Guide on Patent and Sequence Searches and Submissions Related to Genetic Resources and Genetic Resource Data in the Life Sciences

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Draft for comments

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1 INTRODUCTION

Genetic resource sequence data have become the lifeblood of innovation in almost all sectors of the life sciences.

They are the simplest and fastest way to describe genetic resources (GRs) and protein structures, and they are the largest and most complex big data sets that life science innovators are working with everywhere today. They are the most accessible and cheapest to produce molecular characterization data, and they are among the most expensive for which to receive sophisticated legal and intellectual property (IP) analysis. They are also the largest big data sets entering the digital environment in the next twenty years and they are the most widely accessible big data sets in a structured and standardized form.

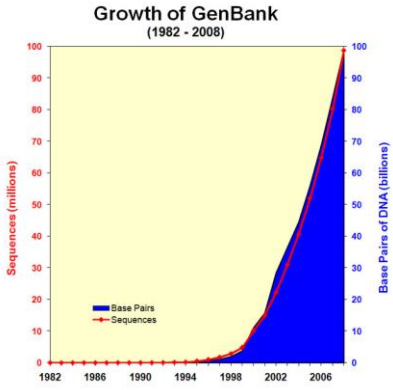


Fig.1: Growth of sequence data in Genbank

Innovators, big and small, in developing and developed countries, want, and need to use GR sequence data and amino acid sequence data to accelerate their biological innovation at all levels and stages of development. Thus, GR sequence data have become one of the most widely accessible and useful intangible resources for biotechnological innovation and the life sciences generally all over the world today.

An innovation resource for everyone everywhere

Sequence data have also become a ubiquitous global innovation tool that cannot be ignored by GR stakeholders or innovators today at any level of development. Even when located in a developing or least developed country (LDC), or among Indigenous Peoples or local communities (IPLCs), GR stakeholders and innovators working with GRs today will need to deal with sequence data search and management tools, the way we use libraries and word processors for research and innovation in other fields of technology. The more they can become familiar with utilizing these library catalogues, word processors and search tools, the more life science innovation will progress, even if these may appear unfamiliar or slightly daunting at the outset. Sequence data are growing globally at an exponential rate and their accessibility is being democratized through the public databases of the International Nucleotide Sequence Database Cooperation (INSDC). See, for example, the growth of sequence data available to GRs stakeholders and innovators from two INSDC databases, namely Genbank (Fig.1) and the European Molecular Biology Laboratory (EMBL) databases (Fig.2). Even beyond the INSDC databases, genomic sequence data are expected to become the largest data set entering the digital environment by 2050 globally (Fig.3). Accordingly, this Guide of the WIPO Toolkit for Rights Management in GRs and Data provides GR stakeholders and innovators a practical introductory user guide for sequence searches and submissions when using these valuable and indispensable information resources in the modern life sciences.

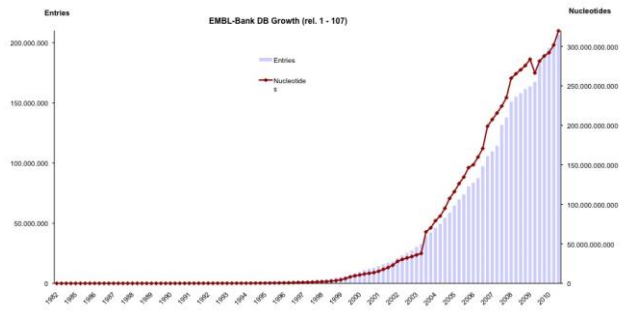


Fig.2: Growth of sequence data in the EMBL databases

A new innovation ecosystem in the life sciences

In their aggregated form, within the global biological research information infrastructure, genetic and amino acid sequence data have formed an emerging innovation ecosystem of their own, connected and embodied by such standards and structures as WIPO ST.26,[1] the global patent information systems related to the PCT, and the data repositories of INSDC. The Patentscope database is a database which releases sequence listings received through applications under the Patent Cooperation Treaty (PCT) for public availability, and is accessible free of charge. These standards and structures house an increasing amount of sequence data with increasing accessibility and ease of searching and submission. If all innovators can have access to and make good use of such sequence data, it is less likely that any will fall behind in the utilization and leveraging of GRs data in their innovations.

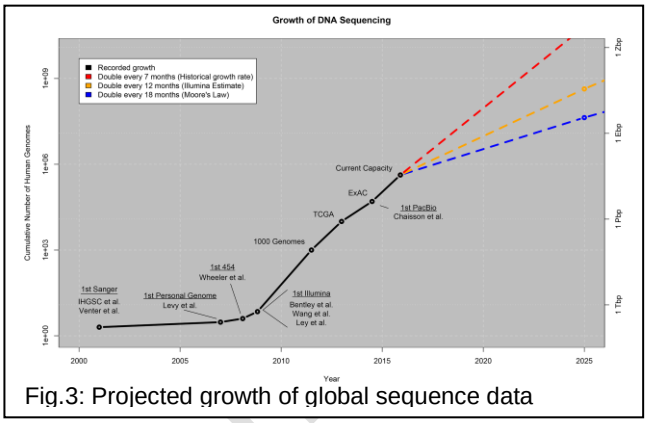
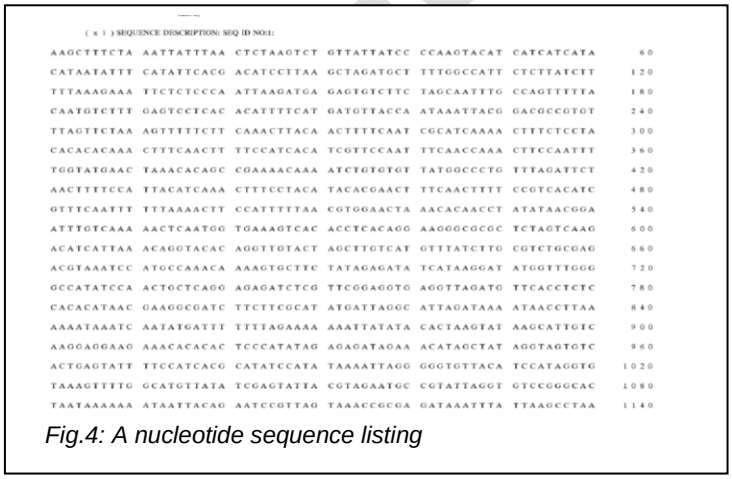


Fig.3: Projected growth of global sequence data

While the characterization of genetic and other biological resources has been an essential part of creating and maintaining legal certainty in the patent protection of biotechnological inventions ever since IP rights were introduced in biotechnology, such characterization of genetic and other biological resources has gone through a paradigm shift since the introduction of automated, high-throughput molecular sequencing of these resources in the early 2000s.

This paradigm shift has led to an expansion of the role of sequence data and other GRs data in at least two ways: firstly, *qualitatively* not only are sequence listings essential in claiming and disclosing biotechnological inventions, as well as in searching, discovering and analyzing relevant prior art for the examination of biotechnological patent applications, but these GRs sequence data have *in themselves* become a source of innovation for innovators in the life sciences, independent of their proximity to or anticipation of patented sequences. Secondly, *quantitatively* the availability of such sequence data sets has over time become so large, that they are stored in large data repositories, such as the membership databases of the INSDC. Legally, certain submission of sequence data by innovators to such repositories is equally important for many such innovators, as is their search and retrieval.


(x) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGCTTTCTA AATTATTTAA CTCTAAGTCT GTTATTATCC CCAAGTACAT CATCATCATA 60
CATAATATTT CATATTCACG ACATCCTTAA GCTAGATGCT TTTGGCCATT CTCTTATCTT 120
TTTAAAGAAA TTCTCTCCCA ATTAAGATGA GAGTGTCTTC TAGCAATTTG CCAGTTTTTA 180
CAATGTCTTT GAGTCCTCAC ACATTTTCAT GATGTTACCA ATAAATTACG GACGCCGTGT 240
TTAGTTCTAA AGTTTTTCTT CAAACTTACA ACTTTTCAAT CGCATCAAAA CTTTCTCCTA 300
CACACACAAA CTTTCAACTT TTCCATCACA TCGTTCCAAT TTCAACCAAA CTTCCAATTT 360
TGGTATGAAC TAAACACAGC CGAAAACAAA ATCTGTGTGT TATGGCCCTG TTTAGATTCT 420
AACTTTTCCA TTACATCAAA CTTTCCTACA TACACGAACT TTCAACTTTT CCGTCACATC 480
GTTTCAATTT TTTAAAACTT CCATTTTTAA CGTGGAACTA AACACAACCT ATATAACGGA 540
ATTTGTCAAA AACTCAATGG TGAAAGTCAC ACCTCACAGG AAGGGCGCGC TCTAGTCAAG 600
ACATCATTAA ACAGGTACAC AGGTTGTACT AGCTTGTCAT GTTTATCTTG CGTCTGCGAG 660
ACGTAAATCC ATGCCAAACA AAAGTGCTTC TATAGAGATA TCATAAGGAT ATGGTTTGGG 720
GCCATATCCA ACTGCTCAGG AGAGATCTCG TTCGGAGGTG AGGTTAGATG TTCACCTCTC 780
CACACATAAC GAAGGCGATC TTCTTCGCAT ATGATTAGGC ATTAGATAAA ATAACCTTAA 840
AAAATAAATC AATATGATTT TTTTAGAAAA AAATTATATA CACTAAGTAT AAGCATTGTC 900
AAGGAGGAAG AAACACACAC TCCCATATAG AGAGATAGAA ACATAGCTAT AGGTAGTGTC 960
ACTGAGTATT TTCCATCACG CATATCCATA TAAAATTAGG GGGTGTTACA TCCATAGGTG 1020
TAAAGTTTTG GCATGTTATA TCGAGTATTA CGTAGAATGC CGTATTAGGT GTCCGGGCAC 1080
TAATAAAAAA ATAATTACAG AATCCGTTAG TAAACCGCGA GATAAATTTA TTAAGCCTAA 1140

Fig.4: A nucleotide sequence listing

[1] WIPO Standard 26, "Recommended standard for the presentation of nucleotide and amino acid sequence listings using XML (eXtensible Markup Language)".

1.1 OBJECTIVES OF THIS GUIDE

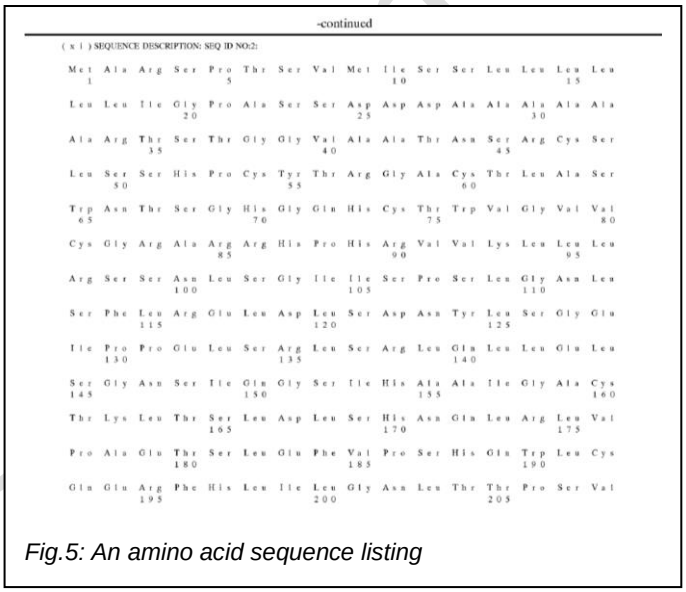
This Guide addresses in particular the challenges for users with lower resources or patent information know-how to conduct prior art searches and submissions involving biological sequence listings in publicly accessible patent and non-patent literature database. It may be read as a specialized addition to the WIPO IP Guide for GRs and Genetic Sequence Data (hereinafter referred to as the Subject Guide).

1.1.1 How to use this Guide

This section will provide you with practical tips on how to use this Guide for the practical use and rights management of sequence data in a patent law context.

1.1.1.1 Quick reference table for use of this Guide

For accessibility and simplicity of use, you will find here a Quick Reference Table to the different stages of the different search types for sequence data – referring you to the corresponding (sub)chapters of this Guide. The table is based on the typology of searches and submissions described in section 1.2.4. below. This typology is non-exhaustive, not static, and not fixed, since objectives and elements from different search types can be combined in a single search, but it may nevertheless provide you with a starting point to efficiently access those parts of this Guide, which you wish to use. You might wish to look at a specific stage of searching within different types of searches, which are often connected in practice, such as Freedom to Operate (FTO) searches and patentability/prior art searches.


-continued

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Arg Ser Pro Thr Ser Val Met Ile Ser Ser Leu Leu Leu Leu
1 5 10 15

Leu Leu Ile Gly Pro Ala Ser Ser Asp Asp Asp Ala Ala Ala Ala Ala
20 25 30

Ala Arg Thr Ser Thr Gly Gly Val Ala Ala Thr Asn Ser Arg Cys Ser
35 40 45

Leu Ser Ser His Pro Cys Tyr Thr Arg Gly Ala Cys Thr Leu Ala Ser
50 55 60

Trp Asn Thr Ser Gly His Gly Glu His Cys Thr Trp Val Gly Val Val
65 70 75 80

Cys Gly Arg Ala Arg Arg His Pro His Arg Val Val Lys Leu Leu Leu
85 90 95

Arg Ser Ser Asn Leu Ser Gly Ile Ile Ser Pro Ser Leu Gly Asn Leu
100 105 110

Ser Phe Leu Arg Glu Leu Asp Leu Ser Asp Asn Tyr Leu Ser Gly Glu
115 120 125

Ile Pro Pro Glu Leu Ser Arg Leu Ser Arg Leu Gln Leu Leu Glu Leu
130 135 140

Ser Gly Asn Ser Ile Gln Gly Ser Ile His Ala Ala Ile Gly Ala Cys
145 150 155 160

Thr Lys Leu Thr Ser Leu Asp Leu Ser His Asn Gln Leu Arg Leu Val
165 170 175

Pro Ala Glu Thr Ser Leu Glu Phe Val Pro Ser His Glu Trp Leu Cys
180 185 190

Glu Glu Arg Phe His Leu Ile Leu Gly Asn Leu Thr Thr Pro Ser Val
195 200 205

Fig.5: An amino acid sequence listing

Fig.3: Quick reference table to chapters describing different stages of different search and submission types.

	A. Prior art/ patentability searches	**B. FtO searches**	**C. Technology trends / patent landscape searches**	**D. Market analysis**
Stage 1	Chapter 3.3.1.1	Chapter 3.3.2.1	Chapter 3.3.3.1	Chapter 3.3.4.1
Stage 2	Chapter 3.3.1.2	Chapter 3.3.2.2	Chapter 3.3.3.2	Chapter 3.3.4.2
Stage 3	Chapter 3.3.1.3	Chapter 3.3.2.3	Chapter 3.3.3.3	Chapter 3.3.4.3
Stage 4	Chapter 3.3.1.4	Chapter 3.3.2.4	Chapter 3.3.3.4	Chapter 3.3.4.4
Stage 5	Chapter 3.3.1.5	Chapter 3.3.2.5	Chapter 3.3.3.5	Chapter 3.3.4.5
Stage 6	Chapter 3.3.1.6	Chapter 3.3.2.6	Chapter 3.3.3.6	Chapter 3.3.4.6
Stage 7	Chapter 3.3.1.7	Chapter 3.3.2.7	Chapter 3.3.3.7	Chapter 3.3.4.7

Stage A	Chapter 3.4.1
Stage B	Chapter 3.4.2

1.1.1.2 Icons used in this Guide

This Guide is written as a practical resource for GR and IP practitioners who work with the practical needs for the utilization of IP information relating to GRs and GR data, so it assumes a basic familiarity with some fundamentals of IP as well as the science and technology basics of your GR sector and technologies, although it does not require the user to be a scientist. The Guide contains supplementary information intended to offer additional resources where legal, scientific, or technological aspects are unfamiliar.

The Guide defines different stages of a search and frames the full sequence data life cycle as a storyline of these stages, including both search and submission phases. You may read the sections sequentially from beginning to end. However, it also has a modular structure, and you can use it as a reference book. Throughout the Guide you will find icons indicating the following practical elements:

Practical Tip: Action-oriented tips and tricks on IP or GR rights management.

Caution: Common legal, policy, strategic or operational risks, threats, or challenges in GR characterization, research, and innovation. The criteria for their inclusion is their practical relevance for the success or failure of GR characterization, innovation, or research projects.

Additional resources, tools, and references: Other related practical instruments, decision-making tools, and standards, for both legal and scientific/technological aspects of this Guide's subject matter.

Get legal advice: The most important message of the WIPO Toolkit for Rights Management in GRs and Data is to obtain legal advice on managing the rights and obligations attaching to any GRs, GR data and IP portfolio. The second most important message is that this Toolkit does not provide such individualized advice. These icons point to some key legal issues which require customized legal considerations and some sources to obtain such advice.

