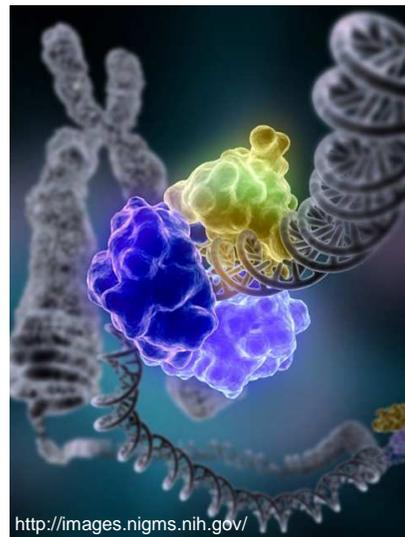


**SLING**

Serving Life-science Information for the Next Generation



## Comprehensive Bio molecular Databases: a worldwide cooperation ?



Stéphane Nauche

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Ana Richart de la Torre

EMBL-EBI



Europäisches  
Patentamt  
European  
Patent Office  
Office européen  
des brevets

**enzymeta**  
GmbH



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## Historical Background

**WIPO**



PCT/MIA/V/2  
ORIGINAL: English  
DATE: November 25, 1994

WORLD INTELLECTUAL PROPERTY ORGANIZATION  
GENEVA

INTERNATIONAL PATENT COOPERATION UNION  
(PCT UNION)

**MEETING OF INTERNATIONAL AUTHORITIES  
UNDER THE PCT**

**Fifth Session**

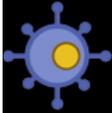
**Geneva, November 28 to December 1, 1994**

THE TRILATERAL PATENT-EJU-SEQUENCE DATABASE:  
POSSIBILITIES TO USE THAT DATABASE BY  
DESIGNATED AND/OR ELECTED OFFICES

The present document is intended to inform the representatives of the international authorities not being parties to the EPO-JPO-USPTO Cooperation of the ongoing activities relating to the Trilateral Patent Sequence Database.

### **I. The Trilateral Patent Sequence Database**

1. In the framework of the Trilateral Cooperation, the three Offices have decided to capture all nucleotide and amino acid sequences from all published patent documents. In order to capture these sequence data, each Office is collaborating with a contractor. The JPO is collaborating with JAPIO, the USPTO with the NCBI (National Center for Biotechnology Information) and the EPO with the EMBL Data Library in Heidelberg, Germany (to be changed in the European Bioinformatics Institute, Hinxton, United Kingdom in September 1994).



# Sequence Listing

Description

Claims

Sequence Listing

Figures

1

**TITLE OF THE INVENTION**  
Binding molecules against SARS-coronavirus and uses thereof

**FIELD OF THE INVENTION**  
The invention relates to medicine. In particular the invention relates to binding molecules capable of specifically binding to SARS-coronavirus (SARS-CoV). The binding molecules are useful in the diagnosis of SARS-CoV and the prophylaxis and/or treatment of a condition resulting from SARS-CoV.

**BACKGROUND OF THE INVENTION**  
Recently a new and in several cases deadly clinical syndrome was observed in the human population, now called severe acute respiratory syndrome (SARS) (Holmes, 2003). The syndrome is caused by a novel coronavirus (Raikawa, 2003), referred to as the SARS-CoV. The genome of SARS-CoV has been determined (Bata et al., 2003). However, much remains to be learnt about the means and methods for diagnostics, prophylaxis and treatment of the virus and the syndrome are needed. The present invention provides means and methods for

**CLAIMS**

1. A binding molecule capable of specifically binding to a SARS-CoV.

2. A binding molecule according to claim 1, which is a human binding molecule.

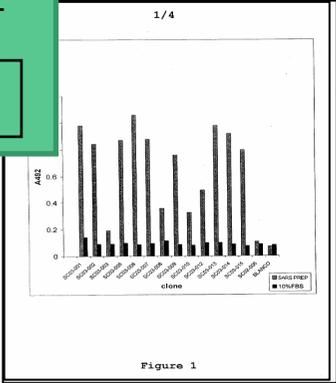
3. A binding molecule according to claim 1 or 2, wherein the binding molecule comprises at least a CDR3 region comprising the amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12 and SEQ ID NO:13.

