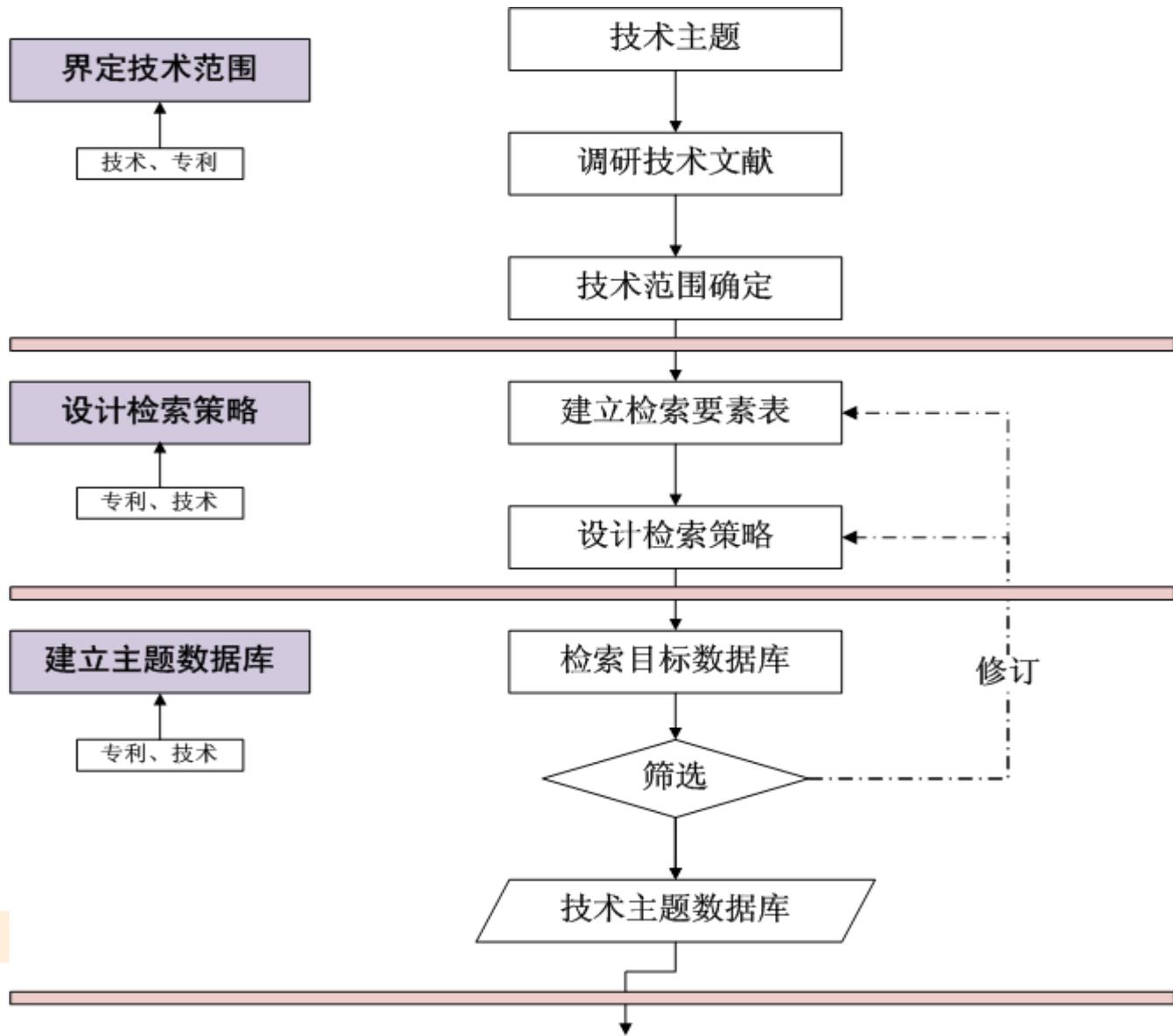
法律风险

- 可专利性、稳定性、主被动侵权风险、技术规避、防御进攻策略



知识产权诊断

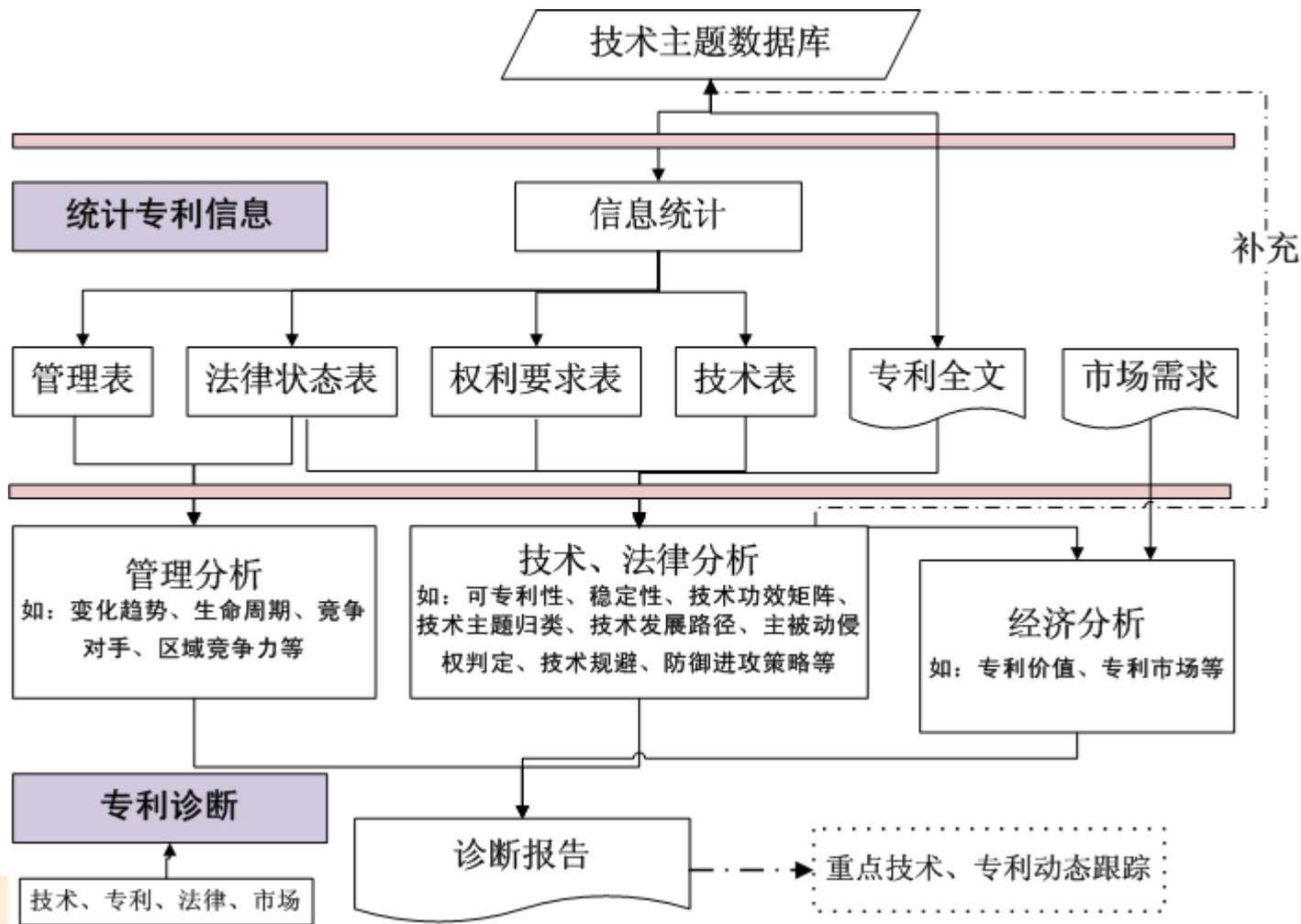
知识产权诊断流程

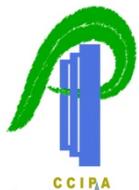




知识产权诊断

知识产权诊断流程





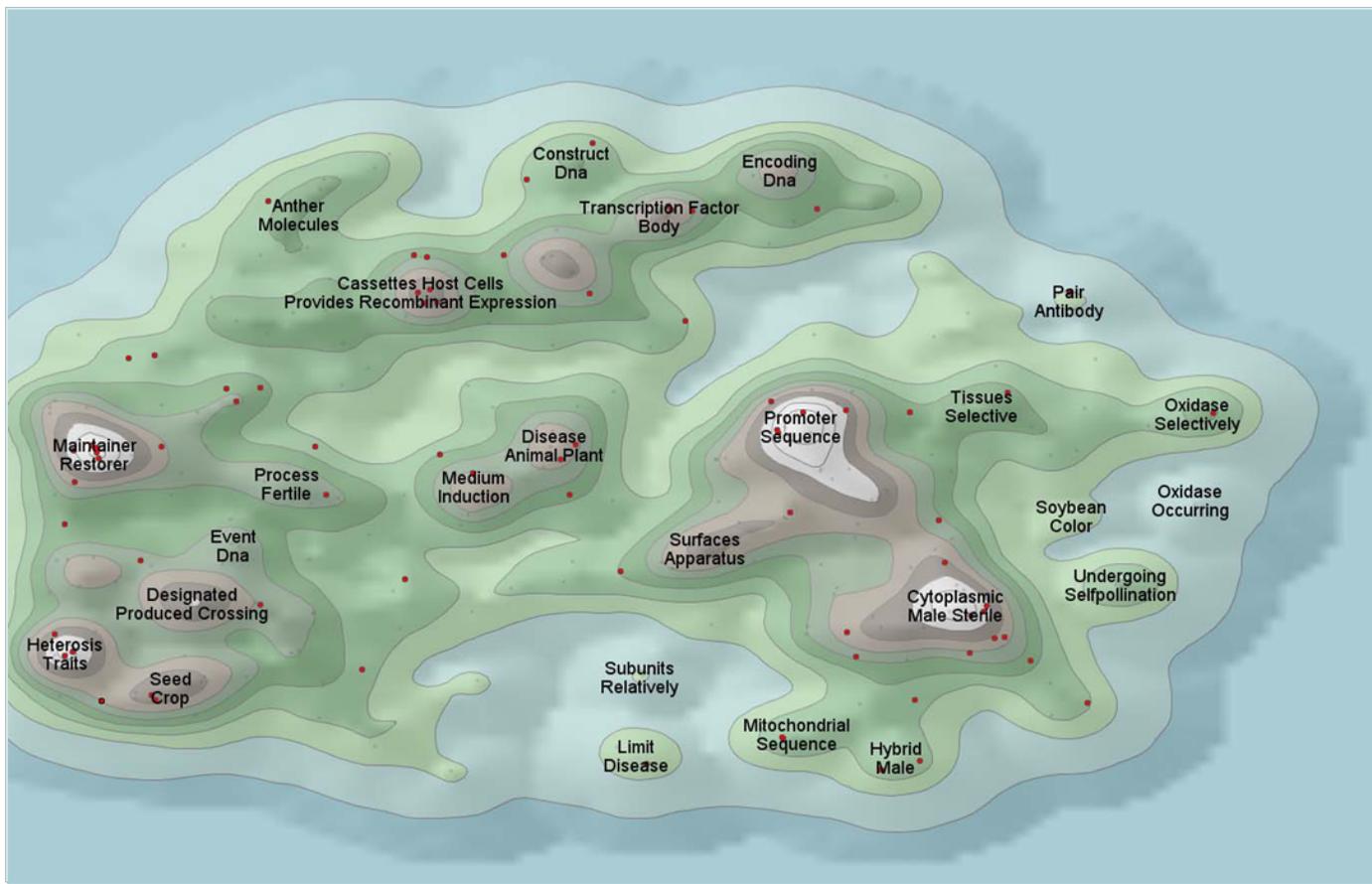
CCIPA



诊断方法

知识产权诊断

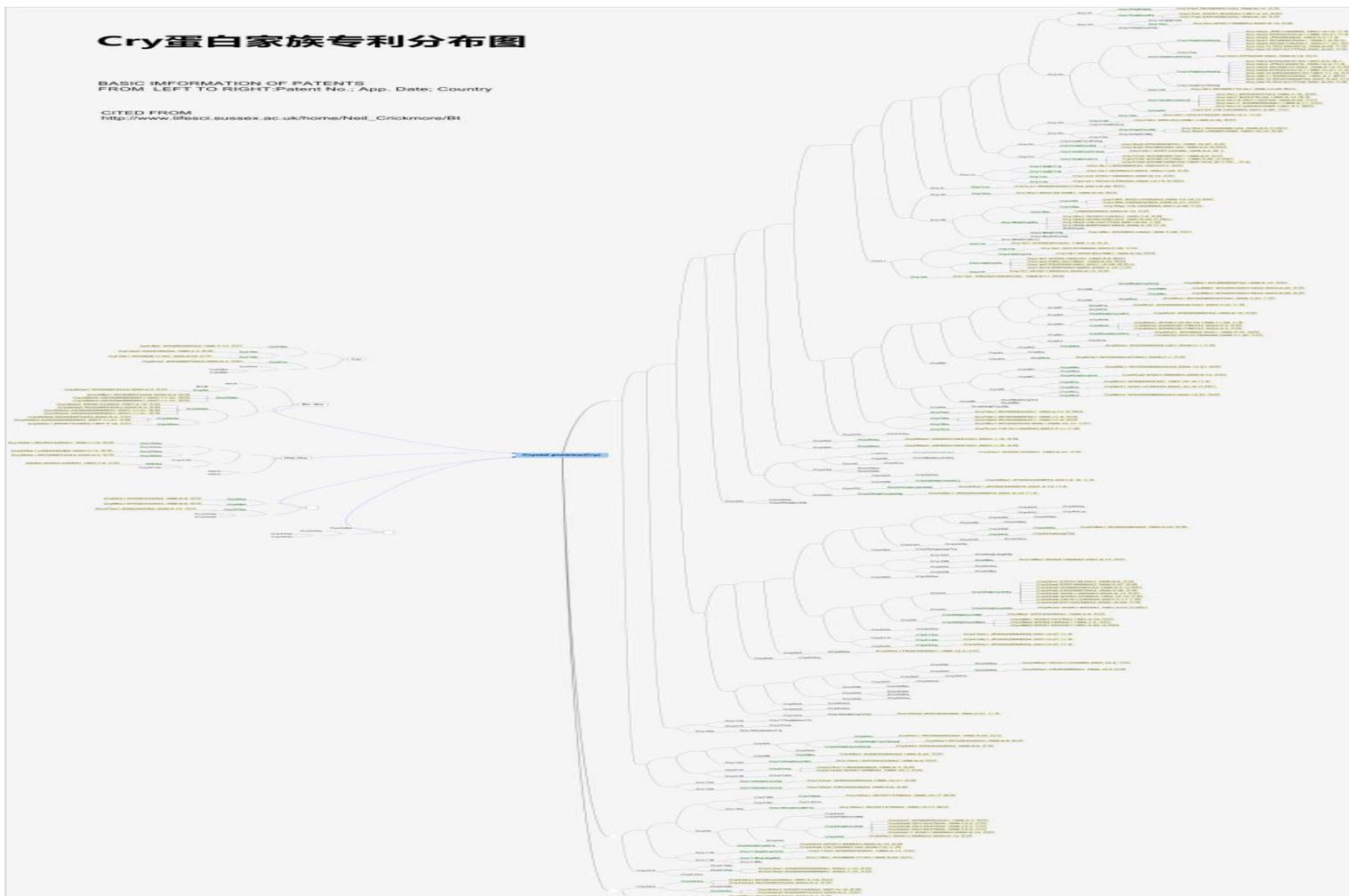
占领技术高地，站在巨人的肩膀上再创新！



专利地图



知识产权诊断





知识产权诊断

技术/功效矩阵

	测量物质成分				测量物质浓度				测量物质透明度				降低成本			
	1987	1992	1997	2002	1987	1992	1997	2002	1987	1992	1997	2002	1987	1992	1997	2002
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	1991	1996	2001	2006	1991	1996	2001	2006	1991	1996	2001	2006	1991	1996	2001	2006
利用光谱性质分析		6	12	50			8	15								
利用偏振性质分析			5	26				4								
利用散射性质分析				15			5	16					4			
利用透射率分析	8			11							12	16				
利用折射率分析		2			3			5				16				26

找出技术空白点，
确定研发重点



知识产权诊断

European Patent Office **espacenet**

Home | Contact English Deutsch Français Help index 7

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Corn event MON810 and compositions and methods for detection thereof

Bibliographic data Description **Claims** Mosaics Original document INPADOC legal status

The EPO does not accept any responsibility for the accuracy of data and information originating from other authorities than the EPO; in particular, the EPO does not guarantee that they are complete, up-to-date or fit for specific purposes. Claims of US 2002102582 (A1) [Translate this text](#) [Claims Tree](#)

What is claimed is:

1. An isolated polynucleotide sequence comprising at least one junction sequence of corn event MON810 selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:1, and complements thereof.
2. The isolated DNA sequence of claim 1 comprising at least 10 contiguous nucleotides of insert DNA sequence from corn event MON810 and at least 10 contiguous nucleotides of corn plant genome flanking DNA sequence from corn event MON810.
3. The isolated DNA sequence of claim 1 comprising at least 20 contiguous nucleotides of insert DNA sequence from corn event MON810 and at least 20 contiguous nucleotides of corn plant genome flanking DNA sequence from corn event MON810.
4. The isolated DNA sequence of claim 1 comprising at least 50 contiguous nucleotides of insert DNA sequence from corn event MON810 and at least 50 contiguous nucleotides of corn plant genome flanking DNA sequence from corn event MON810.
5. An amplicon comprising the DNA sequence of claim 1.
6. An isolated nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1 and SEQ ID NO:2 and complements thereof.
7. A polynucleotide primer sequence for detecting corn event MON810 in a sample comprising at least 15 contiguous nucleotides from position 1-244 of SEQ ID NO:3 or the complement thereof.
8. A pair of polynucleotide primer sequences for detecting corn event MON810 DNA in a sample comprising the primer sequence of claim 7 and a second primer sequence complementary to a sequence comprising at least 15 contiguous nucleotides from position 245-566 of SEQ ID NO:3.
9. A polynucleotide primer sequence for detecting corn event MON810 in a sample comprising at least 15 contiguous nucleotides from position 274-879 of SEQ ID NO:4 or the complement thereof.
10. A pair of polynucleotide primer sequences for detecting corn event MON810 DNA in a sample comprising the primer sequence of claim 9 and a second primer sequence complementary to a sequence comprising at least 15 contiguous nucleotides from position 1-273 of SEQ ID NO:4.
11. A method of detecting the presence of DNA corresponding to the corn event MON810 in a sample, the method comprising:
 - (a) contacting the sample comprising DNA with a pair of primers that, when used in a nucleic-acid amplification reaction with genomic DNA from corn event MON810, produces an amplicon that is diagnostic for corn event MON810;
 - (b) performing a nucleic acid amplification reaction, thereby producing the amplicon; and
 - (c) detecting the amplicon.
12. The method of claim 11 wherein said amplicon is selected from the group consisting of SEQ ID NO:1 and SEQ ID NO:2 and complements thereof.
13. A method of detecting the presence of a DNA corresponding to the MON810 event in a sample, the method comprising:
 - (a) contacting the sample comprising DNA with a probe that hybridizes under stringent hybridization conditions with genomic DNA from corn event MON810 and does not hybridize under the stringent hybridization conditions with DNA of a control corn plant;
 - (b) subjecting the sample and probe to stringent hybridization conditions; and
 - (c) detecting hybridization of the probe to the DNA.
14. A kit for detecting the presence of MON810 nucleic acids in a sample, said kit comprising at least one DNA molecule of sufficient length of contiguous nucleotides homologous or complementary to SEQ ID NO:1 or SEQ ID NO:2 that functions as a DNA primer or probe specific for corn event MON810 and its progeny.
15. A method of detecting corn event MON810 in a biological sample and progeny thereof comprising the steps of (a) extracting protein from a sample of corn event MON810 tissue; (b) assaying the extracted protein using an immunological method comprising antibody specific for the insecticidal protein produced by the MON810 event; and (c) detecting the binding of said antibody to the insecticidal protein.

Data supplied from the **espacenet** database — Worldwide

权利要求书

Corn event MON810 and compositions and methods for detection thereof

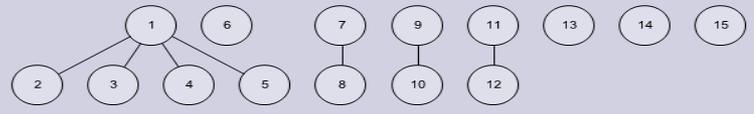
Bibliographic data Description **Claims** Mosaics Original document INPADOC legal status

The EPO does not accept any responsibility for the accuracy of data and information originating from other authorities than the EPO; in particular, the EPO does not guarantee that they are complete, up-to-date or fit for specific purposes. Claims of US 2004180373 (A1) [Translate this text](#) [Original claims](#)

1. An isolated polynucleotide sequence comprising at least one junction sequence of corn event MON810 selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:1, and complements thereof.
2. The isolated DNA sequence of claim 1 comprising at least 10 contiguous nucleotides of insert DNA sequence from corn event MON810 and at least 10 contiguous nucleotides of corn plant genome flanking DNA sequence from corn event MON810.
3. The isolated DNA sequence of claim 1 comprising at least 20 contiguous nucleotides of insert DNA sequence from corn event MON810 and at least 20 contiguous nucleotides of corn plant genome flanking DNA sequence from corn event MON810.
4. The isolated DNA sequence of claim 1 comprising at least 50 contiguous nucleotides of insert DNA sequence from corn event MON810 and at least 50 contiguous nucleotides of corn plant genome flanking DNA sequence from corn event MON810.
5. An amplicon comprising the DNA sequence of claim 1.
6. An isolated nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1 and SEQ ID NO:2 and complements thereof.
7. A polynucleotide primer sequence for detecting corn event MON810 in a sample comprising at least 15 contiguous nucleotides from position 1-244 of SEQ ID NO:3 or the complement thereof.
8. A pair of polynucleotide primer sequences for detecting corn event MON810 DNA in a sample comprising the primer sequence of claim 7 and a second primer sequence complementary to a sequence comprising at least 15 contiguous nucleotides from position 245-566 of SEQ ID NO:3.
9. A polynucleotide primer sequence for detecting corn event MON810 in a sample comprising at least 15 contiguous nucleotides from position 274-879 of SEQ ID NO:4 or the complement thereof.
10. A pair of polynucleotide primer sequences for detecting corn event MON810 DNA in a sample comprising the primer sequence of claim 9 and a second primer sequence complementary to a sequence comprising at least 15 contiguous nucleotides from position 1-273 of SEQ ID NO:4.
11. A method of detecting the presence of DNA corresponding to the corn event MON810 in a sample, the method comprising:
 - (a) contacting the sample comprising DNA with a pair of primers that, when used in a nucleic-acid amplification reaction with genomic DNA from corn event MON810, produces an amplicon that is diagnostic for corn event MON810;
 - (b) performing a nucleic acid amplification reaction, thereby producing the amplicon; and
 - (c) detecting the amplicon.
12. The method of claim 11 wherein said amplicon is selected from the group consisting of SEQ ID NO:1 and SEQ ID NO:2 and complements thereof.
13. A method of detecting the presence of a DNA corresponding to the MON810 event in a sample, the method comprising:
 - (a) contacting the sample comprising DNA with a probe that hybridizes under stringent hybridization conditions with genomic DNA from corn event MON810 and does not hybridize under the stringent hybridization conditions with DNA of a control corn plant;
 - (b) subjecting the sample and probe to stringent hybridization conditions; and
 - (c) detecting hybridization of the probe to the DNA.
14. A kit for detecting the presence of MON810 nucleic acids in a sample, said kit comprising at least one DNA molecule of sufficient length of contiguous nucleotides homologous or complementary to SEQ ID NO:1 or SEQ ID NO:2 that functions as a DNA primer or probe specific for corn event MON810 and its progeny.
15. A method of detecting corn event MON810 in a biological sample and progeny thereof comprising the steps of (a) extracting protein from a sample of corn event MON810 tissue; (b) assaying the extracted protein using an immunological method comprising antibody specific for the insecticidal protein produced by the MON810 event; and (c) detecting the binding of said antibody to the insecticidal protein.