Further reading: The law and science of GRs is evolving and expanding at an unprecedented rate. More information and suggestions for further reading are available on the WIPO website[3] and in the present text marked by this icon.

WIPO products and services: WIPO is continuously developing new products and services on GRs, GR data and the life sciences, as the field evolves. These icons indicate references to WIPO products and services and other programs. Contact WIPO at info@wipo.int for further information.

Example/case study: Examples are taken *inter alia* from the *WIPO Distance Learning Course on Intellectual Property and Genetic Resources in the Life Sciences* (DL-427) and other sources.

Key Legal Issue: Pointers related to core legal choices, issues, and decisions in scientific, innovation, conservation, or commercial practice.

Since, to our knowledge, there is no other tool available that provides this information on sequence searching for GRs users with low resources, budget and legal/scientific know-how, if this Guide does not give you enough detail to conduct your sequence searches to the full extent, or in case you are feeling challenged by either legal or technical aspects of your searches, it is important to recall that this Guide is *not* intended to be an exhaustive resource. You can always access additional WIPO resources and training, such as the *WIPO Executive Course on IP and Genetic Resources in the Life Sciences*, which provides you tutored support for such searches.

1.2 SCOPE OF THIS GUIDE

1.2.1 Scope of users

This Guide is an introduction for beginners, not for advanced users. It is written for all those life science researchers and scientists in developing and developed countries, who are not yet intimately familiar with IP law and management. The goal of this Guide is to give you a simple and accessible starting point for searching, submitting, and using GR sequence data, when you know the science of your GRs, but you are not familiar with the IP dimensions.

1.2.2 Overview of IP rights relevant to GRs and GR data

This Section provides you with an overview and introduction to the main branches of IP law relevant for the protection of GRs as well as GR information and data – i.e., which type of GR subject matter is covered and which rights are involved.

Further Reading:
For additional context information regarding the searches and submissions described in this Guide, see the WIPO IP Guide for GRs and Genetic Sequence Data ("Subject Guide"), available here.

1.2.2.1 Patents

A patent generally grants the patent owner the exclusive right to control who makes, uses, sells, offers for sale and/or imports any invention protected by the patent's claims. Patent claims are sets of sentences, typically appearing at the end of the patent, which describe the invention being protected. In order to obtain a patent, the patent claims must typically describe an invention that is new, useful and non-obvious in view of the "prior art" (a technical term that generally refers to all the public knowledge and inventions that existed before the filing date of a patent application).

What is a patent?

A patent is an award of a time-limited set of exclusive rights from a government for an invention. As explained in the Subject Guide, an "invention" in the meaning of patent law is a solution to a specific and practical problem in the field of technology. GRs cannot become the subject of a patent *as a natural resource*, but only if they constitute an invention. At present, most patent terms are set at 20 years from the date of the application's filing.

The patent must also satisfy other legal requirements, such as time limits related to how long the invention was disclosed to the public prior to the filing of the patent application. Generally, patents will be denied if the invention has been made public prior to the filing of the application, excluding any grace period that may apply. Patents are granted following a formal and substantive examination in which the patent application is thoroughly reviewed by a patent-granting authority. Among other things, the patent examiner will compare the prior

art relating to a pending application against the application's claims in order to determine if the claimed invention provides a novel and non-obvious advance over the prior art.

Caution:

A patent application must be filed *before* publicly disclosing any important results of your GR characterization, innovation, and research activities, such as nucleotide or amino acid sequences that may lead to a valuable product or technology. If you intend to keep open the possibility of filing patent applications, this caution applies also for public research institutions and academic research institutions. You should therefore *not* disclose your characterization or research results prior to having considered if you might file a patent application in the future to which those results might constitute material prior art and, if so, you should file the patent application *before* publishing the research results.

Practical Tip

If your research institution requires the publication of your sequence data as research or academic works, the necessity for you to regularly issue such publications can be accommodated by implementing a publication clearance procedure within your institution, which reviews draft journal and conference submissions for patentable inventions prior to their publication. Necessary measures to safeguard your options for filing potential future patent applications can then be taken at the right time, depending on the IP policy and strategy of your institution, and your GR characterization and research project. Before publishing sequence or other data which could constitute prior art that might be material to potential future patent applications which you might file, you should seek legal advice.

Based on the principle of territoriality of patents, a patent title is valid always only in the limited jurisdiction for which the patent-granting authority that has issued it is competent. It is also only valid if it has not had a successful challenge against it in a court or before the relevant patent-granting authority. Additionally, it is also only valid as long as the maintenance fees for the patent have been paid. For additional IP considerations regarding data exclusivity for such sequence data, please see Section IV.A.1 of the Subject Guide, to which this Guide forms an Annex.

Patent laws normally recognize patent protection for different types of GR-related inventions. At the same time, most patent systems provide uniform treatment for all inventions, regardless of the type of invention and the field of technology, i.e., they implement a principle of non-discrimination as to the field of technology for the availability of patents. The term "patents" usually refers to "patents of invention", which are also referred to as "utility patents", and which protect chemical compositions, machines, processes, and other kinds of inventions that are valuable because of their industrial applicability.

1.2.2.2 Plant Variety's Right and Plant Patent

Plant patents

Some jurisdictions also grant " plant patents", which are relevant to GR-based inventions. For example, in the United States, plant patents may be obtained on "any distinct and new variety of plant, including cultivated sorts, mutants, hybrids, and newly found seedlings, other than a tuber propagated plant or a plant found in an uncultivated state".

Additional resources

If you intend to protect outcomes of your GR characterization or research project in jurisdictions which make available plant patents and you believe your characterization and research results might be eligible for plant patent protection, please consult specialized legal advice.

1.2.2.3 Data Exclusivity

For sequence data which are part of data sets that are submitted for regulatory approvals of life science products, the sequence data may fall under data exclusivity protection. For additional IP considerations regarding data exclusivity for such sequence data, please see Section IV.A.3 of the Subject Guide, to which this Guide forms an Annex.

1.2.2.4 Copyright

Compilations of sequence data and sequence data sets that constitute scientific works have numerous copyright aspects which are widely discussed in other WIPO Guides. See in particular, for the copyright aspects of such sequence data, Section IV.A.2 of the Subject Guide, to which this Guide forms an Annex.

1.2.3 Scope of databases and information systems

Regarding the scope of databases and other information systems covered by this Guide, it is important to recognize and explicitly mention a few limitations.

1.2.3.1 Patent databases

This Guide focuses only on publicly available patent databases. Fee-based, commercial databases for sequence listings in patent literature exist, but are not covered in this Guide. Descriptions of those commercial database providers are available in the WIPO INSPIRE database of patent literature repositories.

A list of existing databases which are covered or not covered by this Guide is contained in the Annex. The focus of this Guide when illustrating patent search and submission principles for patent data is on PATENTSCOPE, the WIPO global database containing sequence listings from the entire PCT collections of patent literature. Practical tips for the use of PATENTSCOPE are provided throughout this Guide.

1.2.3.2 Sequence databases

This Guide focuses only on publicly available sequence databases. Fee-based, commercial databases for sequence listings in non-patent literature exist but are not covered in this Guide. The focus of this Guide when illustrating sequence search and submission principles for sequence data is on the publicly available INSDC collections. Some practical tips for the use of such collections are provided throughout this Guide, but without any assumption of exhaustiveness or up-to-date nature of the information. For up-to-date and complete documentation on using the INSDC databases, it is highly recommended to visit the websites of the relevant databases, which all provide detailed instructions for their use.

1.2.3.3 Need for combining use of databases in practice

In practice, however, it is normal to use a combination of both patent literature and non-patent sequence databases for your searches. Sequence searches in patent databases and sequence searches and submissions in non-patent literature databases may thus be seen as

complementary parts of the full sequence data innovation ecosystem and it is therefore recommended to combine the use of both types of databases in practice.

1.2.4 Scope and types of searches and submissions

The *scope* of a sequence search is the most important factor of the search. This Guide focuses on helping you define the scope of your search in publicly available databases. Additional features for scope delineation are available in fee-based, commercial databases for sequence listings. They are not covered in this Guide, but descriptions of those commercial database providers are available in the WIPO INSPIRE database.

There are numerous *types* of sequence searches that can be performed, and in practice you will probably mostly be using combinations of functions and features from the different search types. For simplicity and accessibility, the searches have been categorized into a few fundamental types in this Guide. This typology is not exclusive and not exhaustive. It is an intentional simplification to give you a simple starting point for making your own searches and practicing the different types of search techniques, so you can eventually combine them as is best for your own purposes.

1.2.4.1 Patentability-related searches

Patentability is one of the most important issues in patent searches since this is critical in formulating an effective portfolio of patents and other IP titles for your life science innovations.

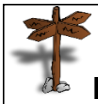
Patentability-related searches may be conducted with various starting points, including subject matter, applicants, inventors, and the like. Subject matter may be searched by using keywords, classifications, GR/biological resource (BR) related sequence information, chemical structure, and the like. Here is a brief overview of the standard starting points you could choose from:

Searches by subject matter – technical keywords

Not all patents and patent applications relating to biological sequence listings/information are associated with the actual GR/BR related sequence information. This means that a significant proportion of patentability searches need to rely on technical keyword information. This Guide covers such searches using keywords by subject matter, which is relevant to GR/BR related sequence information. The Guide explains how you can conduct such subject matter searches by using technical keyword as query utilizing formulae, technologies, and the like.

Searches by subject matter – classifications

All patents/patent applications are classified by various kinds of patent classifications, including in particular the International Patent Classification (IPC) and the Cooperative Patent Classification System (CPC), which is the result of a partnership between the European Patent Office (EPO) and the United States Patent and Trademark Office (USPTO), “F term” developed by the Japan Patent Office (JPO), and the like.



Practical Tip

Searches using classifications are particularly useful when a bulk search and/or general search is required. On the other hand, when a specific search using a particular GR/BR related sequence data is required, classification may not be sufficient and other means such as keywords and actual sequence information may be necessary to obtain satisfactory results.

Searches by subject matter – GR/BR related sequence information

Of course, GR/BR related sequence information such as nucleic acid sequence and/or amino acid sequence information may be directly used to conduct patentability searches. Especially, when novelty is to be verified, specific sequence information needs to be included for your search strategy since such direct searches using sequence information will give you direct results indicating whether your particular sequence of interest is already in the public domain or not. However, care must be taken when GR/BR related sequence information is used, since such information may include errors or uncertain/undetermined sequence information. Such ambiguity needs to be taken into account and therefore similar/variant sequences should always be of consideration. As such, sequence information is a necessary tool for conducting patentability searches, but it is always important to take into account that this is not sufficient and thus a combination of other means, such as keywords, classifications and the like need to be considered.

Searches by subject matter – amino acid or nucleic acid sequences

It should be noted that GR/BR related inventions are often described in the form of amino acid or nucleic acid sequences. In current patent practice, such a sequence-described invention is recited in the form of SEQ ID Nos in patent specifications with the use of sequence listings (currently ST.26 format for patent applications having a filing date of July 1, 2022 or later, but most of the existing patent literature currently still uses ST.25 format). The sequence listings are not included in the description of a patent specification in a normal text, but with a special format. As such, a search with a text or classification will not produce any satisfactory results. In this regard, one has to use special search measures to locate a search result with adequate contents. In this respect, one has to use sequence information *per se* of your search interest as a query in an appropriate database, which allows one to conduct searches directly using sequence information, such as amino acid or nucleic acid sequences. In WIPO PatentScope, such a function is yet to come, but there are a number of paid or free databases. The Subject Guide makes use of publicly available databases to provide you with tips for conducting such searches, using sequence information as basis of your query.

Searches by subject matter – chemical structure

It should be noted that materials relating to GR/BR related sequences are chemical substances. Inventions relating to GR/BR related sequences are often modified into chemical substances which cannot be directly expressed as nucleic acid or amino acid sequences. For example, a number of successful mRNA vaccines are chemically modified nucleotides/nucleosides which may be novel in the art. As such, such modified nucleotides/nucleosides need to be searched by using chemical structure searches. This Guide also provides you with tips for conducting such searches using chemical structures as basis of your query.

Searches by patent applicants and/or inventors

Searches may also be conducted by using applicants' information. Information related to applicants can include applicant's name, inventor's name, etc.

Applicants' names may be searched by looking at the relevant commercial entity name but it needs to be kept in mind that although patent applications are usually filed in the name of commercially known company names, often they are also filed in the name of IP specified entity's names, such as a patent management company and the like. Furthermore, until 2012, in the United States of America (U.S.) only inventors were able to file a patent application because the U.S. followed a first-to-file approach, so it is necessary to keep in mind that inventors' names can be used to conduct a search as applicant's query.

As such, inventors' names are also important information to conduct efficient patent searches. In addition to the above-mentioned U.S. circumstances, it is often the case that some of the inventors are Key Opinion Leaders (KOL) and thus such KOL inventors should be watched for a particular invention regardless of the field. Of course, inventions relating to GR/BR related sequence information are not exceptions. Therefore, inventor's information is often important to conduct effective patentability searches.

When conducting inventors and applicants searches, not only the individual entities are to be searched, but also networks between the inventors and/or applicants are sometimes useful in patentability searches.

There are also two other special searches which fall into this search type:

Searches covering different knowledge systems, such as traditional knowledge systems

Several patent granting authorities have issued distinct examination guidelines for patent applications claiming GR/BR sequences related to traditional knowledge (TK). Such GR/BR related sequences may be searched using patent databases and, more importantly, sequence databases provided by a number of academic/governmental organizations should be considered for exhaustive searches. Additionally, some jurisdictions have prepared local databases that allows searches on TK and such databases may be a good source of searches relating to GR/BR related sequences.

WIPO Resource:

The Traditional Knowledge Division of WIPO maintains a list of databases which contain TK, including TK associated with GRs.

You can access the list here.

Searches by patent examiners/search report conducted by a patent office

Many patent offices, including those of PCT Contracting States, provide search reports, including international search reports (ISRs). Such information should be considered.

1.2.4.2 Freedom-to-operate (FtO) searches

FtO searches are not fully covered by this Guide. FtO searches are also called "Clearance" searches and are conducted as a part of due diligence work. FtO searches may be conducted using several patent databases.

As FtO clearance searches eventually require professional legal opinions, this Guide provides you only with preliminary searches for this purpose, so that you can obtain a general sense of infringement/non-infringement of your particular project/target.

For this, you will have to undertake case law searches too.

In order to actually and finally clear the FtO search, it is necessary to clear the "literal", "direct" infringement test, but also the "indirect" infringement test. In addition, and in particular, the "doctrine of equivalents" infringement test needs also to be cleared. Furthermore, any other defense, such as invalidity, prior user rights and the like need to be considered. Where case law needs to be heavily considered, it is often necessary to take a final decision as to whether the particular search target is ultimately an infringement risk or not.

For this, the present Guide recommends seeking professional FtO analysis services from patent professionals. In any event, before going to consult with IP professionals, readers may be able to prepare for the consultation. This Guide will provide information about such preparatory FtO clearance searches ***only***.

Caution:

It is important to note that this Guide does ***NOT*** – categorically ***NOT*** – provide any advice on any specific FtO searches, methods, parts, or processes thereof and does not assume any responsibility or liability on the part of WIPO for any FtO searches conducted by using this Guide, including their results, implications, interpretations, or any resulting consequences thereof.

1.2.4.3 IP landscaping searches

IP landscape (IP landscaping) analysis is an analysis of patent and other IP data that reveals business, scientific and technological trends. IP landscape reports usually focus on a single industry, technology, geographic region, or combination thereof. IP landscaping analysis requires not only patent information, including patentability searches, FtO searches, but also patent and non-patent information relating to the target technology of interest should be included within the search scope.

Based on an efficiently done IP landscaping analysis, one can know how the technology of interest may be patented, so that you can create an efficient IP/patent portfolio. Furthermore, an IP landscaping analysis provides you with an overview about business models and business opportunities for your particular technology of interest. Such information can include whether "dangerous" patents exist (which limit your freedom-to-operate) and whether licensing-in activities may therefore be necessary, how the market of interest has developed, who the main scientific and business stakeholders are and the like.

1.2.4.4 Due diligence searches

Due diligence is the evaluation of an entity or target, which includes legal due diligence, IP due diligence and the like. An IP due diligence is the evaluation of the intangible assets owned or used by an entity (which may be the entire company or a part of a company) in order to obtain reliable knowledge about their value. Due diligence is often practiced when mergers and acquisitions (M&A) are conducted, but also needs to be conducted when one company wants to obtain a particular business unit within another company.

IP due diligence includes multiple (direct) IP searches, including the patentability and FtO searches mentioned above and other IP related searches, plus additionally the review of any contracts relating to IP. Increasingly of particular interest in due diligence searches relating to GR/BR sequences is compliance with the Convention on Biological Diversity (CBD), its Nagoya Protocol (NP) and other matters concerning access and benefit-sharing (ABS) for GRs.

