Understanding Patent Documents and Data Fields

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WIPO Open Source Patent Analytics Project

What is a Patent?

- A patent can be described in two main ways:

  1. As a particular form of intellectual property right.

  2. As a type of document.

As a form of intellectual property right

1. A patent is a temporary grant of an exclusive right to a patentee to prevent others from making, using, offering for sale, or importing, a patented invention without their consent, in a country where a patent is in force.

2. Patent rights are territorial rights - they are only valid in the territory of the country where granted.

3. Patents are typically granted for a period of 20 years from the filing data of an application but may be opposed or revoked.

4. To be eligible a claimed invention must: a) Involve patentable subject matter; b) Be new or novel; c) Involve an inventive step; d) Be susceptible to industrial application or useful.

Patents as a type of document

- For patent analytics we need to concentrate on patents as documents and to understand:

  1. The structure of patent documents and their data fields.

  2. The strengths and weaknesses of patent databases as a means for obtaining patent data.

- In this session we deal with the basics of patent documents and their data fields.

Basic Data Types

When performing patent analysis we are dealing with data of seven different types:

1. **Dates** (priority, application and publication dates)

2. **Numbers** (priority number, application number, publication number, family members, citations)

3. **Names** (Applicants - also known as Assignees - and Inventors)

4. **Classification codes** (e.g. International Patent Classification/Cooperative Patent Classification)

5. **Text fields** (Title, Abstract, Description, Claims, Sequence data)

6. **Images** (Diagrams)

7. **Additional Information** (Legal Status, Public Registry etc)

NATURE | TECHNOLOGY FEATURE

Synthetic genomes: The next step for the synthetic genome

Monya Baker

Nature **473**, 403–408 (19 May 2011) | doi:10.1038/473403a
Published online 18 May 2011

Biologists have copied an existing genetic code, but haven't yet commercialized it or written their own. What will it take for a tour de force to reach industrial force?

Subject terms: Biotechnology · Genetics and genomics

Introduction

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A year ago this week, headlines trumpeted that humans had created artificial life. Scientists at the J. Craig Venter Institute in Rockville, Maryland, had chemically synthesized DNA and placed it inside a bacterial cell emptied of its own genetic material. Tests a few days after the insertion showed that the 1-million-base-pair-long synthetic genome was able to run the cellular machinery[1].

Whole-genome engineering could one day create cells unbound by biochemistry as we know it, says George Church, a geneticist at Harvard Medical School in Boston, Massachusetts. Researchers might even be able to design a new genetic code, one that could incorporate more than the 20 or so amino acids used by natural living systems. That achievement is "going to be more than an increment", says Church, "that's going to be a game-changer". But current reality is more prosaic. As

Original Front Page

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(19) World Intellectual Property Organization
International Bureau

PCT

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28 February 2008 (28.02.2008)

(10) International Publication Number
WO 2008/024129 A2

(51) International Patent Classification:
C07H 21/04 (2006.01) *C12P 1/04* (2006.01)
C12N 5/06 (2006.01)

(21) International Application Number:
PCT/US2006/046803

(22) International Filing Date:
6 December 2006 (06.12.2006)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/742,542 6 December 2005 (06.12.2005) US

(71) Applicant *(for all designated States except US)*: **J. CRAIG VENTER INSTITUTE** [US/US]; 9704 Medical Center Drive, Rockville, MD 20850 (US).

(71) Applicant *(for US only)*: **HUTCHISON, Clyde, A., III** [US/US]; c/o J. Craig Venter Institute, 9704 Medical Center Drive, Rockville, MD 20850 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **VENTER, Craig, J.** [US/US]; c/o J. Craig Venter Institute, 9704 Medical Center Drive, Rockville, MD 20850 (US). **SMITH, Hamilton, O.** [US/US]; c/o J. Craig Venter Institute, 9704 Medical Center Drive, Rockville, MD 20850 (US).

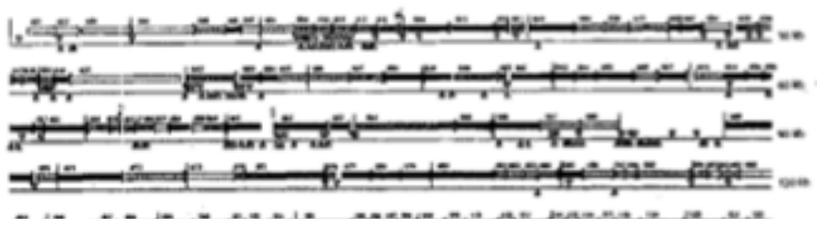
(74) Agents: **BATHURST, Brian** et al.; Carr & Ferrell LLP, 2200 Geng Road, Palo Alto, CA 94303 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LV, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH,

[Continued on next page]

(54) Title: SYNTHETIC GENOMES



(57) Abstract: Methods are provided for constructing a synthetic genome, comprising generating and assembling nucleic acid cassettes comprising portions of the genome, wherein at least one of the nucleic acid cassettes is constructed from nucleic acid components that have been chemically synthesized, or from copies of the chemically synthesized nucleic acid components.