4. A binding molecule according to any one of the claims 1 - 3, wherein the binding molecule comprises a heavy chain comprising the amino acid sequence selected from the group consisting of SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29 and SEQ ID NO:37 and

SA0000001

**SEQUENCE LISTING**

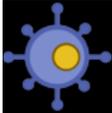
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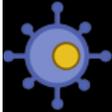
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## XML Sequence Listing

### General Information ↷



HANDBOOK ON INDUSTRIAL PROPERTY INFORMATION AND DOCUMENTATION

Ref.: Standards – ST.36

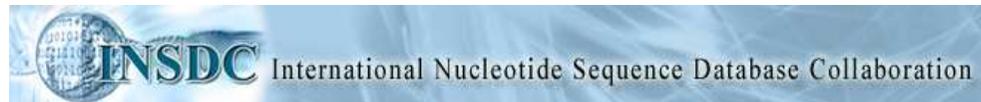
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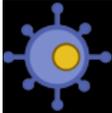
#### **STANDARD ST.36**

Version 1.2

RECOMMENDATION FOR THE PROCESSING OF PATENT INFORMATION USING XML  
(EXTENSIBLE MARKUP LANGUAGE)

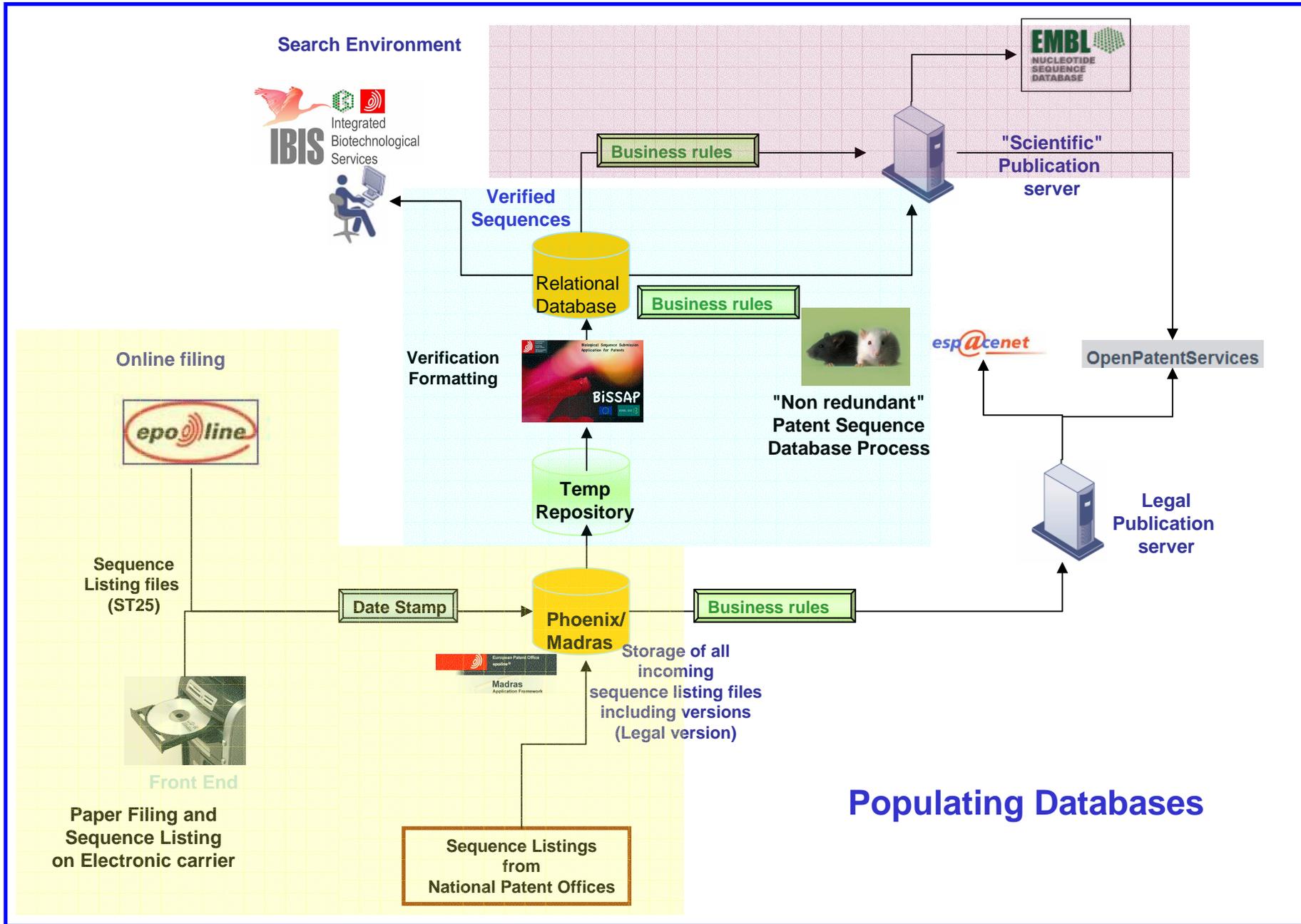
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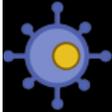