Data supplied from the **espacenet** database — Worldwide

找出权利空白点，
规避专利陷阱，
减少侵权风险

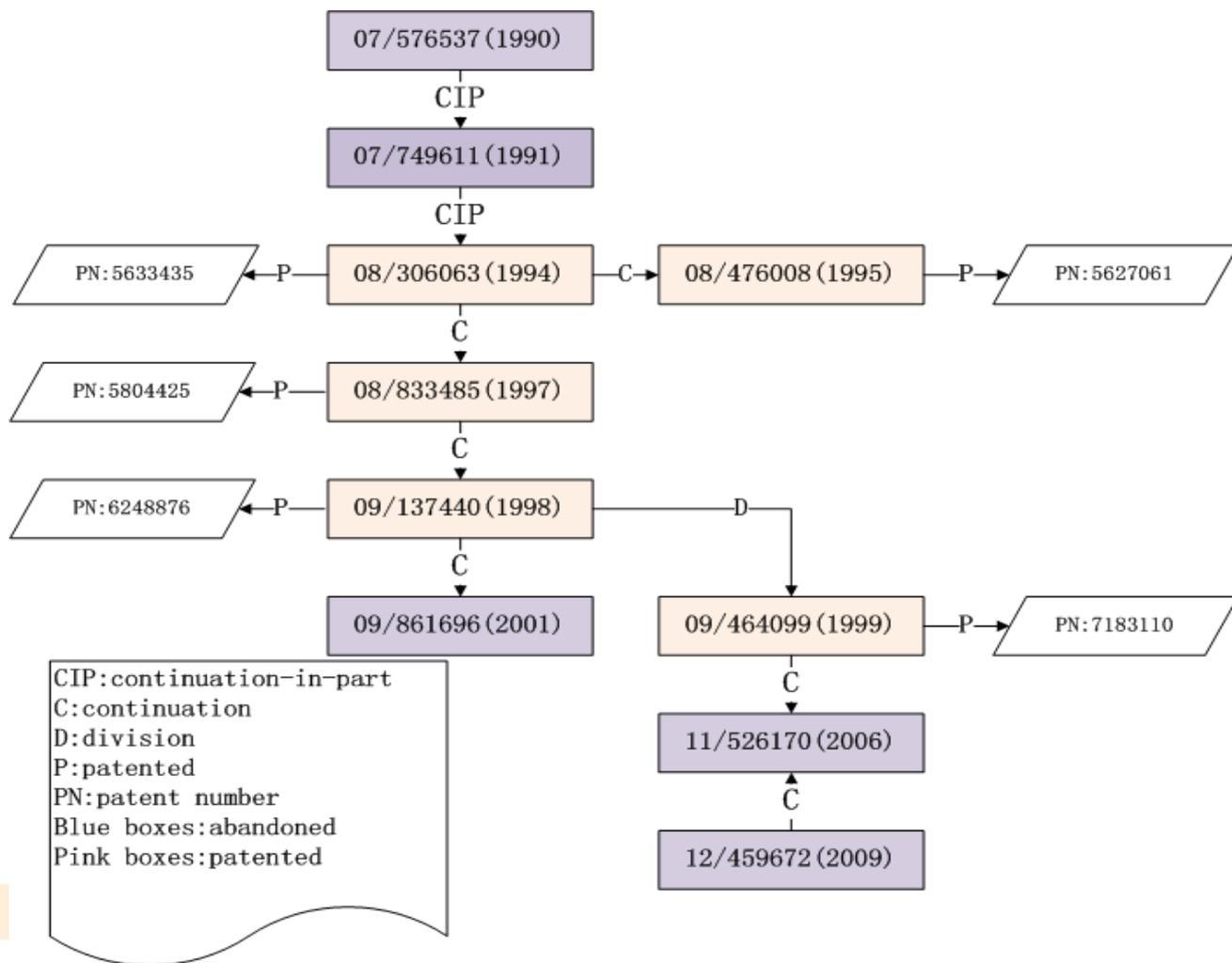




知识产权诊断

案例介绍

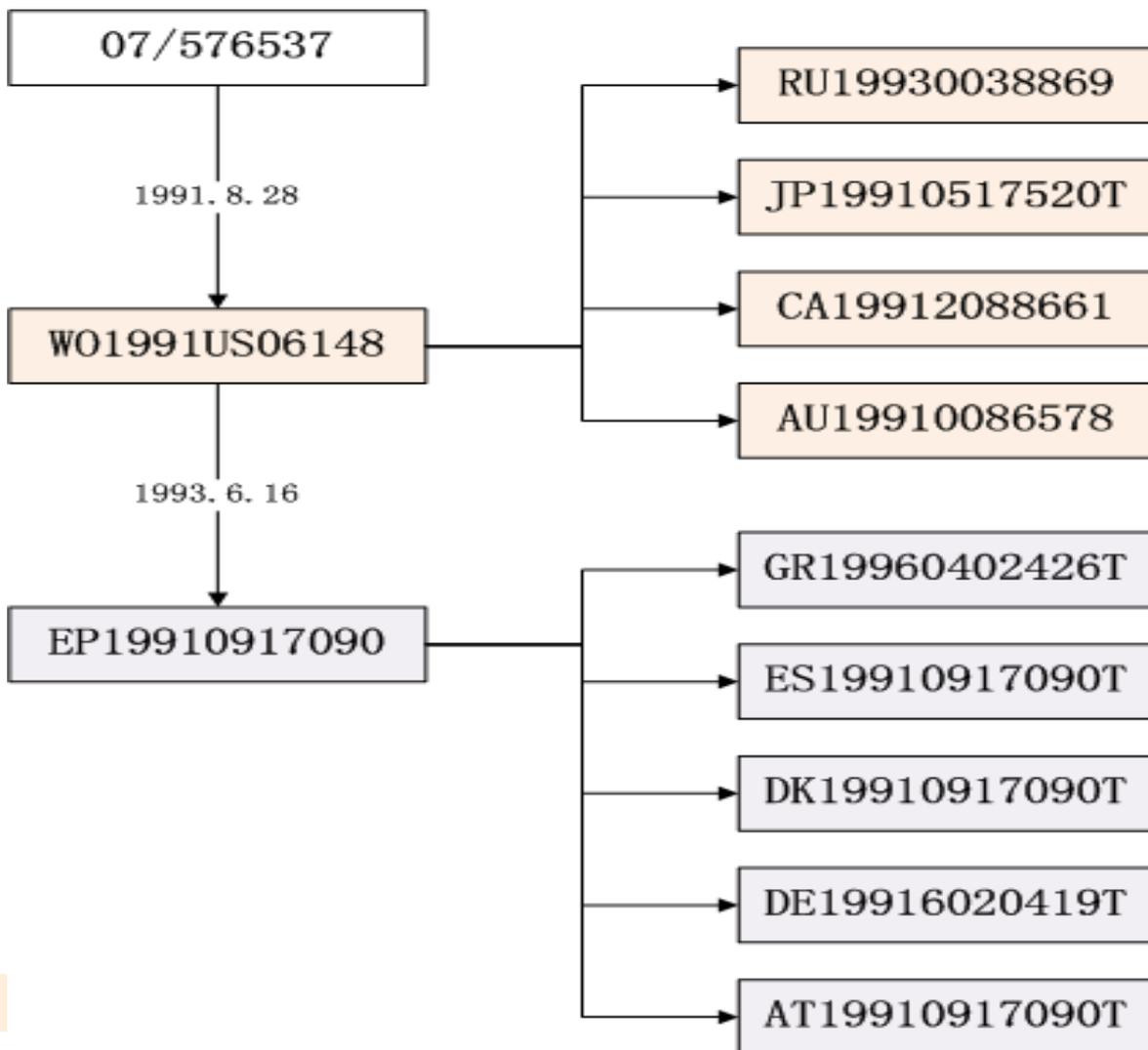
CP4 EPSPS 专利— 美国同族





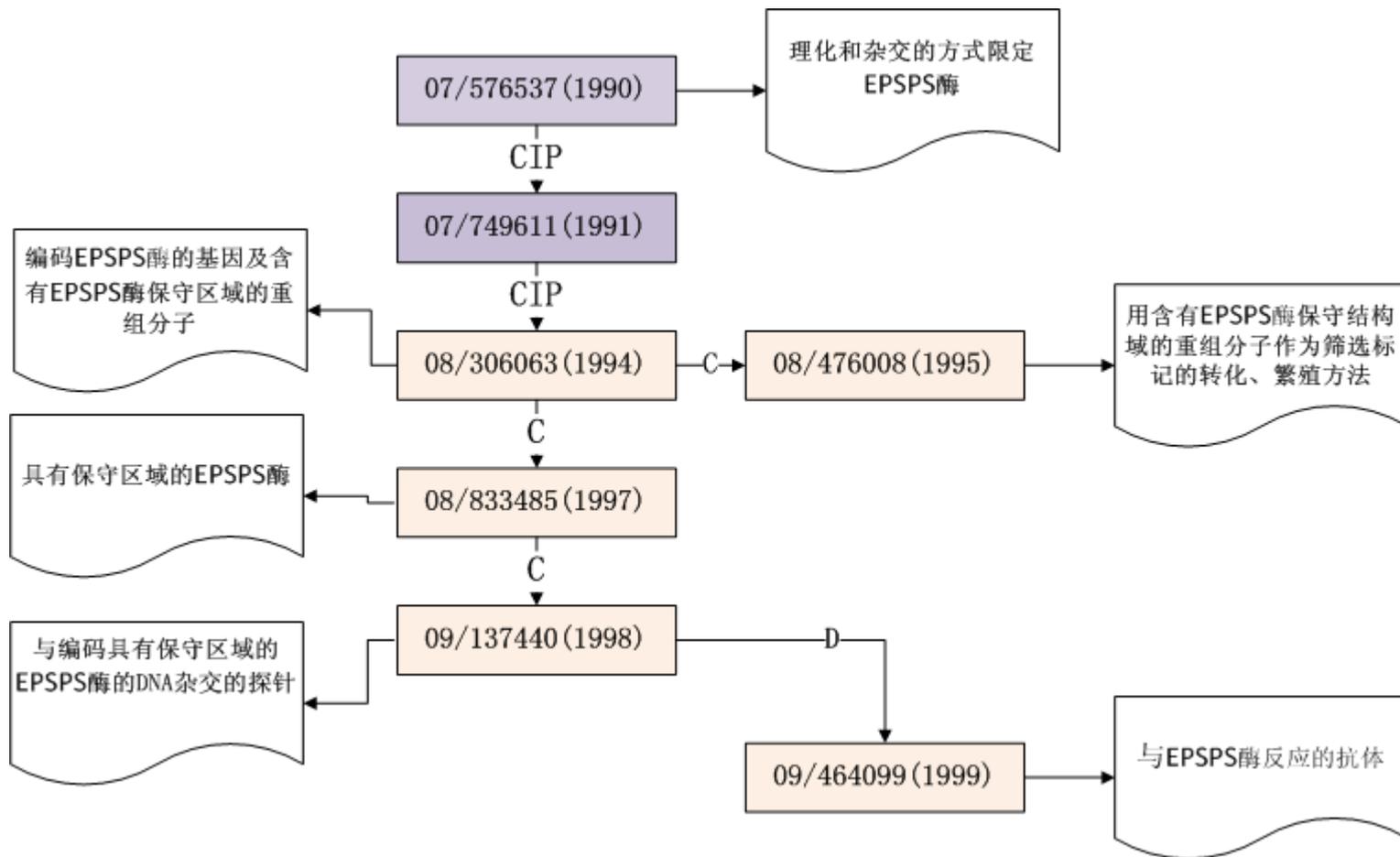
知识产权诊断

CP4
EPSPS
专利—
世界同族





知识产权诊断



CP4 EPSPS 专利部分保护范围简示



知识产权诊断

SEQ ID NO: 2

```

1 Met Asn Ala Asn Asp Leu Ile Phe Leu Ala Gln Pro Gly Gly Arg Leu Asn Gly Arg Ile
2 | Arg Val Pro Gly Asp Lys Ser Ile Ser His Arg Ser Ile Met Leu Gly Ser Leu Ala Glu
4 | Gly Thr Thr Glu Val Glu Gly Phe Leu Glu Gly Glu Asp Ala Leu Ala Thr Leu Gln Ala
6 | Phe Arg Asp Met Gly Val Val Ile Glu Gly Pro Asn His Gly Arg Val Thr Ile His Gly
8 | Val Gly Leu His Gly Leu Lys Pro Pro Pro Gly Pro Leu Tyr Val Gly Asn Ser Gly Thr