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Bibliographic data: WO2008024129 (A2) — 2008-02-28

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SYNTHETIC GENOMES

Page bookmark WO2008024129 (A2) - SYNTHETIC GENOMES

Inventor(s): VENTER CRAIG J [US]; SMITH HAMILTON O [US] +

Applicant(s): CRAIG VENTER INST J [US]; HUTCHISON CLYDE A III [US]; VENTER CRAIG J [US]; SMITH HAMILTON O [US] +

Classification: - international: ***C07H21/04; C12N5/06; C12P1/04***

- cooperative: **C12N15/10; C12N15/1093; C12N15/66**

Application number: WO2006US46803 20061206

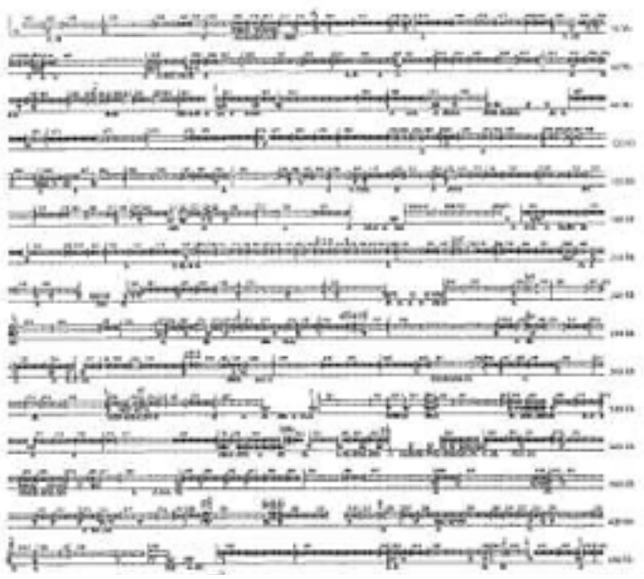
Priority number(s): US20050742542P 20051206

Also published as: WO2008024129 (A3) US2007264688 (A1) JP2009518038 (A) JP5106412 (B2) IL192041 (A) → more

Abstract of WO2008024129 (A2)

Translate this text into Albanian patenttranslate powered by EPO and Google

Methods are provided for constructing a synthetic genome, comprising generating and assembling nucleic acid cassettes comprising portions of the genome, wherein at least one of the nucleic acid cassettes is constructed from nucleic acid components that have been chemically synthesized, or from copies of the chemically synthesized nucleic acid components. In one embodiment, the entire synthetic genome is constructed from nucleic acid components that have been chemically synthesized, or from copies of the chemically synthesized nucleic acid components. Rational methods may be used to design the synthetic genome (e.g., to establish a minimal genome and/or to optimize the function of genes within a genome, such as by mutating or rearranging the order of the genes).; Synthetic genomes of the invention may be introduced into vesicles (e.g., bacterial cells from which part or all of the resident genome has been removed, or synthetic vesicles) to generate synthetic cells. Synthetic genomes or synthetic cells may be used for a variety of purposes, including the generation of synthetic fuels, such as hydrogen or ethanol.



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SYNTHETIC GENOMES

Description of WO2008024129 (A2)

A high quality text as facsimile in your desired language may be available amongst the following family members:

SYNTHETIC GENOMES

By J. Craig Venter, Hamilton O. Smith and Clyde A. Hutchison III

CROSS-REFERENCE TO RELATED APPLICATIONS

[001] The present application claims benefit and priority from U.S. Provisional Patent Application Serial No. 60/742,542 filed on Dec. 6, 2005, entitled, "Synthetic Genomes;" the present application is related to U.S. Provisional Patent Application Serial No. 60/752,965 filed on Dec. 23, 2005, entitled, "Introduction of Genomes into Microorganisms;" U.S. Provisional Patent Application Serial No. 60/741,469 filed on Dec. 2, 2005, entitled, "Error Correction Method;" and U.S. Non-Provisional Patent Application Serial No. 11/502,746 filed on Aug. 11, 2006, entitled "In Vitro Recombination Method," all of which are incorporated herein by reference.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

[002] This invention was made with U.S. government support (DOE grant number DE-FG02-02ER63453). The government has certain rights in the invention.

Patent Claims

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Claims of WO2008024129 (A2)

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Original claims | **Claims tree**

CLAIMS What is claimed is:

1. A method for constructing a synthetic genome comprising: assembling nucleic acid cassettes that comprise portions of the synthetic genome, wherein at least one of the nucleic acid cassettes is constructed from nucleic acid components that have been chemically synthesized, or from copies of chemically synthesized nucleic acid components.