(a) IP searches

As mentioned, IP due diligence includes multiple (direct) IP searches, including the patentability and FtO searches described in the preceding subsections, and other IP related searches. Additionally, any contracts relating to IP may need to be reviewed.

(b) Contractual terms and conditions

A number of agreements and contracts are associated with IP matters. As this is important to decide who would be the owner of the particular IP assets, contracts are always important to check.

(c) ABS searches

Inventions relating to GR/BR sequences may be within the scope of coverage of the CBD or other ABS instruments on GRs. Thus, it should always be cleared that the inventions relating to GR/BR related sequences are legally, legitimately, and authentically obtained and thus the IP assets relating thereto can be properly enforced. As of December 2022, the CBD Conference of the Parties decided to establish a benefit-sharing mechanism which relates to digital sequence information (DSI), yet to be implemented. Compliance in relation to such mechanisms should be ensured in the context of due diligence searches.

(d) M&A

When an M&A is conducted, every single matter needs to be checked. Readers should consult with M&A professionals when actually conducting this kind of due diligence. This Guide only provides an overview of general due diligence searches and does ***not*** cover M&A due diligence.

1.2.4.5 Submissions for technical public disclosure to sequence databases

It is often important and useful to submit data and information relating to GR/BR sequence to public sequence data repositories. This is important because a legally certain submission and registration on a public repository renders to the target technology a level of legal certainty, which is otherwise not available, and thus technical public disclosure is important to that extent. On the other hand, after submitting your technology to the database, which eventually discloses it to the public, the novelty of that particular technology will be permanently lost.

This Guide also provides directions for direct submissions and facilitated submissions, including on particular aspects and options that should be kept in mind from an IP perspective, such as:

(a) Legal certainty and technical public disclosure

(b) Layers and functions of disclosure for biological sequences

(c) Direct submissions, and

(d) Facilitated submissions.

1.2.5 Scope of GRs or BRs

Please note a few important qualifications regarding the scope of GRs and BRs, as covered and addressed in this Guide:

(a) This Guide also covers the technical aspects for searches on human GRs, but it does not cover the related data protection, privacy, and regulatory aspects thereof;

(b) The Guide covers both GRs and BRs, i.e., it covers both nucleotides and amino acid sequences;

(c) This Guide can be used to explore/investigate antibody claims, but there are limitations regarding what is the best description regarding antibody claims;

(d) Antibodies are a good example to explain patent searches relating to GRs and BRs. Antibodies are typical embodiments of biopharmaceuticals. It is also important to learn how such antibodies may be described in patent claims. To this end, it is noted that antibodies are glycoproteins that are generated by the immune system of homo sapiens and other animals to tag and target pathogenic agents (antigens) for destruction. Therefore, antibodies may be described through [1] Composition of matter

claims (antibody as product), which is very important; [2] Use/indication claims (method of treatment/diagnostic); and [3] Manufacture claims. This Guide will explain how such antibody claims may be constructed and protected through a patent and thereby allow readers to consider how to efficiently search for antibody inventions.

1.2.6 The relevance of prior art searches and submissions for global public health and pandemic preparedness

It is also pertinent to note the importance of prior art searches and submissions in public health since the effective availability and use of sequence data is of paramount importance for pandemic preparedness and response in the case of repeated or future pandemics. The Covid-19 pandemic illustrated more than any event in human history how important sequence searches and sequence availability are for global public health and the future of human health on the planet including all societies, whether in developed or developing countries, or IPLCs. Particularly important for public health related searches, such as searches for mRNA vaccines, are combined sequence and chemical structure searches.

This Guide will use some examples of searches for mRNA vaccines as illustrations on how to conduct GR sequence searches for public health.

2 DISCLAIMERS

In this Guide, WIPO neither endorses nor opposes any particular policy or approach to IP rights in GRs management. This Guide does not provide:

- Legal advice on IP rights for specific uses of GRs or specific GR-based innovations and creativity. References to information sources, where such advice or related information are available, are included in the relevant chapters and text boxes;
- an introduction to genetics, GR/BR management or GR/BR characterization techniques;
- current information on the status of national or regional legislation applicable to GRs and GR-based innovation. Information on such legislation is available from the WIPO Lex database, and additional references to information sources are in the relevant chapters and text boxes;

Furthermore, it is important to note that the information contained in this Guide:

- does not constitute legal advice;
- does not claim to be up-to-date on constantly evolving databases and their functionalities;
- is not exhaustive and does not assume any responsibility for any searches or submissions;
- does not cover FtO searches or any similar legal analysis of search results;
- creates no liability of WIPO on any searches or submissions conducted by readers.

3 PRACTICAL SEARCH PROCESSES AND PRACTICES

3.1 INTRODUCTION

Practically speaking, once you have decided that a search is necessary, you have to think over what is the object of your search.

For example, if you wish to prepare and file a new patent application relating to a genetic resource, you will have to conduct a search of such genetic resource of your interest. Such a prior art search would result in clarifying whether the invention relating to your gene of interest would be novel and/or non-obvious vis-à-vis the state of the art. Additionally, before filing a new application, you may wish to do some investigation on the state of the art and analyze what types of patent applications are out there to consider and take them into account in your patent application strategy, and create an effective patent portfolio accordingly.

On the other hand, if you wish to launch a product relating to GRs, but you are unsure if there is no IP bar to enter into the market, you would need to conduct a clearance search, i.e., a freedom-to-operate search. Based on this freedom-to-operate search, you can ensure that the product and/or service of your business does not infringe any patents except those held by you or by parties which grant you a license to practice the invention underlying your product and/or service.

Once you find a patent that might prevent you from entering into your market of interest, you may wish to invalidate and/or narrow down the scope of such a patent. Then you would have to conduct a prior art search. Typically, it is possible to narrow the scope of claims of such a patent by providing relevant prior art information to the relevant patent-granting authority.

From a business point of view, patent information is a good information source of “future” business. Therefore, patent search may also be conducted as a marketing tool.

Finally, technology trends can also be analyzed based on patents and other IP searches for GRs.

3.2 TYPE OF SEARCHES

First, you need to decide what your search objectives are.

3.2.1 Prior art searches/Patentability searches/Invalidity searches

Prior art searches/Patentability searches/Invalidity searches are similar in performing such searches: all of them are related to patentability of certain subject matter.

Prior art searches are mainly undertaken to conduct patentability searches for your new patent filing, and for invalidation purposes of existing patents and/or patent applications. These are similar but there are some differences and thus their relation is explained in terms of similarity and difference in this section.

Patentability searches are typically conducted to obtain information as a basic information source for new patent filings. In this regard, in the case of new patent filings, often you may not be sure of the patent claims to be searched. However, that is no reason for concern since this is common. Perhaps you may have some information from the inventors in your hand, but often such information is not in patent claims format.

Generally speaking, nucleic acids of GRs are claimed in patent applications through product and process claims, which could be described through the following categories:

1. *Product claims for nucleic acids*

   (a) which characterize a nucleic acid by the nucleic acid sequence itself (in full or in part);
   (b) which characterize a nucleic acid by functional terms;
   (c) which characterize a nucleic acid by the amino acid sequence of the encoded protein (in full or in part);
   (d) which characterize a nucleic acid by reference to a deposited microorganism or deposited DNA;
   (e) which characterize a nucleic acid by parameters;
   (f) which characterize a nucleic acid by a process for its preparation;
   (g) which comprise nucleic acids as essential elements;
   (h) for certain types of nucleic acids and methods of using same.

2. *Process claims for nucleic acids*

   (a) involving isolation from a nucleic acid source;
   (b) claims involving genetic engineering or synthesis;
   (c) Use claims/purpose-limited product claims for nucleic acids.
      c-1. medical/pharmaceutical use
         c-2. agricultural/plant/animal(non-human) use
         c-3. microbial use
         c-4. biotechnological use.

In this regard, depending on the type of claims you wish to search for patentability, your search strategy may differ.

Invalidity searches are conducted to obtain information to attempt to invalidate an existing patent and/or patent application. Therefore, you would need to obtain accurate information on the patent/patent application on record in order to conduct an effective and efficient search for it, including its time of application/examination/grant, jurisdiction, stage, etc.

3.2.2 Freedom-to-Operate(FtO)/Clearance searches

Once you have decided to conduct a freedom-to-operate (FtO) search, you need to define your search from the point of view of your interest. When you are considering your FtO to develop, make and put on the market a new product or process resulting from your GR characterization and innovation work, an FtO analysis is done by systematically and fastidiously disaggregating the product or process into its basic constituent elements and then analyzing each one for the attached IP or other rights which could constitute encumbrances for future product(s) or process(es).

If you have identified results of your GR work, which you would like to develop into a product or process for production, then a thorough FtO analysis will inform you and your institution whether the development and commercialization of the new product or process can go forward with a limited risk of infringing unlicensed IP or other GR-related rights of others.

However, since the IP and other legal landscapes surrounding your GR characterization results are continuously changing and evolving, the outcomes of your FtO analysis may also change and need to be updated over time. New patent titles might be granted, or old ones expire, or some might

Get legal advice:

If you are conducting FtO searches, it is important that you seek legal advice from an IP professional with legal expertise and an in-depth technical understanding of your field of technology. It is important to note that this Guide does ***NOT*** provide any advice on any specific FtO searches, methods, parts or processes thereof.

be invalidated; patent portfolios or parts thereof may be transferred, assigned, or licensed; licenses may be issued and terminated. All these developments continuously change your FtO.

An FtO analysis is a systematic and thorough exercise, which should be completed by specialized counsel. However, several steps can be well prepared. Some of the preparations that you can do at this stage include:

- Composing your team for FtO analysis;
- disaggregating and analyzing the product or process to be developed;
- compiling and using your laboratory notebooks and other materials;
- assessing GR pedigrees;
- interviewing the GR researchers and scientists;
- identifying relevant contractual agreements, such as MTAs, shrink-wrap licenses, and other contracts concerning the GRs and related property titles;
- defining FtO questions and issues;
- selecting patent literature and non-patent literature databases;
- dealing with sectorial specific information resources for pharmaceutical patent information;
- managing the “grace period”;
- ensuring due diligence during the FtO analysis and beyond.

3.2.3 Technology trends searches/ patent landscape searches

Technology trends searches/ patent landscape searches are similar to each other, and such technical trends may also be elucidated by conducting patent and non-patent searches. Thus, please refer to the other search types most relevant to you as listed above.

3.2.4 Market searches

Market information may be obtained by an organization or a private sector entity.

3.3 DETAILED EXPLANATION IN ACCORDANCE WITH THE RESPECTIVE STAGES:

In order to provide you with a simple, accessible, non-technical framework for all sequence search types, hereinafter, each type of above-listed search types is described within a unified frame of the following stages:

STAGE 1: Defining the objectives of your search.
STAGE 2: Building your initial query building blocks.
STAGE 3: Refining your search query: Trial and error and modification processes.
STAGE 4: Analyzing your search results.
STAGE 5: Applying your search results to your objectives.
STAGE 6: Recognizing the limitations of your search results.
STAGE 7: Finalizing your search: preparing reports.

3.3.1 Prior art/ patentability searches

Here you will find a slightly more detailed example and an explanation of how a **prior art/patentability search/**invalidity search is practically conducted.

3.3.1.1 STAGE 1: Defining the objectives of your search

A subject matter related to a specific genetic resource is characterized and explained. Let us assume one (relatively) newly identified gene is to be searched: gene GR1 having a SEQ ID No: 1 (a nucleotide sequence) and SEQ ID No: 2 (an amino acid sequence corresponding thereto) having the Gene name "XYZ" also known as "ABCase," having Gene ID X000001. The sequence of this gene will be used as the object of your search.

The first task is to define the exact questions you are trying to answer. If your goal is a final product, then consider such a final product first. But do not forget to consider preparation methods, intermediate products, and any relevant tools to prepare such a final product. Once you have identified your questions, do an additional brainstorming to create questions about the gene or identified sequence from different angles.

The above-mentioned sequence related inventions have the sequence information relating to either amino acid or nucleotide sequences. You can begin with the sequence of your interest, and you may wish to start your preliminary search with the sequence. You will soon realize whether your sequence is unique enough to distinguish itself from other existing and known sequences or not. In addition, one has to keep in mind that partial sequences need to be analyzed since many patent applications often identify their inventions using partial sequences. Further, many genetic sequences have unique domains or regions, which are a representative form of partial sequences. Such domains or regions may be a good starting point for partial sequences. If there are similar sequences, alignment amongst such multiple similar sequences or any other search query tools may be used for preparing your search strategy.

Some tips at this stage: There are a number of search tips and the most fundamental is to connect your search to your business objectives. Refer to some relevant document reference that explains business objectives when considering your objectives of your search. IP search are always related to business either directly or indirectly.

3.3.1.2 STAGE 2: Building your initial query building blocks

Next, you will build your initial query building blocks. Before doing so, you need to decide which database functions you will use.

Building your initial search queries is the first step: Queries and formulae are important and the most essential framework for your search activities. For this, you may start by defining the following building blocks:

- **Keywords**
  Keywords are the most common and easy starting points for conducting IP searches. There are a number of ways to identify your keywords of interest. The respective means of keyword listing have their own specific considerations.

- **Starting from gene names**
  No comprehensively coherent nomenclatures like in other fields of technology exist in the field of the life sciences.
  One of the simplest ways to prepare your search queries for GRs is to use gene names. Usually, you come with your source of information relating to your project relating to GRs, and such sources usually are associated with names of genes. In this regard, such names are usually expressed using the "currently" recognized gene names. However, genes have usually their own history of developments of research, and there are variations in terminology relating to the same gene over time. As such, you have to consider the history of the gene of your interest. In this regard, there are usually some references regarding the synonyms of the same gene, and you can refer to the relevant literature or references.

When you go to the websites of most scientific resources, you will usually find such a history of the gene of interest. There could be a number of synonyms and changes of nomenclature and/or biological classifications.

- **Starting from enzyme or other protein names**
  Enzyme and other proteins such as structural proteins and the like also have a large number of synonyms and genus/species in classification categories (e.g., hydrolyzing enzyme can include lipase, esterase, etc.).
  Genes usually encode a particular enzyme or other proteins. Similar to the gene names of genes, proteins have also numbers and synonyms. Enzymes and proteins have been codified and can be used as queries.
  Historically speaking, there are many cases where enzymes and proteins were first identified and only later genes coding for the particular enzymes and proteins were identified.

- **Dictionaries of synonyms**
  Dictionaries of synonyms may be easily found. Most biological sequence databases provide life science dictionaries which focus on two categories of issues. These issues can be listed as follows:
    1. Taxonomic naming issues: Enzymes per se are classified from taxonomic point of view using EC numbers.
    2. Species, genus, and other taxonomic terms.

- **Pre-clinical, clinical, and post-clinical trials naming**
  It is also possible to conduct searches based on the names of pre-clinical, clinical, and post-clinical trials. There are considerable naming issues in the pharmaceutical sector that are worth taking into account and are relevant to a global health context.

- **Traits and phenotypic nomenclature**
  These descriptions relate to the phenotypic, not the genotypic, traits of the relevant plants or other organisms. They may also serve as important starting points for searches.

- **Specific relevance in plant breeding**
  Types of sequences:

    1. Nucleotide sequence
    2. Amino acid sequences
    3. Other sequences such as carbohydrate sequences and the like

- **Sequence similarity (homology) searches**
  These similarity searches are mostly conducted with two main types of search tools:
    1. Basic Local Alignment Search Tool (BLAST) searches
    2. INSDC databases (DNA Data Bank of Japan (DDBJ), the National Center for Biotechnology Information (NCBI) and EMBL-EBI) are a good source of searches. Within the WIPO Patent Analytics Manual, there is a distinct section on *The Lens*, which may provide a useful feature.
    3. FASTA searches

  These are powerful searches, but they can be complicated searches, as some degree of algorithms has to be used. You may wish to consider claims languages, using variation language, such as “#%identity”. There can also be one or more variations, such as addition, deletion, or substitutions. You may wish to use a partial sequence as query for conducting your search, as it often is the case where important

inventions are described using specific features of genetic information such as specific domains or regions.

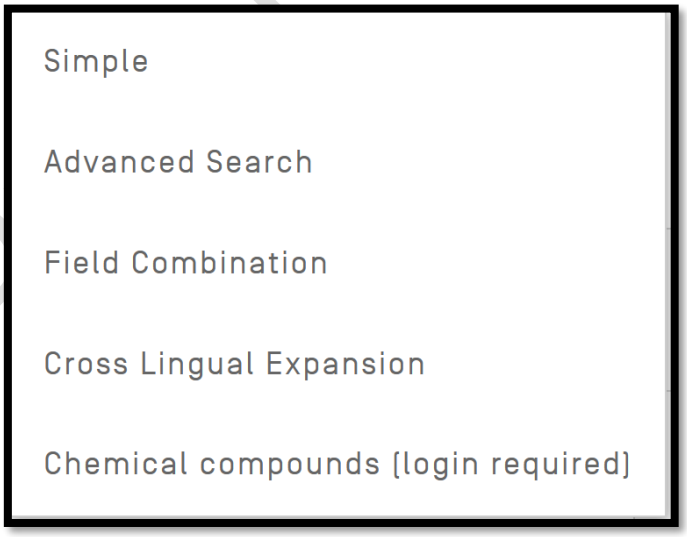
- **Chemical Structure**
  Chemical structure searches are closely related to sequence searches and form important building blocks in combination with them. They can be undertaken with the PATENTSCOPE Chemical Structure Search Tool, which provides ease of searching and user-friendly search results display for the chemical structures.
  The combination of chemical structure searches with sequence searches is particularly relevant for pharmaceutical inventions in a global health context.