10 | Ser Met Arg Leu Leu Ser Gly Leu Leu Ala Gly Gln Ser Phe Asp Val Thr Met Thr Gly
12 | Asp Ala Ser Leu Ser Lys Arg Pro Met Asn Arg Val Ala Asn Pro Leu Arg Glu Met Gly
14 | Ala Val Val Glu Thr Gly Pro Glu Gly Arg Pro Pro Leu Thr Ile Arg Gly Gly His Lys
16 | Leu Lys Gly Leu Thr Tyr Thr Leu Pro Met Ala Ser Ala Gln Val Lys Ser Cys Leu Leu
18 | Leu Ala Gly Leu Tyr Ala Glu Gly Lys Thr Thr Val Thr Glu Pro Ala Pro Thr Arg Asp
20 | His Thr Glu Arg Met Leu Arg Gly Phe Gly Tyr Ser Val Glu Ser Asn Gly Pro Val Ala
22 | Ser Leu Gln Ser Gly Gly Lys Leu Thr Ala Thr Arg Ile Glu Val Pro Ala Asp Ile Ser
24 | Ser Ala Ala Phe Phe Leu Val Ala Ala Ser Ile Ala Glu Gly Ser Glu Leu Val Leu Glu
26 | His Val Gly Ile Asn Pro Thr Arg Thr Gly Val Ile Asp Ile Leu Arg Leu Met Gly Gly
28 | Asp Ile Thr Leu Glu Asn Gln Arg Glu Val Gly Gly Glu Pro Val Ala Asp Leu Arg Val
30 | Arg Gly Ala Gln Leu Lys Gly Ile Asp Ile Pro Glu Ala Leu Val Pro Leu Ala Ile Asp
32 | Glu Phe Pro Val Leu Phe Val Ala Ala Ala Cys Ala Glu Gly Arg Thr Val Leu Arg Gly

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国内某研究所
申请文本中的
SEQ: 2

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Ser Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser
20 25 30
G D K S

COG ACG CCG ATC ACC TAC CGC GTG CCG ATG GCC TCC GCA CAG GTG AAG
Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val Lys
165 170 175
S A Q V K

ACG GTC ATC GAG CCG ATC ATG ACG GGC GAT CAT ACG GAA AAG ATG CTG 682