2. The method of claim 1, wherein one or more of the nucleic acid cassettes are prepared by assembling chemically synthesized, overlapping oligonucleotides of about 50 nucleotides.

3. The method of claim 1, wherein the cassettes are about 4 kilobases to about 7 kilobases in length.

4. The method of claim 1, wherein the cassettes are about 4.5 kilobases to about 6.5 kilobases in length.

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9 application(s) for: **WO2008024129 (A2)**

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	Inventor:	Applicant:	CPC:	IPC:	Publication info:	Priority date:
1. SYNTHETIC GENOMES	VENTER CRAIG J [US] SMITH HAMILTON O [US] (+2)	CRAIG VENTER INST J [US] HUTCHISON CLYDE A III [US]	C12N15/10 C12N15/1093 C12N15/66	C07H21/04 C12N5/06 C12P1/04	WO2008024129 (A2) 2008-02-28 WO2008024129 (A3) 2008-10-09	2005-12-06
2. Synthetic genomes	SMITH HAMILTON O VENTER CRAIG J	CRAIG VENTER INST J	C12N15/10 C12N15/1093 C12N15/66	C07H21/04 C12N5/06 C12P1/04	AU2006347573 (A1) 2008-02-28 AU2006347573 (B2) 2013-01-17	2005-12-06
3. SYNTHETIC GENOMES	HUTCHISON CLYDE A III [US] SMITH HAMILTON O [US] (+1)	CRAIG VENTER INST J [US]	C12N15/10 C12N15/1093 C12N15/66	C07H21/00 C07H21/04 C12N1/00 (+4)	CA2643356 (A1) 2008-02-28	2005-12-06
4. Synthetic genomes	VENTER CRAIG J	CRAIG VENTER INST J [US]	C12N15/10	C07H21/00	CN101501207 (A)	2005-12-06

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International search citation

1. Method for the complete chemical synthesis and assembly of genes and genomes

Inventor:	Applicant:	CPC:	IPC:	Publication info:	Priority date:
EVANS GLEN A [US]	EGEA BIOSCIENCES INC [US]	B01J19/0046 B01J2219/00317 B01J2219/00511 (+17)	B01J19/00 C12N15/10 C12N15/66 (+7)	US6521427 (B1) 2003-02-18	1997-09-16

International search NPL citation

2. Venter aims for maximum impact with minimal genome

Author:	Publication data:	CPC:	Source information:	Publication info:
Erika Check	NATURE, 20021128 Nature Publishing Group, United Kingdom		Vol:420,Nr:6914,Page(s):350	XP008128716

3. Generating a synthetic genome by whole genome assembly: phiX174 bacteriophage from synthetic oligonucleotides

Author:	Publication data:	CPC:	Source information:	Publication info:
SMITH HAMILTON O ET AL	Proceedings of the National Academy of Sciences, 20031223 National Academy of Sciences, US		Vol:100,Nr:26,Page(s):15440 - 15445	XP002301506

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2 documents citing **WO2008024129 (A2)**

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1. BACTERIAL ENGINEERING

Inventor:	Applicant:	CPC:	IPC:	Publication info:	Priority date:
WILLIAMS DAVID HUGH [GB] TURNER ARTHUR KEITH [GB] (+1)	DISCUVA LTD [GB]	C12N15/102 C12N15/1082	C12N15/10	WO2014072697 (A1) 2014-05-15	2012-11-06

2. METHODS FOR CLONING AND MANIPULATING GENOMES

Inventor:	Applicant:	CPC:	IPC:	Publication info:	Priority date:
BENDERS GWYNEDD A [US] GLASS JOHN I [US] (+10)	SYNTHETIC GENOMICS INC [US] BENDERS GWYNEDD A [US] (+11)	C12N15/1031 C12N15/1079 C12N15/66 (+1)	C12N15/10 C12N15/74	WO2011109031 (A1) 2011-09-09 WO2011109031 (A8) 2012-09-20	2010-03-05

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Legal status of WO2008024129 (A2) 2008-02-28; WO2008024129 (A3) 2008-10-09:

WO **F** **2006046803** **W** (Patent of invention)

Event date :	2008/05/07
Event code :	121
Code Expl.:	EP: THE EPO HAS BEEN INFORMED BY WIPO THAT EP WAS DESIGNATED IN THIS APPLICATION
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CORRESP. PATENT D. :	2008544524
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Round Up

In this session we have walked through some of the most important patent data fields.

These fields are the building blocks for sophisticated patent analysis. In future sessions we will focus on:

- Retrieving data with these fields
- Cleaning up the data in these fields
- Mapping trends
- Network Mapping
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