- **Classification codes**
  A selection of classes or sub-classes within the multiple classification systems that have been developed for patent searching can provide valuable additional parameters and building blocks for your sequence searches.
  Within the International Patent Classification (IPC), the Organisation for Economic Co-operation and Development (OECD) has defined a list of IPC codes which they have classified as the Biotechnology IPC codes. These can provide you a starting point for selecting your IPC classes, subclasses, or groups.
  Besides the IPC, also the Cooperative Patent Classification (CPC) system for patent literature will provide you the possibility of defining limiting parameters and filters for your sequence searches.

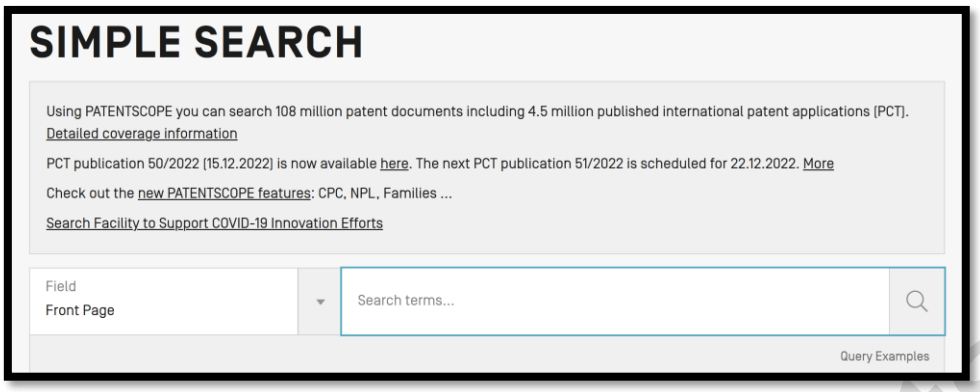
- Patent linkages
  A final building block for your sequence search queries may be the patent linkages of your target sequence(s) and these linkages can provide you additional references to relevant patent and non-patent literature.

Based on these building blocks, you may now be ready to test combinations of your search query building blocks in different search formats. There is a range of search formats you can use for this. In this Guide, we will use the PATENTSCOPE search formats in order to illustrate these formats, which are common to many patent databases.

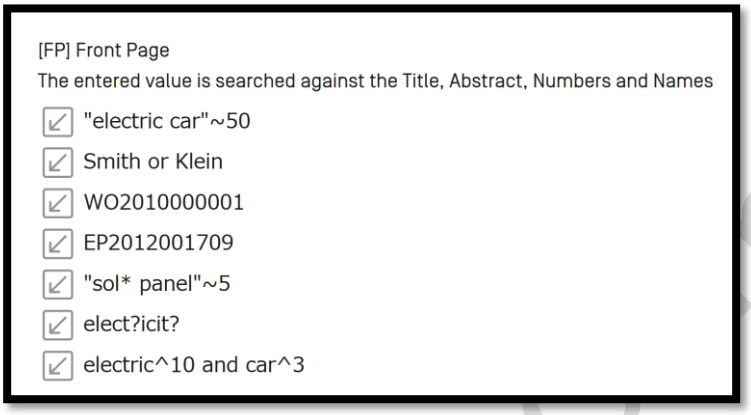
In PATENTSCOPE, there are a number of formats for searches, including the below:



For beginners, it would be easier to start with a “Simple” search.

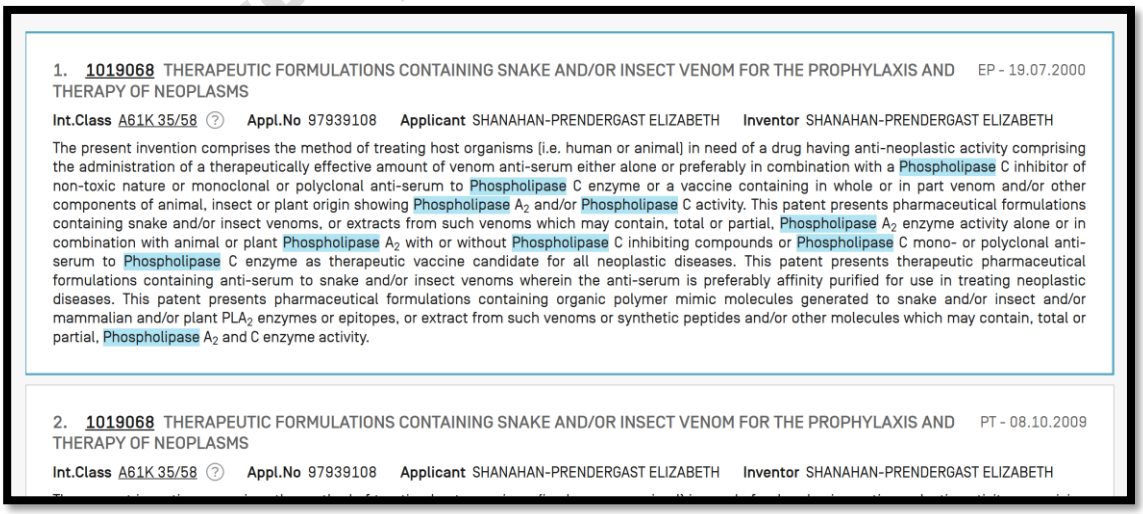


In the query term, you can input a specific term such as the gene name or ID.

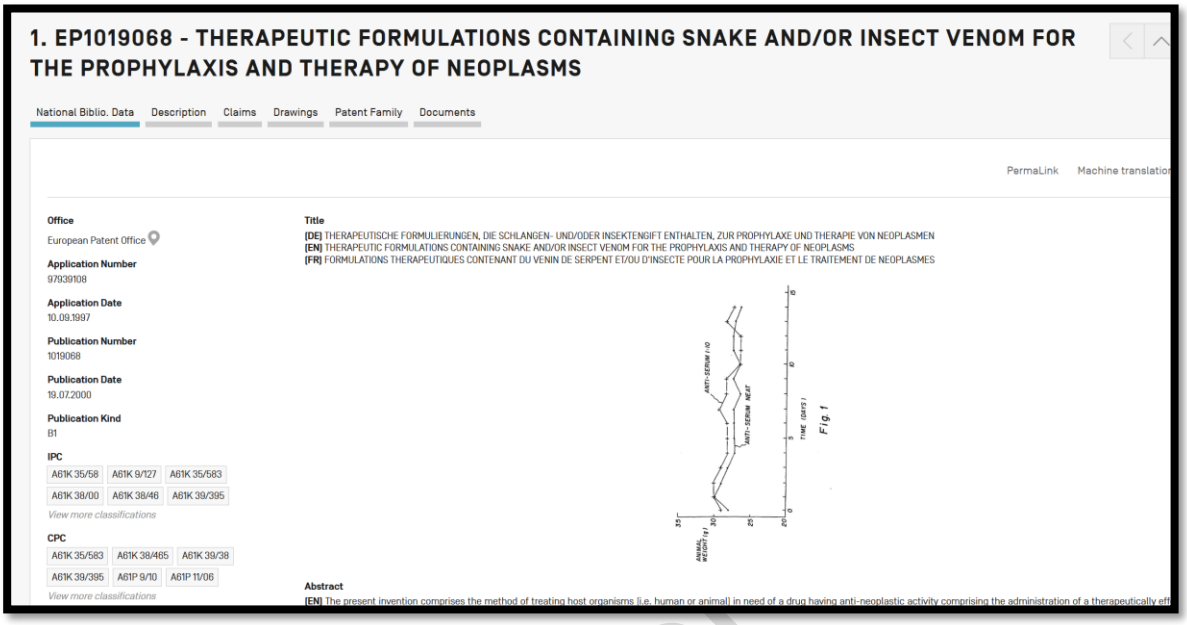


Usually, a specific gene name can be used for searches. For the gene name search, there are usually synonyms and thus you may use the thesaurus dictionary or reference to ensure full coverage for your search.

You will obtain some search results from your initial search (the following is a search result using the term “Phospholipase”)



By clicking the first search result, you will be able to see the individual patent record with its core components of the body of the patent: front-page bibliographic data, description, claims and drawings. In addition, you will receive information on the full patent family, to which your found patent document relates, and other relevant documents of the patent file.



You will see a number of important additional items, including IPC, CPC, and the like, and you may take a look at the Description by tab-clicking. You can also obtain a publication in PDF format.

While reading the abstract and description, you can find synonyms relating to your query term (in this case, PLA_2, lipolytic enzyme, and the like). Depending on the circumstances, you can create query groups for the concept for this term including the synonyms you identified and refine your search using those.

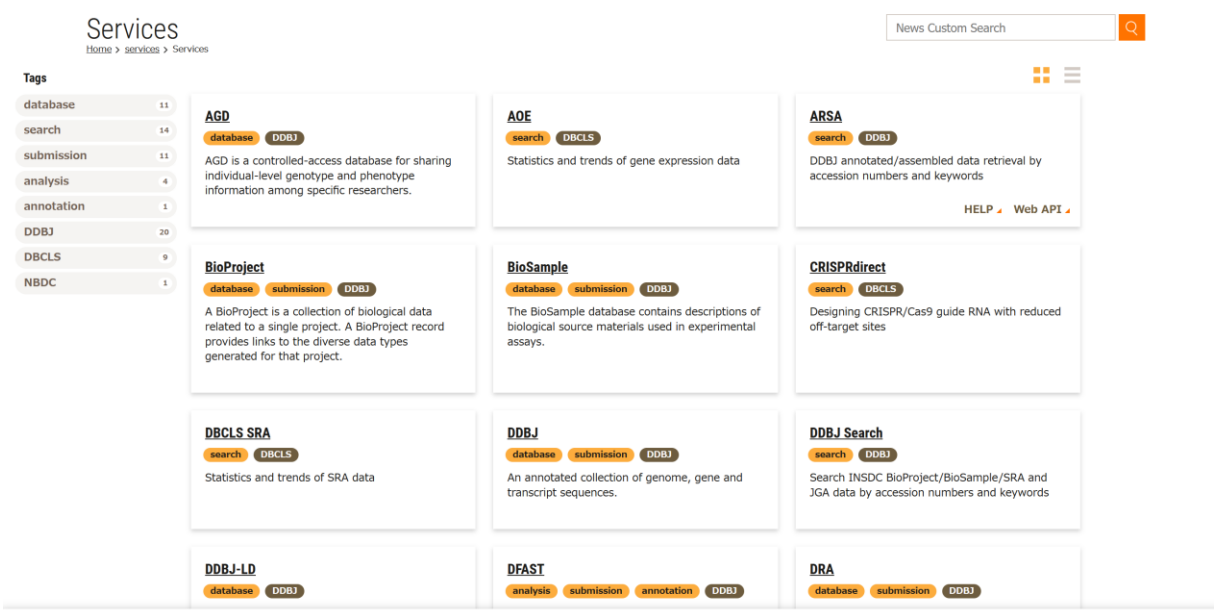
In the publication, classification numbers such as IPC and CPC are included. Here you can find a relevant IPC/CPC such as A61K 38/465 for phospholipase (in this case, this class number corresponds to Hydrolases (3) {acting on ester bonds (3.1), e.g., lipases, ribonucleases}).

IPC/CPC are usually a little bit broader for GRs patent searches, but it may sometimes be good for refine your search strategy.

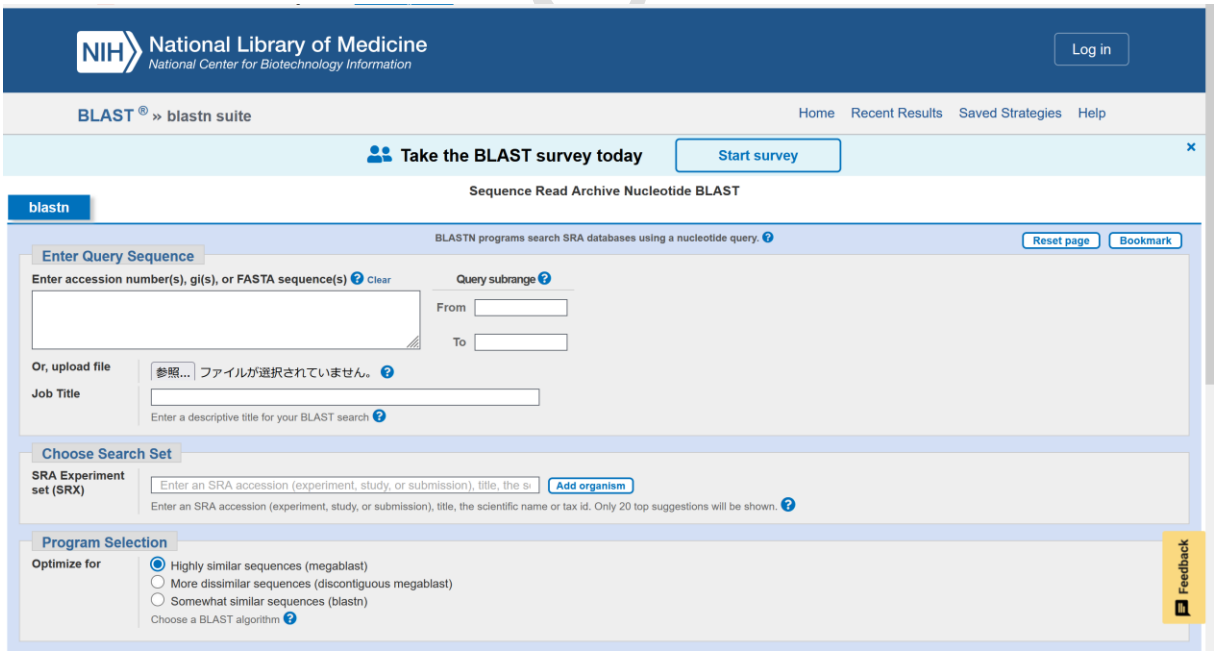
The first search results are usually not the “right” ones that you wish to locate. However, that is no reason for concern, that is normal and not a problem resulting from the technical or legal complexity of the exercise, or your technical error or shortcomings. You could think of this initial search as merely the starting point to endeavor and create better search strategies.

In the sequence information search, for example, DDBJ, one of the trilateral organizations of the INSDC, provides a number of tools for sequence searches.[2]

[2] https://www.ddbj.nig.ac.jp/services/index-e.html



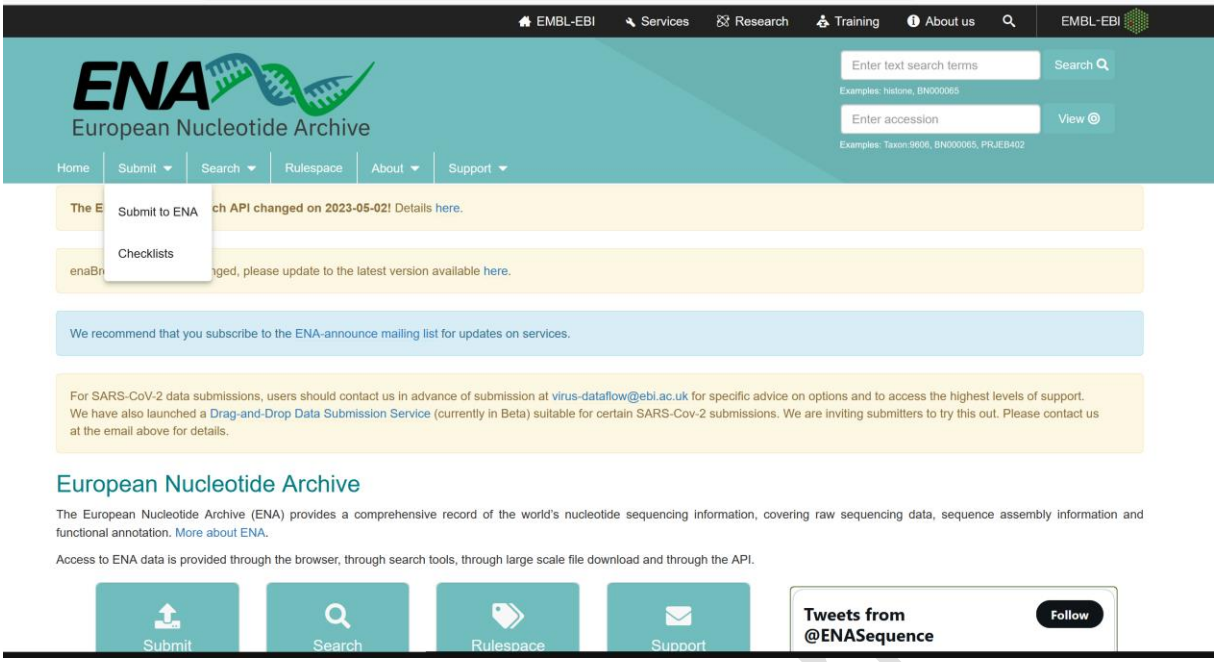
You can also go to NCBI or EBI for equivalent searches. The following is an image of NIH (NCBI) BLAST search query page[3].