Thr Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu
195 200 205
R D H T E

AAC CCC ACC CCG ACC GGC
Asn Pro Thr Arg Thr Gly
275
N P T R

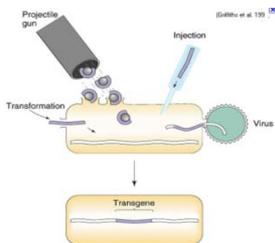
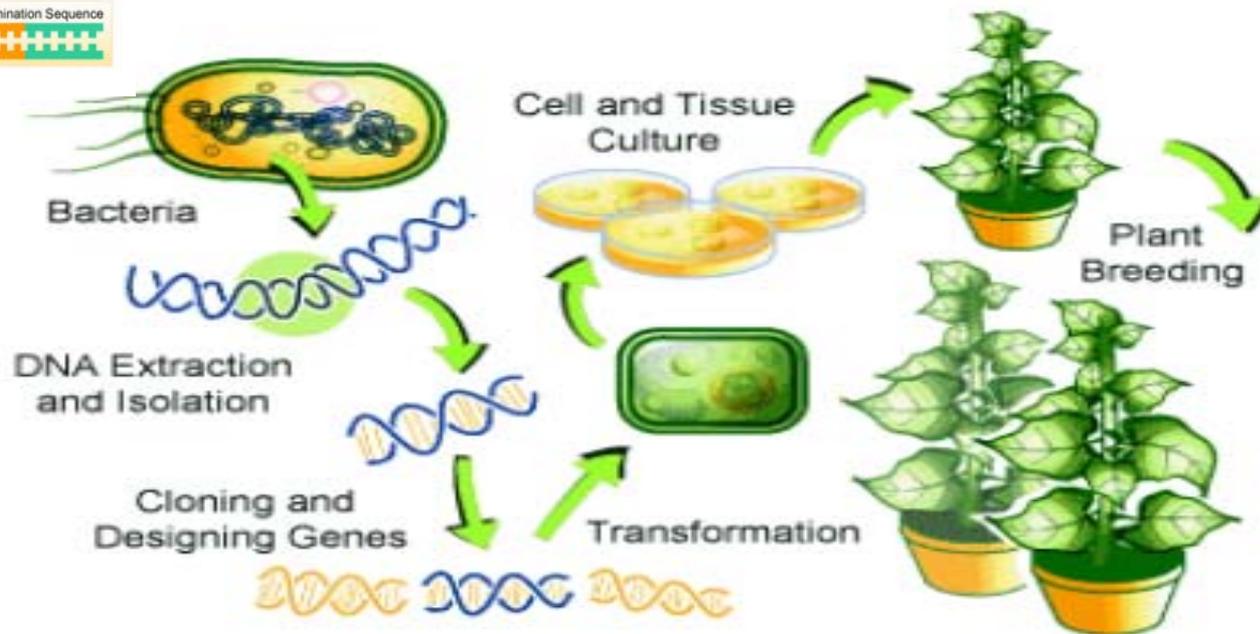
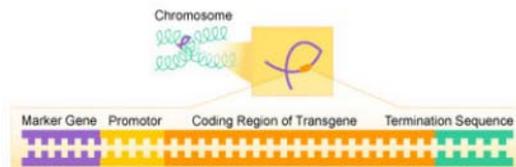
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US5633435中:
SEQ: 3



知识产权提案

- 何时保护研发成果?
- 采取何种方式保护?



专利、商业秘密、合同、遗传资源、植物新品种



知识产权提案

必须建立相应的企业知识产权管理制度：

- 研究数据保密制度
- 成果发表审批制度
- 知识产权工作流程



知识产权提案

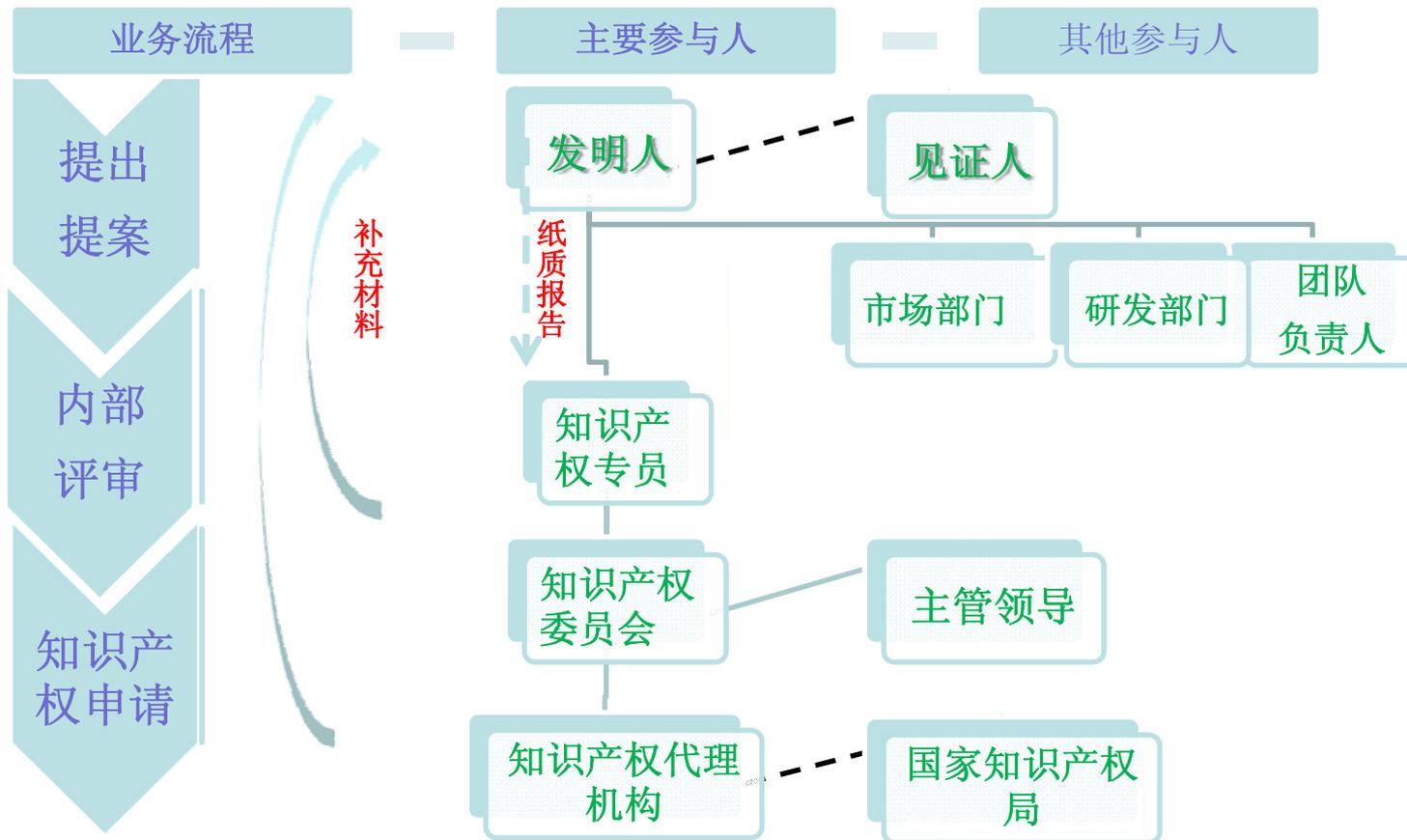
提案的主要内容

- 在常规育种、转基因育种等领域制定清晰可实现的总体目标，常规育种和转基因育种相结合缩短育种周期。
- 估计时间框架、成本和职责。
- 确定预期可交付的成果和结果。
- 确定审计和评估程序方案。





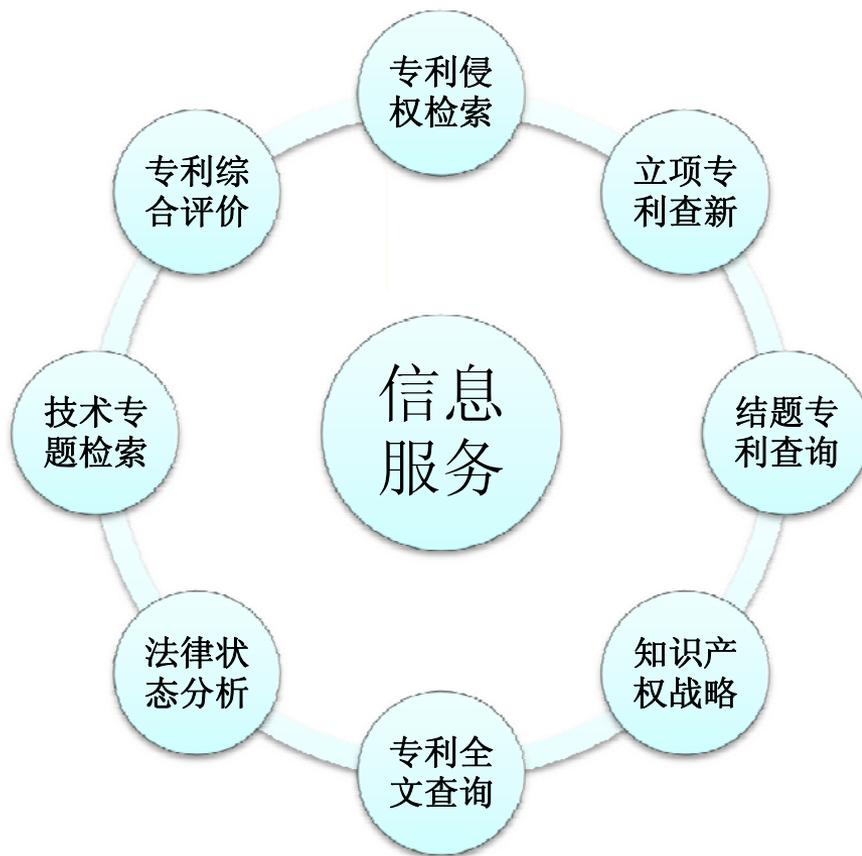
知识产权提案



注：图中实线部分通过内部的管理信息系统实现。



目前我们提供专利信息的查询、诊断、评价等咨询服务：





谢谢大家！
请批评指正