# SLING

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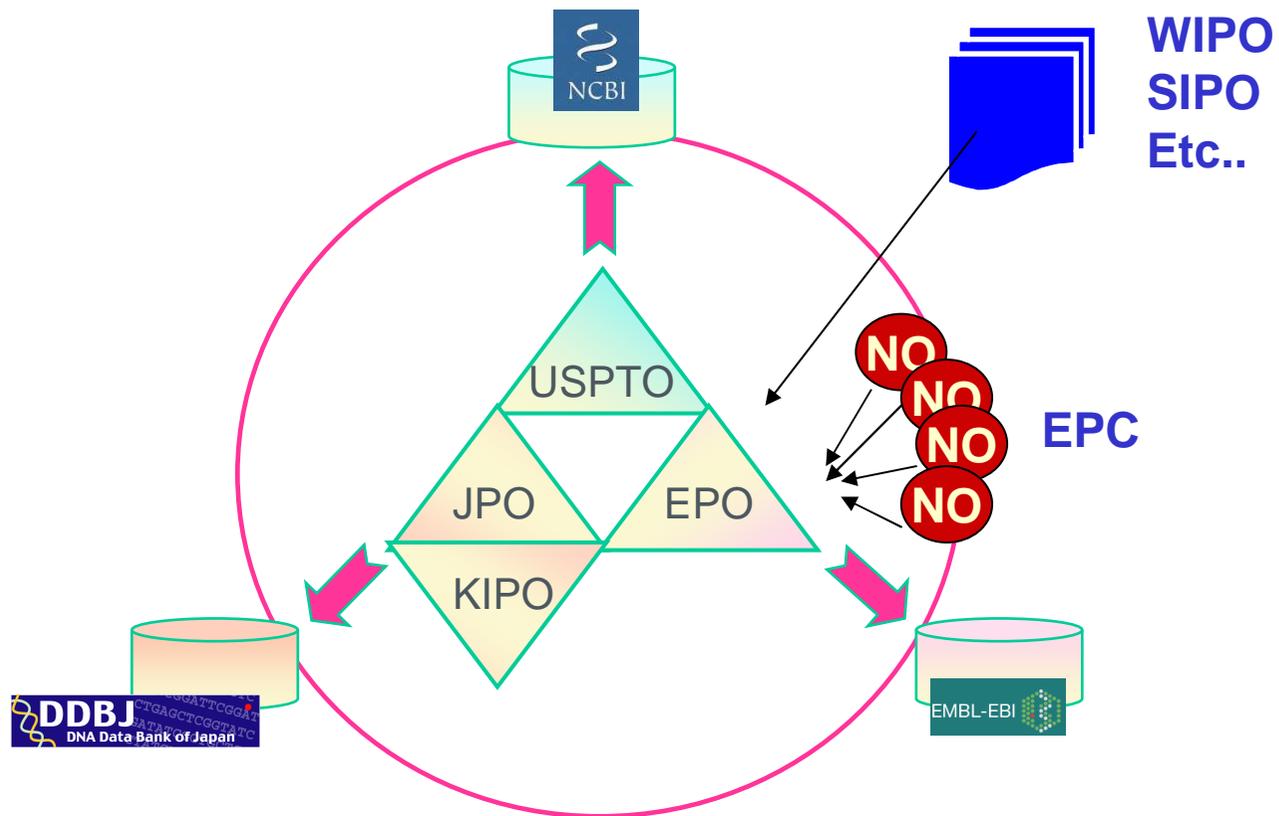