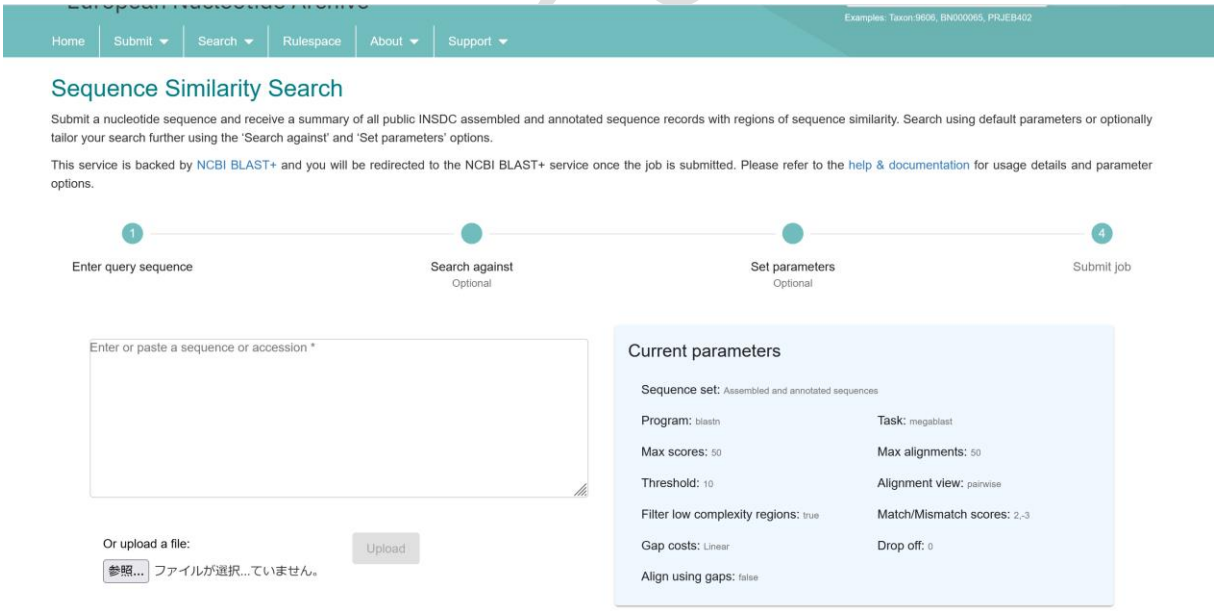
EBI '(ENA) is as follows[4]:

3 https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&BLAST_PROGRAMS=megaBlast&PAGE_TYPE=BlastSearch&BLAST_SPEC=SRA&SHOW_DEFAULTS=on

4 https://www.ebi.ac.uk/ena/browser/home

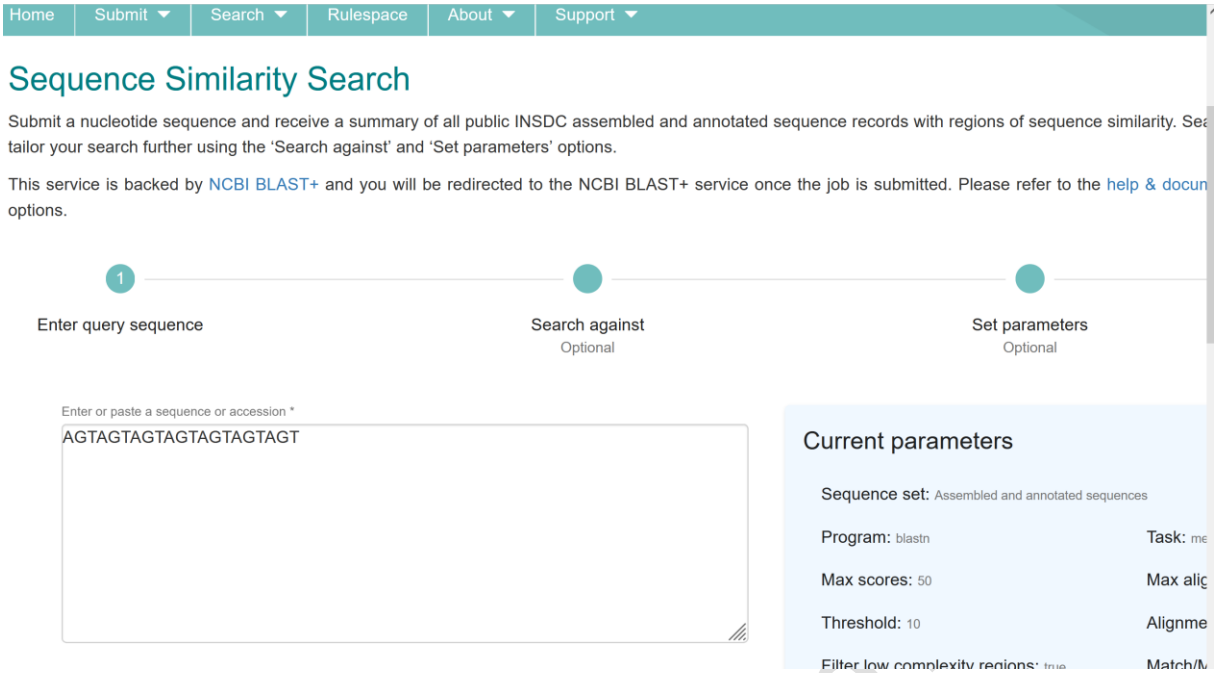


To explain search strategy, we will explain ENA's similarity search[5].

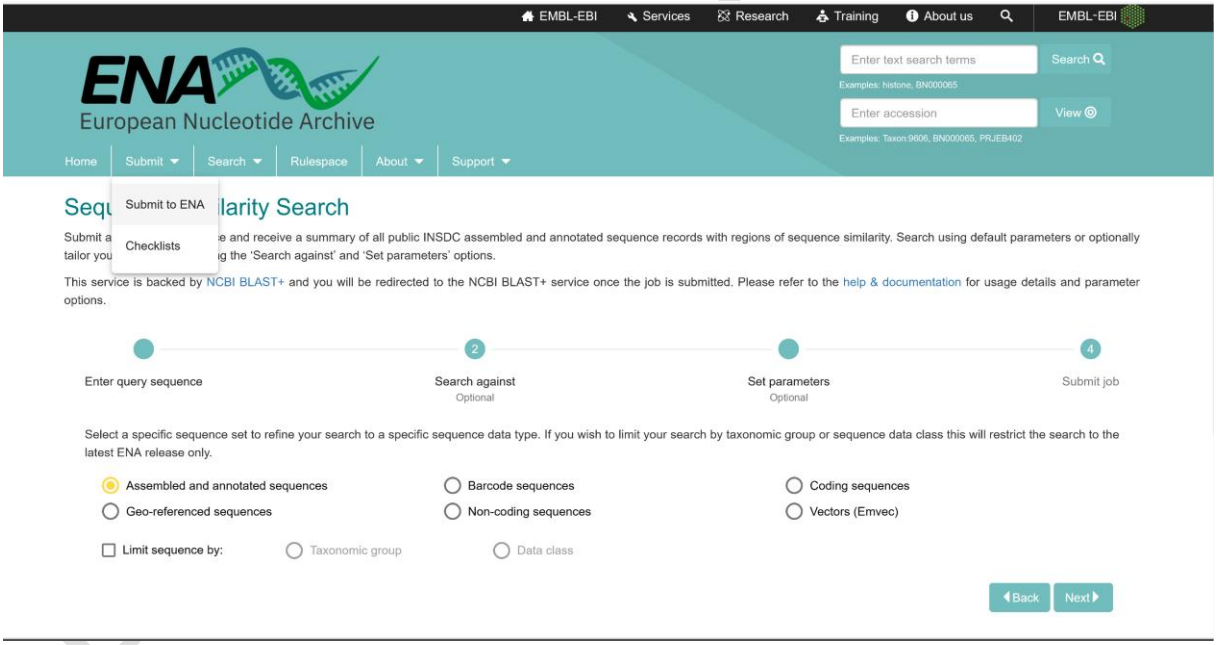


In the first round, you will enter your sequence of your search query as follows:

[5] https://www.ebi.ac.uk/ena/browser/sequence-search

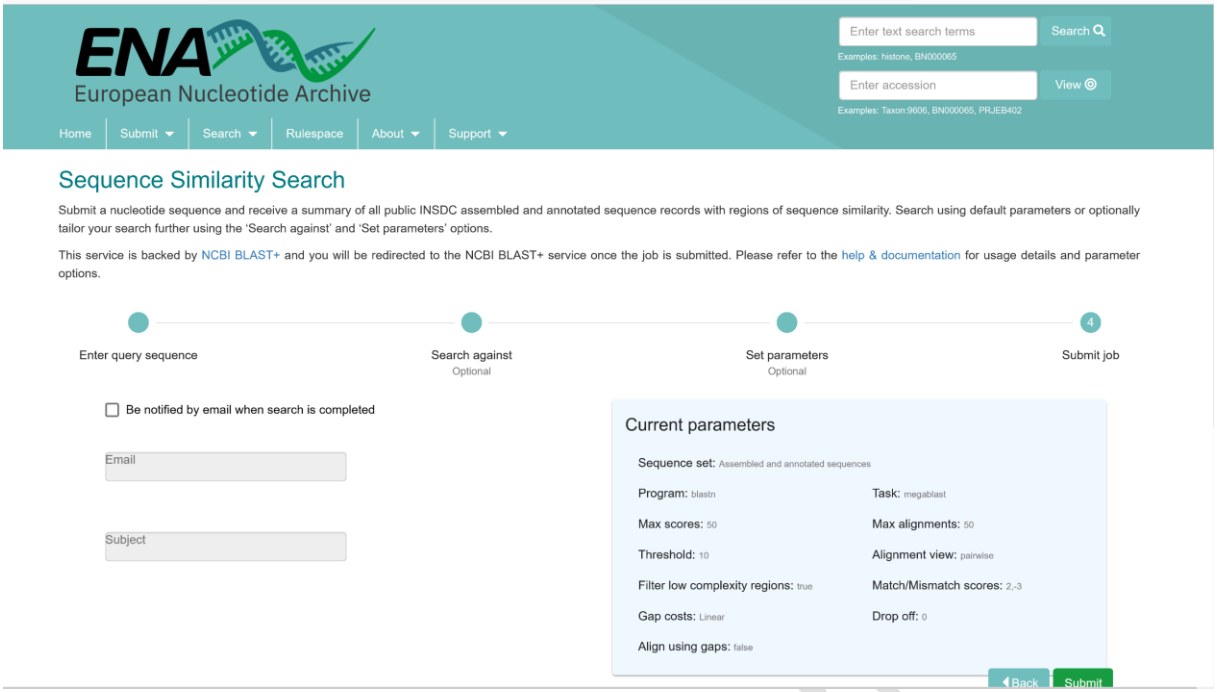


You can optionally choose the database of your interest, or proceed with the default setting.

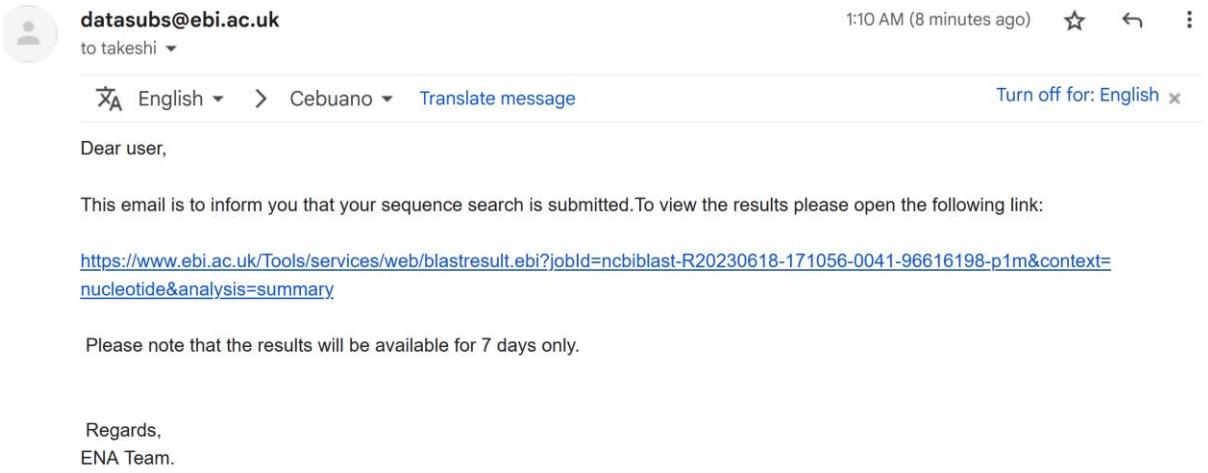


Then you can set your parameters of interests, or you can use default setting.

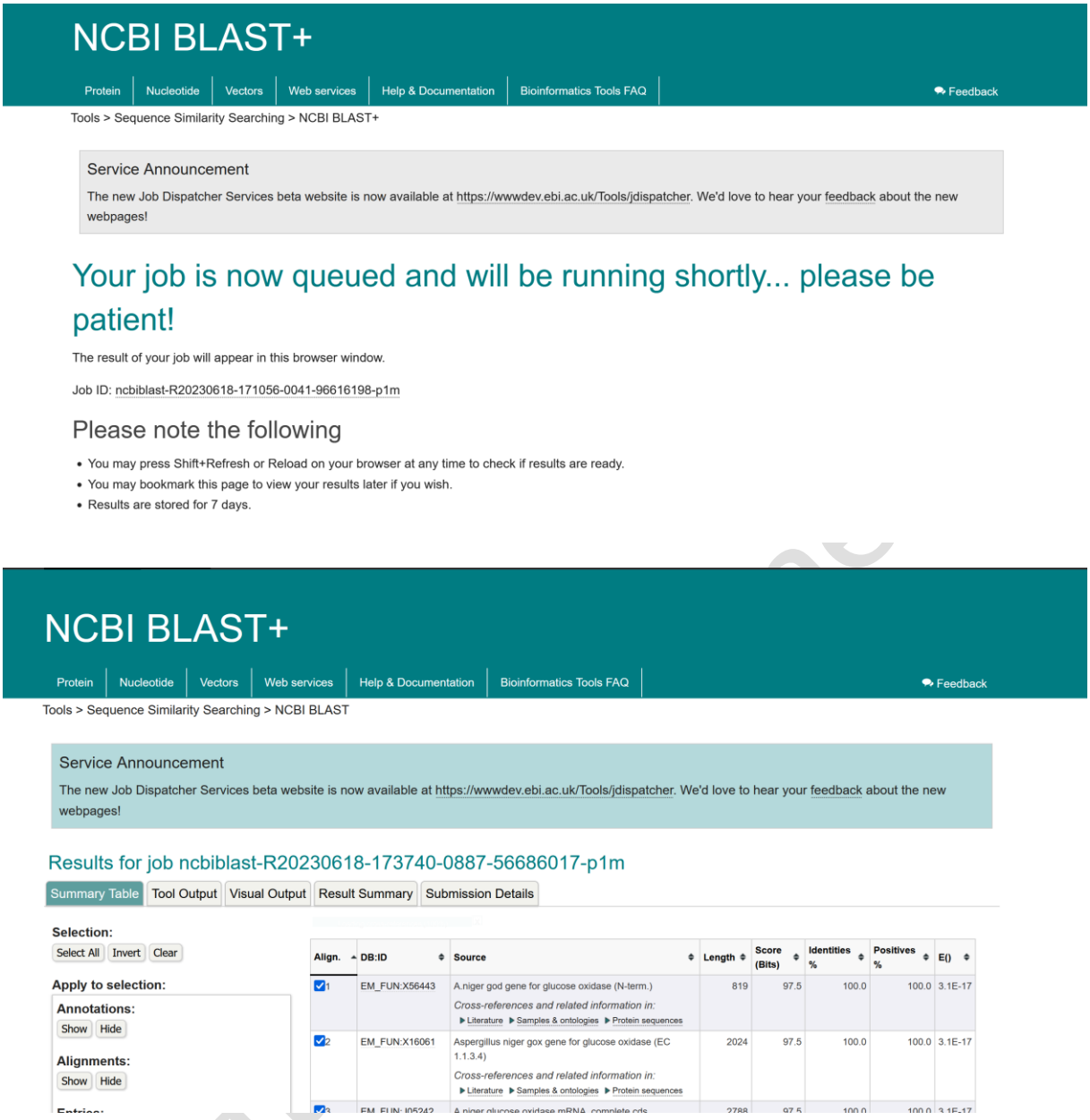
Once the search settings are completed, you will be asked if your search result needs to be sent via email or presented on site.