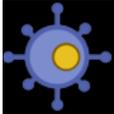
**SLING**

Serving Life-science Information for the Next Generation



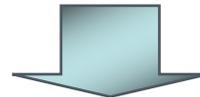
## International Cooperation



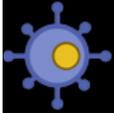


## Necessity to increase coverage and avoid redundant Information

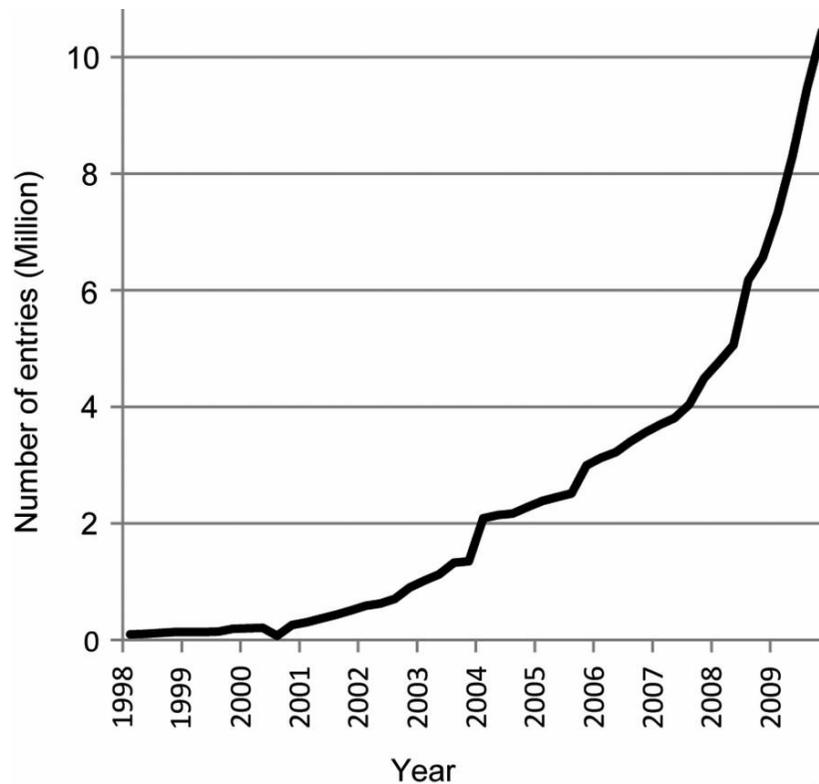
- Increase in Biotechnology applications disclosing biological sequences. To date, only **JPO**, **USPTO**, **EPO** and **KIPO**, send their sequences to the public repositories (NCBI/DDBJ/EBI)
- Data spreading from other patent offices is not included in the exchange flow.
- June 2003: completeness study performed by the EPO.  
*(NCBI/DDBJ/EBI) vs. GeneSeq = Differences in coverage were detected :none is exhaustive !*
- April 2005 (Washington): Project initiation report presented by the EPO to TO's  
*Aims: generation of Non-redundant Patent sequence databases with increased coverage*
- (Tokyo, April 2007, Munich, November 2007 and Washington 2009):
  - *EPO progresses were presented to the TO's*
  - *JPO involved KIPO in the data exchange flow to the public sequence repositories*



**EPO and EBI have completed the generation of Non-redundant Patent sequence Databases, which are publicly available through the EBI services**



## Patent Sequence Databases Figures



**August 2010 :  
17 million entries**

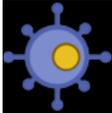
Nucleic Acids Research Advance Access published November 1, 2009

*Nucleic Acids Research*, 2009, 1-5  
doi:10.1093/nar/gkp960

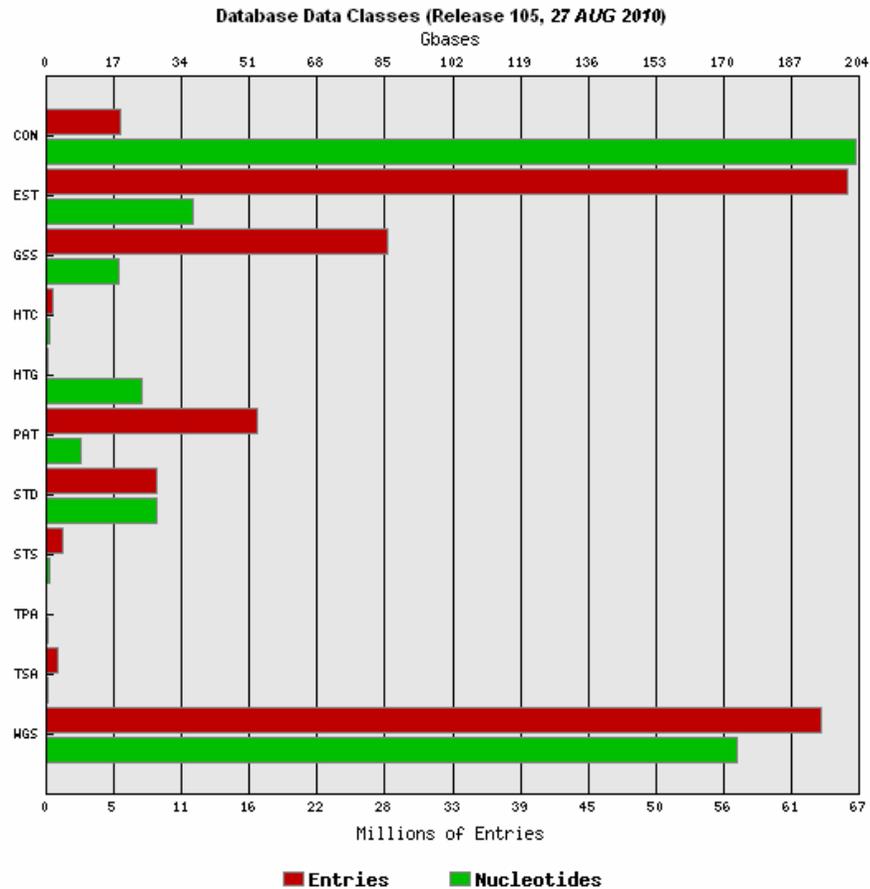
### Non-redundant patent sequence databases with value-added annotations at two levels

Weizhong Li<sup>1</sup>, Hamish McWilliam<sup>1</sup>, Ana Richart de la Torre<sup>2</sup>, Adam Grodowski<sup>2</sup>, Irina Benediktovich<sup>2</sup>, Mickael Goujon<sup>1</sup>, Stephane Nauche<sup>2</sup> and Rodrigo Lopez<sup>1,\*</sup>

<sup>1</sup>European Bioinformatics Institute, EMBL Outstation, Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SD, UK and <sup>2</sup>European Patent Office, IQ Life Sciences, Patentlaan 3-9, 2288 EE Rijswijk, The Netherlands



## Patent Sequence Databases Figures

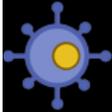


- PRT sequences sent to EMBL - 224196

[4.53% increase of EMBL patent PRT db](#)

- DNA sequences sent to EMBL - 498189

[2.84% increase of EMBL patent DNA db](#)



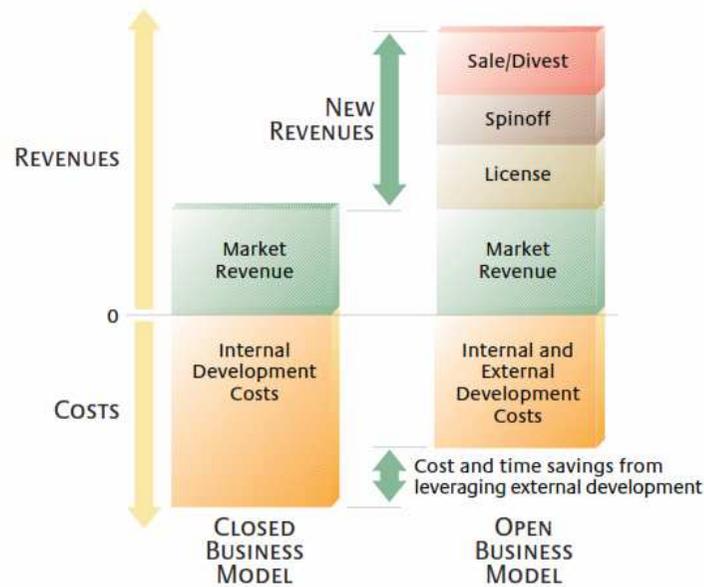
# Open Innovation

## Connect and Develop

Inside Procter & Gamble's New Model for Innovation

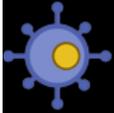
Procter & Gamble's radical strategy of open innovation now produces more than 35% of the company's innovations and billions of dollars in revenue.

Harvard Business Review, 2004, Huston et al."



MIT Sloan Management Review; 2007; Chesbrough h; „Why Companies should have open Business Models“





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## Summary

**Create sequences**



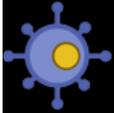
**Collect**

**Populate Patent sequence databases**



**Disseminate Information**  
**Search ,Prior art' in Biotechnology**





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# Questions



Thank  
You