You will receive notifications from ENA once the search is completed.



The link will lead you to the following page:



You will obtain a search result as exemplified above. You can also view it in another format or in a visual format.

```
BLASTN 2.12.0+


Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb
Miller (2000), "A greedy algorithm for aligning DNA sequences", J
Comput Biol 2000; 7(1-2):203-14.


Database: em
           188,844,347 sequences; 1,356,524,713,175 total letters


Query= EMBOSS_001

Length=60

                                                                    Score     E
Sequences producing significant alignments:                        (Bits)  Value

EM_FUN:X56443.1 X56443.1 A.niger god gene for glucose oxidase (N-t...  97.5    3e-17
EM_FUN:X16061.1 X16061.1 Aspergillus niger gox gene for glucose ox...  97.5    3e-17
EM_FUN:J05242.1 J05242.1 A.niger glucose oxidase mRNA, complete cds    97.5    3e-17
EM_FUN:AF234246.2 AF234246.2 Aspergillus niger glucose oxidase (GO...  97.5    3e-17
EM_PAT:HJ225127.1 HJ225127.1 Sequence 6 from patent US 8461320         97.5    3e-17
EM_PAT:AR367928.1 AR367928.1 Sequence 45 from patent US 6376210        97.5    3e-17
EM_PAT:AR361776.1 AR361776.1 Sequence 6 from patent US 6599745         97.5    3e-17
EM_PAT:AR125435.1 AR125435.1 Sequence 6 from patent US 6177261         97.5    3e-17
EM_PAT:FW510124.1 FW510124.1 A novel method to isolate mutants and...  97.5    3e-17
EM_PAT:DI010510.1 DI010510.1 Recombinant vector and recombinant ye...  97.5    3e-17
EM_PAT:AX069381.1 AX069381.1 Sequence 45 from Patent WO00102600        97.5    3e-17
EM_PAT:DI250904.1 DI250904.1 KR 1020130042346-A/9: Recombinant vec...  74.5    4e-10
EM_PAT:I09604.1 I09604.1 Sequence 4 from Patent WO 8912675             70.5    4e-09
EM_FUN:AY842492.1 AY842492.1 Aspergillus niger glucose oxidase gen...  64.1    3e-07
EM_PAT:I09605.1 I09605.1 Sequence 5 from Patent WO 8912675             64.1    3e-07


>EM_FUN:X56443.1 X56443.1 A.niger god gene for glucose oxidase (N-term.)
Length=819

 Score = 97.5 bits (120),  Expect = 3e-17
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query  1    CAACCAGCCTTTCCTCTCTCATTCCCTCATCTGCCCATCATGCAGACTCTCCTTGTGAGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  685  CAACCAGCCTTTCCTCTCTCATTCCCTCATCTGCCCATCATGCAGACTCTCCTTGTGAGC  744
```

The new Job Dispatcher Services beta website is now available at https://wwwdev.ebi.ac.uk/Tools/jdispatcher. We'd love to hear your feedback about the new webpages!

Results for job ncbiblast-R20230618-173740-0887-56686017-p1m

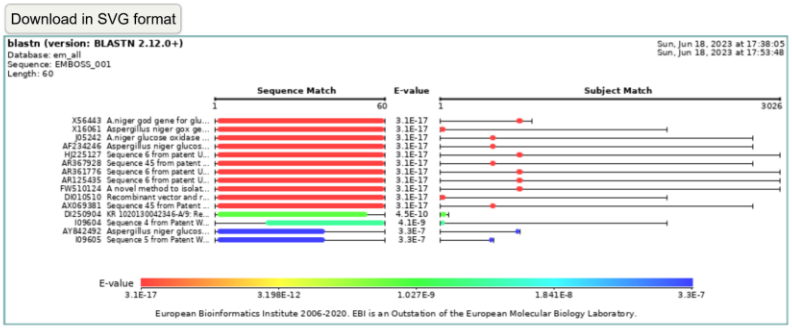
Summary Table | Tool Output | Visual Output | Result Summary | Submission Details

Color scale:

○ fixed

◉ dynamic Update

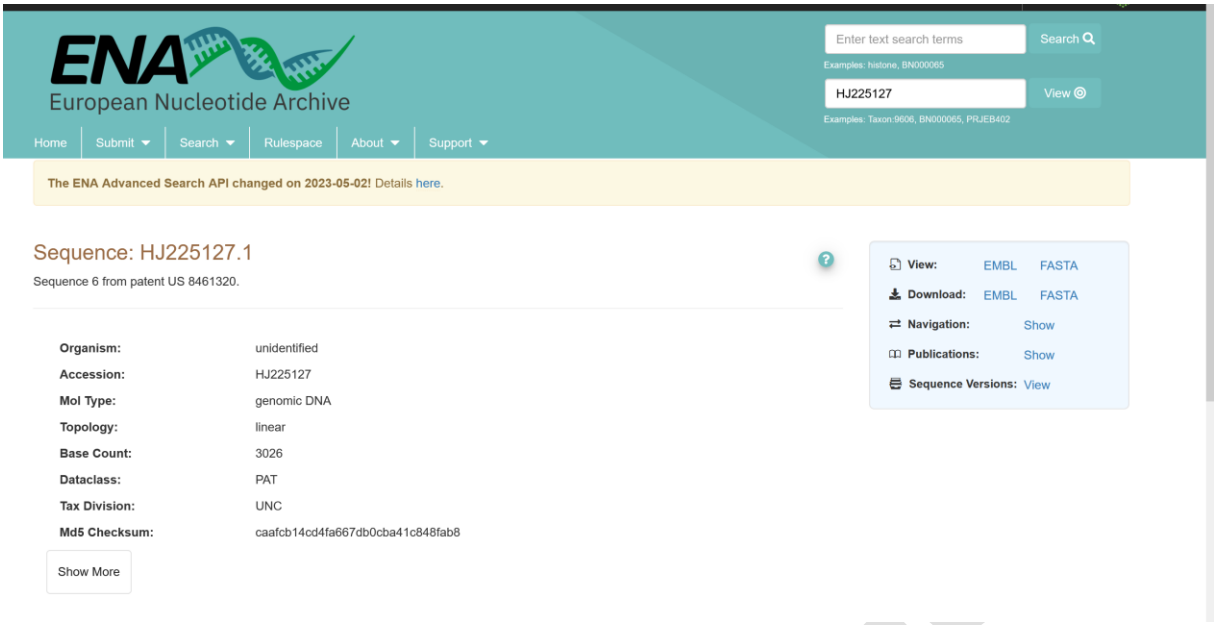
Download in SVG format



You may be interested in the 100% identity hit such as

☑ 5	EM_PAT:HJ225127	Sequence 6 from patent US 8461320. *Cross-references and related information in:* ▶ Samples & ontologies	3026	97.5	100.0	100.0	3.1E-17

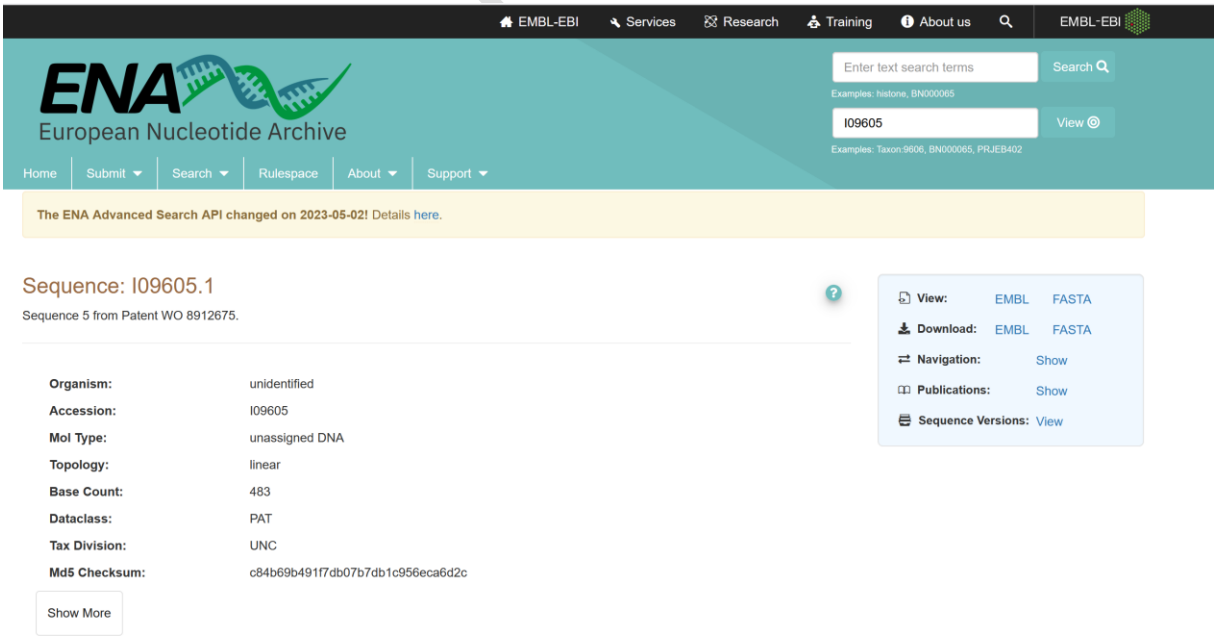
which is a sequence listed in a US patent.



You may also find a result with less score, e.g.

☑ 15	EM_PAT:I09605	Sequence 5 from Patent WO 8912675. *Cross-references and related information in:* ▶ Nucleotide sequences ▶ Samples & ontologies	483	64.1	100.0	100.0	3.3E-7

If you click on the ID, then you will find the result:



This is a sequence listed in an international application, WO89/12675.

PCT WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 4 : **C12N 1/16, 9/04, 15/00** **C07H 21/00**	**A1**	**(11) International Publication Number:** **WO 89/12675** **(43) International Publication Date:** 28 December 1989 (28.12.89)

(21) International Application Number: PCT/US89/02696

(22) International Filing Date: 20 June 1989 (20.06.89)

(30) Priority data:

209,530	21 June 1988 (21.06.88)	US
366,377	19 June 1989 (19.06.89)	US

(71) Applicant: CHIRON CORPORATION [US/US]; 4560 Horton Street, Emeryville, CA 94608 (US).

(72) Inventor: ROSENBERG, Steven ; 2323 Bywood Drive, Oakland, CA 94602 (US).

(74) Agents: MONROY, Gladys, H. et al.; Irell & Manella, 545 Middlefield Road, Suite 200, Menlo Park, CA 94025 (US).

(81) Designated States: AT (European patent), BE (European patent), CH (European patent), DE (European patent), DK, FR (European patent), GB (European patent), IT (European patent), JP, LU (European patent), NL (European patent), NO, SE (European patent), SU.

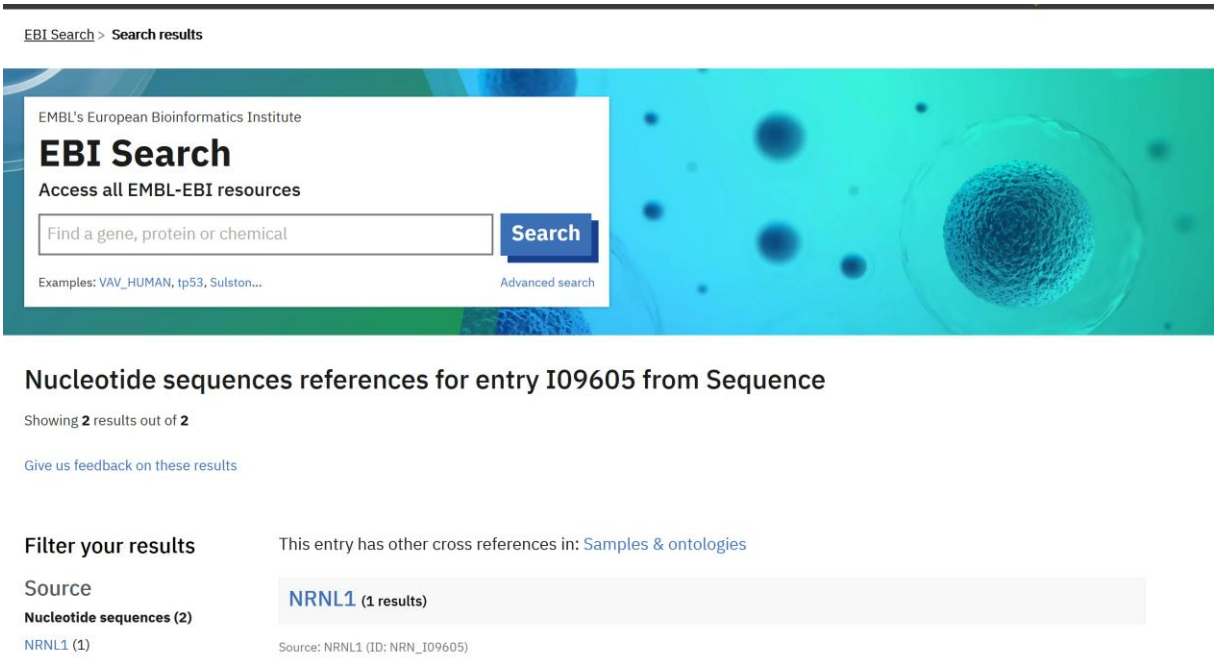
Published
With international search report.

(54) Title: PRODUCTION OF GLUCOSE OXIDASE IN RECOMBINANT SYSTEMS

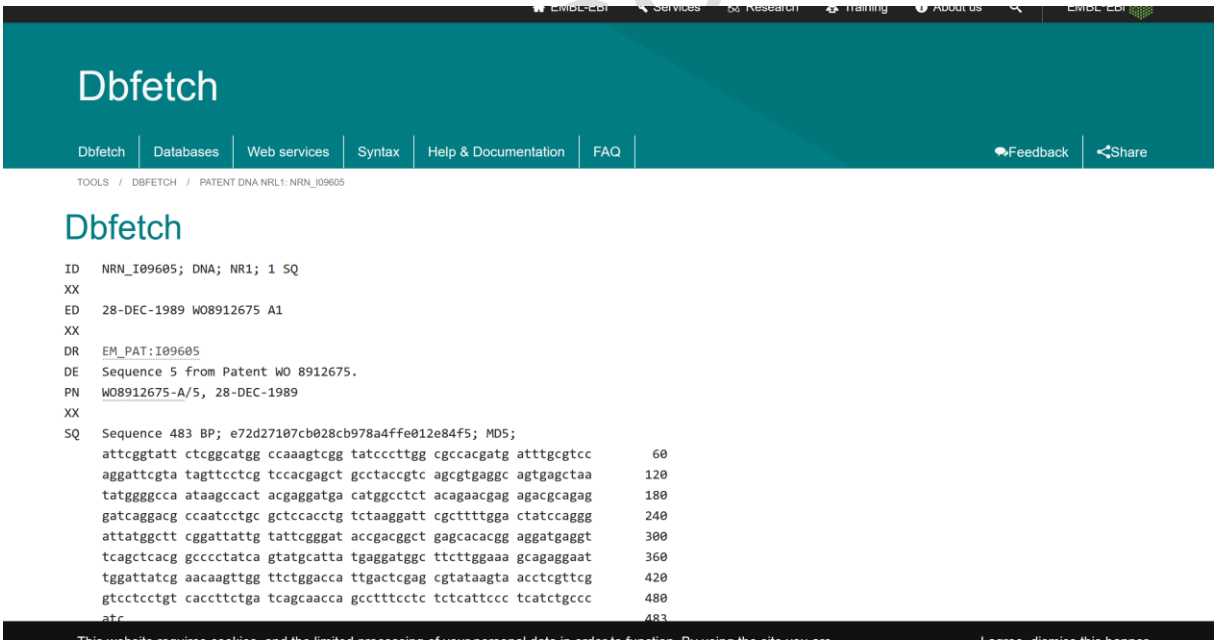
(57) Abstract

The present invention provides recombinant polynucleotides which encode glucose oxidase (GO). It also provides recombinant expression systems which produce, and when desired, secrete active GO and GO analogs into the extracellular medium.

In this case, the search results say SEQ ID No. 5 to be the identified hit. The PCT publication was in 1989, which is well before the sequence listing became systematic. You would need to use another tool to obtain an actual text readable sequence. For example, you can click on the search result as follows:



By clicking on the label NRNL1, you will obtain the following:



This is a computer readable sequence. As such, you will be able to further analyze with computer-based search systems (e.g., BLAST) the scientific literature and the further annotation information which is associated with this sequence and with sequences that are similar to this sequence.

Thus, stage 2 could be called the “brainstorming” phase of your sequence searches.

3.3.1.3 STAGE 3: Refining your search query: Trial and error and modification processes

Once you have done an initial search in Stage 2, pick up some hits from the search results and read and investigate them closely. You may well find some relevant claim language, search terms, phrases, international patent classification, etc., which will be helpful to refine your searches further.

Once you find relevant and important patent documents, you can identify enterprise names and other business-related information. Based on such information, you can develop your search further with the internet websites of those businesses to explore what is going on in the real-world business and innovation landscape surrounding your search object.

Try to use your knowledge of the business and industry sector in order to understand your search and search results, since your entire exercise takes place in a business and innovation context. Discuss with your colleagues and/or instructors about your results. If you are participating in the Traditional Knowledge Division’s distance learning executive course and its time-limited customer journey of follow-up mentoring, you will be able to discuss with your tutor/mentor to obtain feedback and further develop your search query.

Next, in the prior art search, you may wish to try with the “Advanced Search” or the “Field Combination Search” options. “Advanced Search” will require some knowledge of formulating a search formula with Boolean operators as exemplified below. “Field Combination Search” requires less technical and search know-how, and you may wish to use the formula to create a search formula. A search formula can be composed of a combination of queries in the respective fields, including title, claims and the like.

An example of an Advanced Search is:

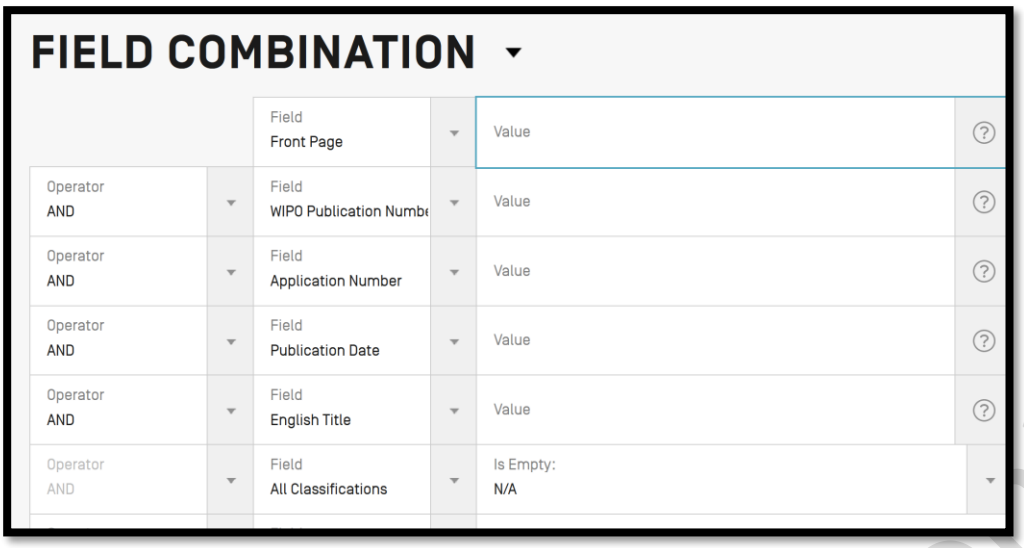
Samples of searches:

wind turbine - general searches, looking everywhere

EN_ALLTXT:(wind turbine) - all the text fields are searched, the relevance of top results is of high quality

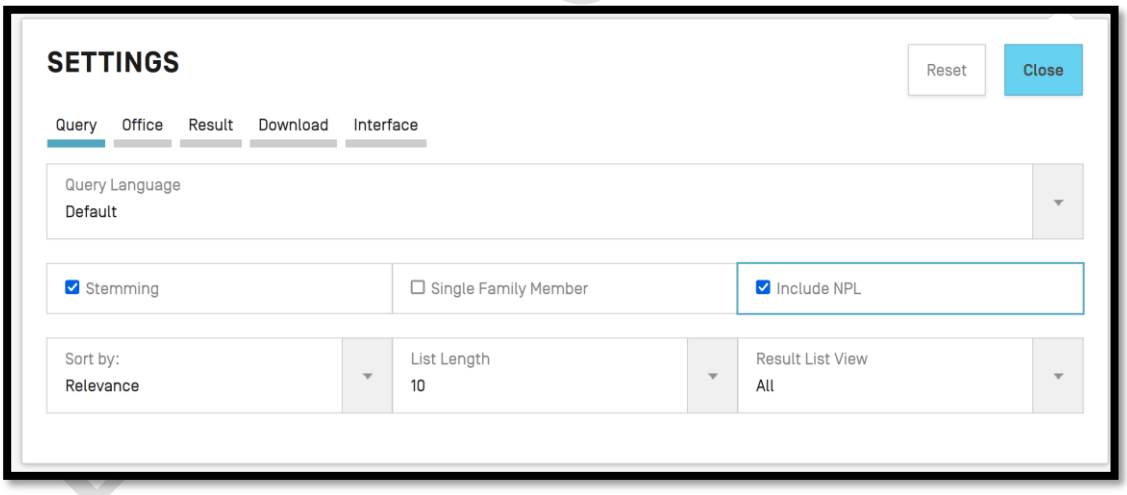
ALLNAMES:(Mao Yumin) - looking for applicant,inventor,agent names

ALLNUM:(DK 2008 123) - looking for IDs, WO, PCT numbers



For the prior art searches, sometimes, you would need to limit the publication date, especially when you wish to retrieve some technology as of a certain date such as a patent having a specific, past filing date. In this case, you can limit the Publication Date by choosing "publication date" as the field of interest, and input the most recent "permissible" date (usually one day before the filing date, or priority date if applicable) to limit the date – and thus find out your real "prior" art.

After iterative refinements of your search, you will have a certain list of literature hits. In the case of PATENTSCOPE, as default, you will only obtain patent/patent application literature. For comprehensive prior art search purposes, you should choose to include non-patent literature (NPL) in the following setting.



Alternatively, or additionally, for the non-patent literature search, academic databases, such as NCBI, PubMed or the like, can also be used. For the non-patent literature searches, you can use similar queries as the ones you have developed in the patent searches. Generally speaking, non-patent literature covers a limited scope of subject matter, whereas patent literature covers broader subject matter by the very nature of those categories of prior art literature.

3.3.1.4 STAGE 4: Analyzing your search results

In any event, once you have your own search result hit list, make sure you take your time to review the results vis-à-vis your search purpose. You may well find relevant hits and then mark such hits with your preferred symbol, such as ☑, X, XXX or the like.

Prior art searches are conducted for the purpose of evaluating patentability: Therefore, when you review the search result, you should formulate your search goal usually in the form of a potential future "claim".

Read and analyze your search results: Summarize your search results using various analyzing tools; discuss with your colleagues and/or your tutor/mentor about your results and your initial impressions and thoughts about them; and make sure to prepare a short summary of your results at this stage.

If you find an important patent document, you should deepen your investigation of the particular case, including patent family searches, analysis of the claims, applicants, inventors and the like.

As discussed above in detail, in certain jurisdictions "gene" *per se* claims are still patent eligible. If that is the case in the jurisdiction(s) you are interested in, a classical claim such as "*a(n isolated) nucleic acid molecule comprising a sequence set forth in SEQ ID XXX*" is the claim format that you might want to consider.

Usually, variations are permissible and thus, when you compare the search result with your search goal, you would need to aim for a homology or genetic similarity of about 90% or the like. In this scenario, you would have to use your homology search tools to compare the results – and see what you find. If your search hits are well above a certain homology with your targeted gene and its known sequence, then such results would be "*relevant*" literature and thus should be included in your list of "material prior art".

3.3.1.5 STAGE 5: Applying your search results to your objectives

If your search goal is a particular application of a gene, then you should prepare your goal in a real "claim" format related to the sequence, such as these:

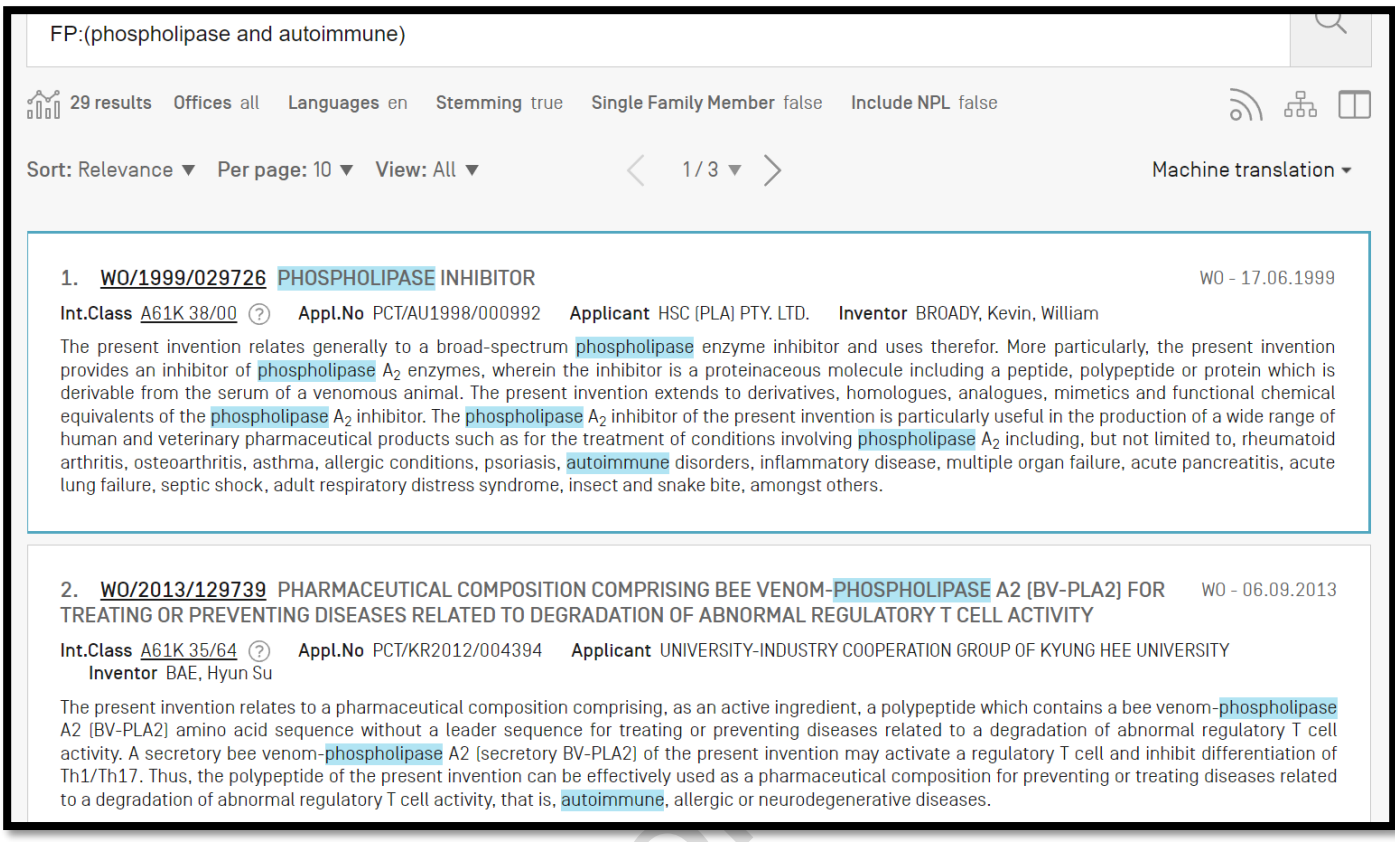
> "Use of a nucleic acid of SEQ ID NO: XXX for treating [for manufacturing a medicament for treating] an autoimmune disease"; or
> "A pharmaceutical composition for treating an autoimmune disease comprising a nucleic acid of SEQ ID NO: XXX"; or
> "A method of treating an autoimmune disease in a subject comprising the step of administering an effective amount of a nucleic acid of SEQ ID NO: XXX".

Alternatively, your claim may read:

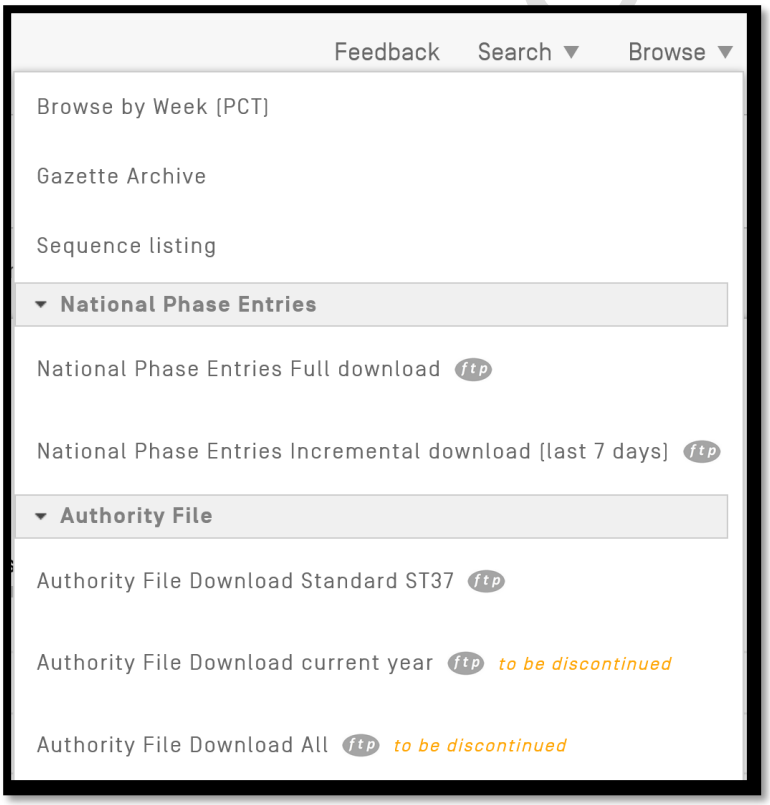
- "A method of treating an autoimmune disease [relating to a nucleic acid of SEQ ID NO: XXX.] in a subject comprising the step of administering an effective amount of an inhibitory compound ZZZ which inhibits a nucleic acid of SEQ ID NO: XXX".

Then, you may be able to search for your terminology of the target gene in combination with a keyword relating to the application (in this case, some query relating to the disease (e.g., autoimmune)).

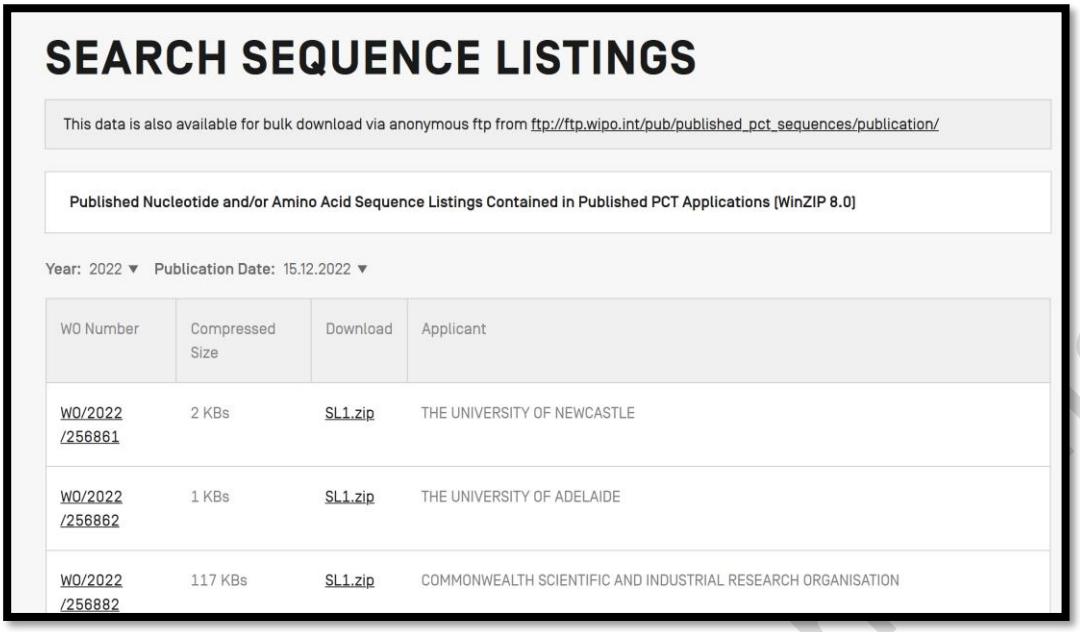
The resulting list may be as follows (for the example of "phospholipase" and "autoimmune"). Specifically, if you have a WIPO account, up to 10,000 hits can be downloaded as an excel file from PATENTSCOPE.



For the purpose of sequence listing information, you can use the “Sequence Listing” function by choosing it in the “Browser.”



You will the obtain GR sequence listing files as follow:



SEARCH SEQUENCE LISTINGS

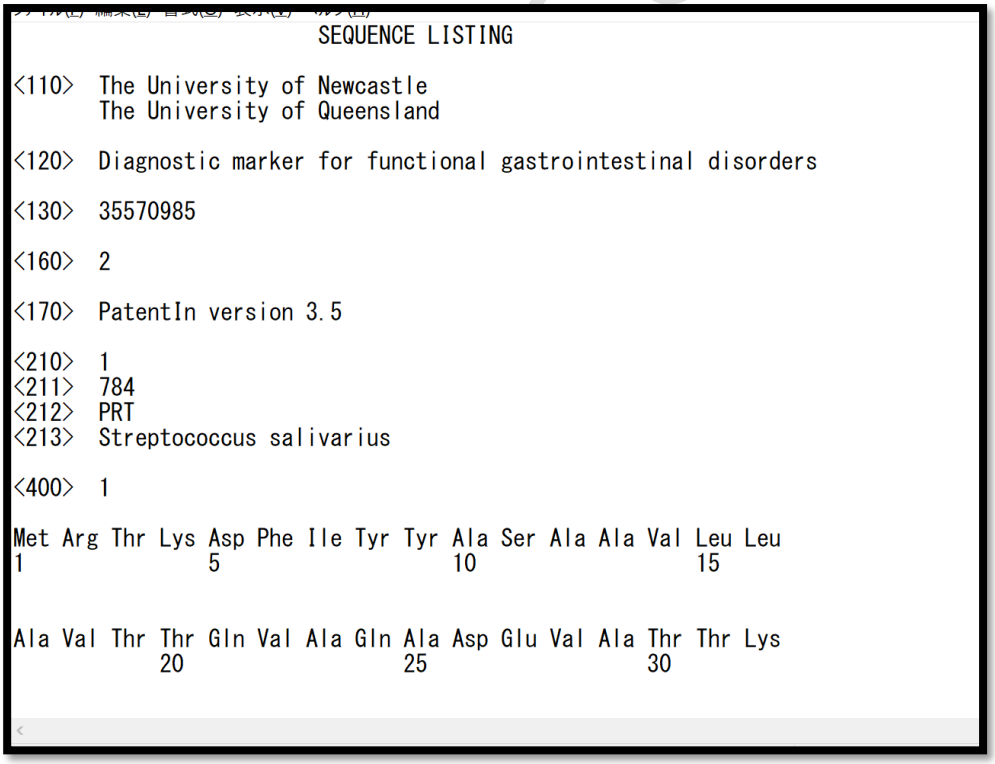
This data is also available for bulk download via anonymous ftp from ftp://ftp.wipo.int/pub/published_pct_sequences/publication/

Published Nucleotide and/or Amino Acid Sequence Listings Contained in Published PCT Applications (WinZIP 8.0)

Year: 2022 ▼ Publication Date: 15.12.2022 ▼

WO Number	Compressed Size	Download	Applicant
WO/2022/256861	2 KBs	SL1.zip	THE UNIVERSITY OF NEWCASTLE
WO/2022/256862	1 KBs	SL1.zip	THE UNIVERSITY OF ADELAIDE
WO/2022/256882	117 KBs	SL1.zip	COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION

As you will see as of the “Big Bang” on July 1, 2022, when ST.26 came into effect globally, most if not all sequence listings will be in the neat and comfortable, machine-readable XML format of ST.26. For example, when you open those of the above-mentioned autoimmune enzyme example, the first one, for example, reads as follows:



```
                        SEQUENCE LISTING

<110>  The University of Newcastle
       The University of Queensland

<120>  Diagnostic marker for functional gastrointestinal disorders

<130>  35570985

<160>  2

<170>  PatentIn version 3.5

<210>  1
<211>  784
<212>  PRT
<213>  Streptococcus salivarius

<400>  1

Met Arg Thr Lys Asp Phe Ile Tyr Tyr Ala Ser Ala Ala Val Leu Leu
1               5                  10                  15


Ala Val Thr Thr Gln Val Ala Gln Ala Asp Glu Val Ala Thr Thr Lys
            20                  25                  30
```

You can use these sequences for further searching. (Currently, PATENTSCOPE is not available for you to enter such sequence information as a query, and therefore you may need to use another database, such as *The Lens* or the INSDC repositories, such as DDBJ, EMBL and NCBI).

3.3.1.6 STAGE 6: Recognizing the limitations of your search results

Your search may behave like a culture of bacteria, rather than a higher plant: it may spread in all directions indiscriminately. Thus, Stage 6 is here for you to remind yourself of the limits of your search. Refocus on the source of light to maximize the photosynthesis and energy of your searches. The earlier you can recognize the limitations of your search results when you are conducting your search, the better for your search process. Self-consciousness in sequence searching is like meditation in front of a Zen Garden: it is useful to continuously stay in touch with the limitations of your perception. Limitations may be derived from the database you used, your search strategy, and the like.

Furthermore, for the purposes of prior art searches, you need to recognize the time lag of publication of your prior art of interest. The time lag may be legal or factual. Legal time lag is due to the eighteen months period of time required for publication, counting from the priority date. As such, some patent literature may not be present due to the time lag, even if the literature of interest may have an earlier filing date than your search interest.

Then ask yourself: what are the challenges you are facing? Three challenges are common at this stage:

Issue of jurisdictions and differences in patentability requirements:

When conducting prior art searches for patentability, such as for new patent filings and/or invalidation purposes, there are a number of issues that need to be considered. Novelty and non-obviousness/inventive step requirements are the main issues of patentability, but one also has to consider the prior filing issue/double patent issue.

In this regard, the non-obviousness/inventive step requirement is similar but different from jurisdiction to jurisdiction. Apparently, the terminology is different such as non-obviousness and inventive step and the like. Non-obviousness is often used in the U.S., while inventive step is often used in the European Patent Convention regions and Japan to name a few.

Moreover, what is important is the practical difference in the non-obviousness/inventive step requirement; the examination standard is different from jurisdiction to jurisdiction, and sometimes different from time to time even in the same jurisdiction.

Challenges related to search result categories

There are sometimes a large number of search results from your initial search. In such a case, you need to refine your search, and/or conduct a second round of search against the first search results.

Technical specificities of GRs:

Additionally, relating to GRs, consideration needs to be given to the GR's technical specificities vis-à-vis other technology fields.

3.3.1.7 STAGE 7: Finalizing your search: preparing reports

You can then improve your search by changing your search queries and formulae. Once you have finished your analysis, it is useful to prepare a summary report for summarizing the results.

The results should usually include relevance and observation of the technological information found in the search hit vis-à-vis your search goal. Specific portions such as paragraph number and/or page and line numbers and excerpts therefrom should be included in the report. Your review analysis thereon should also be included.

If a patentability search is intended, you can mark the relevancy using labels. You may use any labels, but our recommendation is to use similar or identical labels as those used and categorized in PCT International Search Reports. For these labels see WIPO Standard ST.14:

(a) Categories indicating cited documents (references) of particular relevance:

- Category "X": The claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone;
- Category "Y": The claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

(b) Categories indicating cited documents (references) of other relevant prior art:

- Category "A": Document defining the general state of the art which is not considered to be of particular relevance;
- Category "D": Document cited by the applicant in the application and which document (reference) was referred to in the course of the search procedure. Code "D" should always be accompanied by one of the categories indicating the relevance of the cited document;
- Category "E": Earlier patent document as defined in Rule 33.1(c) of the Regulations under the PCT, published on or after the international filing date. Code "E" may be accompanied by one of the categories "X", "Y" or "A";
- Category "L": Document which may throw doubts on priority claim(s), or which is cited to establish the publication date of another citation or other special reason (the reason for citing the document shall be given);
- Category "O": Document referring to an oral disclosure, use, exhibition, or other means. Code "O" should always be accompanied by one of the categories "X", "Y" or "A";
- Category "P": Document published prior to the filing date (in the case of the PCT, the international filing date) but on or after the priority date claimed in the application. Code "P" should always be accompanied by one of the categories "X", "Y" or "A";
- Category "T": Later document published after the filing date (in the case of the PCT, the international filing date) or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention;
- Category "&": Document being a member of the same patent family or document whose contents have not been verified by the search examiner but are believed to be substantially identical to those of another document which the search examiner has inspected.

3.3.2 (Freedom-to-Operate)/Clearance Search:

FtO searches are often conducted as a part of due diligence, and thus this Guide is limited to some basics on how to conduct such a search using a simple database such as PATENTSCOPE. As mentioned above, this Guide does not cover FtO analyses and it is necessary to seek legal advice from IP professionals on the subject.

3.3.2.1 STAGE 1: Defining the objectives of your search

If an FtO Search is intended, please identify your business model, which you wish to practice or investigate. As briefly touched upon, once you have decided to conduct a FtO search, you need to define you target business model, such as your target product profile, target service profile or the like.

- If a plurality of elements is considered, please identify each and every single element (invention) that may have a technical feature. When you are able to define your

business model of interest, such a model often includes a plurality of elements. In such a case, you would need to identify each and every single element (invention) that may have a technical feature. You may also have to further define the order of preference and priority for the respective elements in view of your business interests and the state of the art.

- If the technical feature of your investigation of interest lies in a combination of elements, consider such a combination when preparing your search questions/queries. That is, a single search for the respective element may not be sufficient to cover a full FtO search; the combination of the respective elements may have a different chance of success in patent examination and thus may be a bar to your innovation project or business.

3.3.2.2 STAGE 2: Building your initial query building blocks

An exemplary FtO search will be shown as follows, supposing the following as the exemplary action to be searched:

> "The act of working to launch a pharmaceutical product including an inhibitor of GR XXX for treating disease YYY."

Now you would have to identify what constitutes your innovation and business of interest for the launch of the product. For example, your innovation and business interests might consist of the following: typical key sections for an FtO search would include indications and usage; dosage and administration; dosage forms and strengths; contraindications; warnings and precautions; adverse reactions; drug interactions; use in specific populations; drug abuse and dependence; overdosage; *description*; clinical pharmacology; nonclinical toxicology; clinical studies; references; supply/storage and handling; and patient counseling information.

In this respect, "*description*" (italicized in the list above) is directed to the product itself. The description may include information such as the proprietary name and established name, dosage form and route of administration, qualitative and quantitative ingredients, pharmacologic or therapeutic class, and any other important physical and chemical characteristics.

In a complete FtO, all the following factors need to be considered and analyzed:

A. *The product profile*: Typically for GR XXX, the product of interest will include:
   1. Active Pharmaceutical Ingredient (API): Compound X (e.g., an inhibitor for GR XXX, for treating disease YYY);
   2. Additives/DDS required for the API (e.g., if Compound X is a gene product, such as an mRNA, then it would require a DDS for efficient delivery, such as LNP);
   3. Use of such API (indication);
   4. Dosage and formulation; and
   5. Dosage regiment.

   6. With respect to the sequence *per se*, not only sequence identities, but also a similarity or identity less than 100% needs utmost care in order to adequately analyze and judge whether your target of interest falls within the scope of the claims. Identity percentages may be expressed using BLAST conditions, under certain versions, such as those as of 2010 or the like. You will then have to calculate the percentages based thereupon.

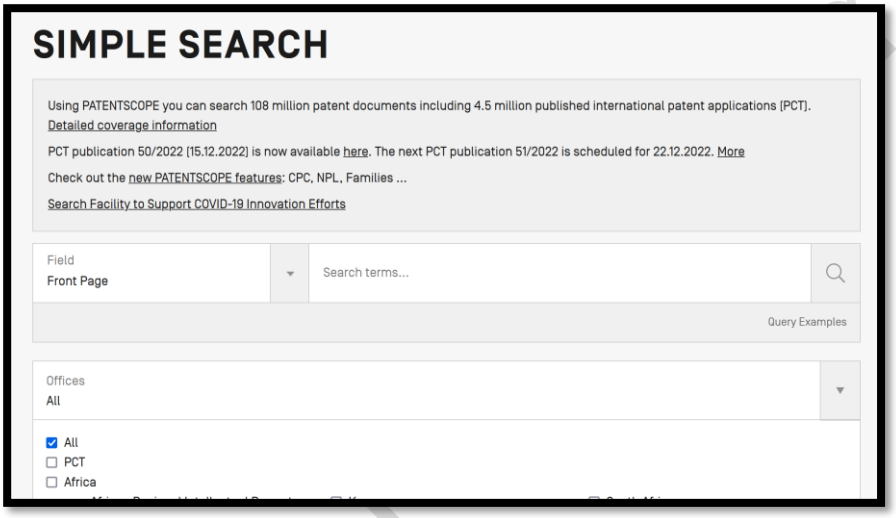
B. *Other factors* relating to and necessary for conducting business of the target product profile (TPP):
   1. Manufacture of the product;
   2. Distribution and Storage of the product;
   3. Others [relevant elements of GR XXX to be supplemented].

All these factors need to be checked in order to perform a full FtO, since, if you are going to develop and protect the prospective invention, for which you are conducting your prior art/patentability search, then you would have to manufacture the product, distribute and sell the product and administer the product, and if necessary store the product. Every single parameter is related to some technical aspects which are supported by a number of (patented) inventions in the product. Such inventions may be encompassed by patents or other IPRs and thus will require you to investigate them in the course of a FtO search.

As for the main API, you would need to conduct searches for any technical matter related to the product. If the product is a nucleic acid product or an amino acid sequence product, then the following would be necessary:

- Name of the product from a chemical point of view [see IUPAC];
- Functional features of the product [such as inhibitory action of GR XXX; function of GR itself, such as cellular/biological pathway ZZZ, modulation of receptor WWW, etc.];

In this context, you can initiate your preliminary searches using representative key words.
At this stage, you may use “Simple Searches” for collection of initial useful information and then improve your search strategy.

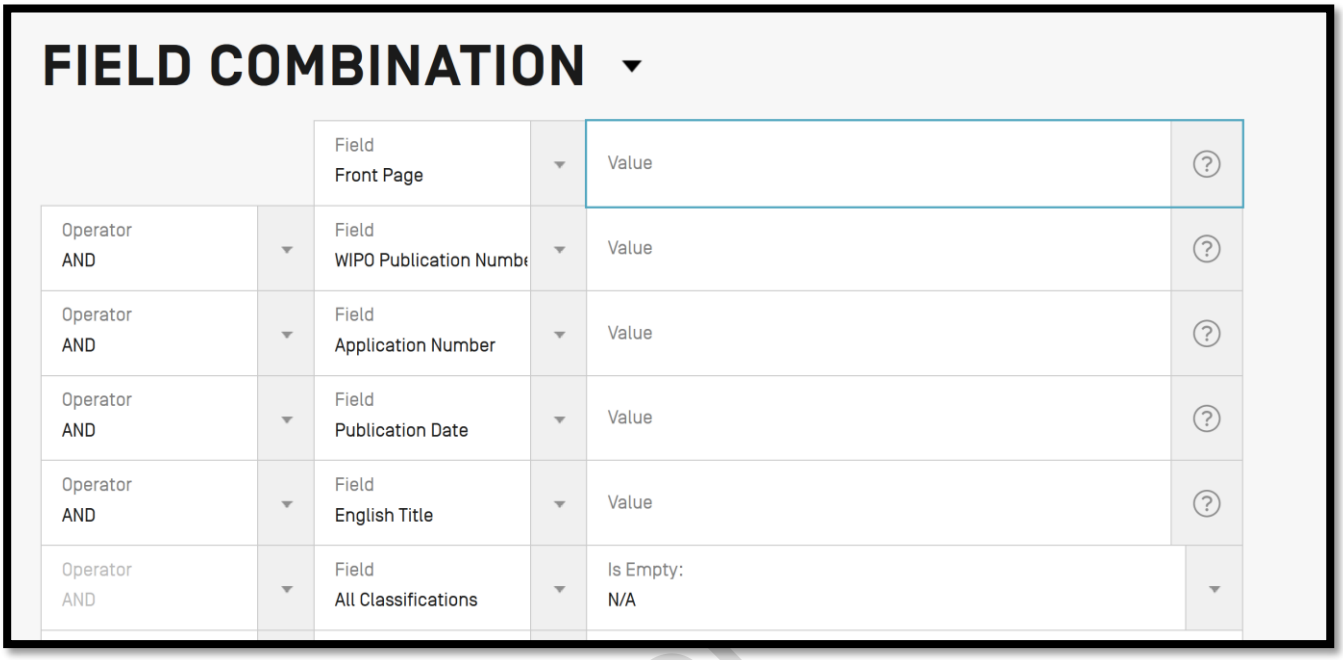


By doing this initial search, you will obtain more information on your target GR sequence, such as additional relevant key words, including other genetic nomenclatures of the particular GR of interest, genetic sequence information, classifications such as IPC and CPC, relevant inventors, relevant stakeholders (patentees and applicants), representative claim formats, technical information, such as technical problems to be solved by the invention, and many other materials.

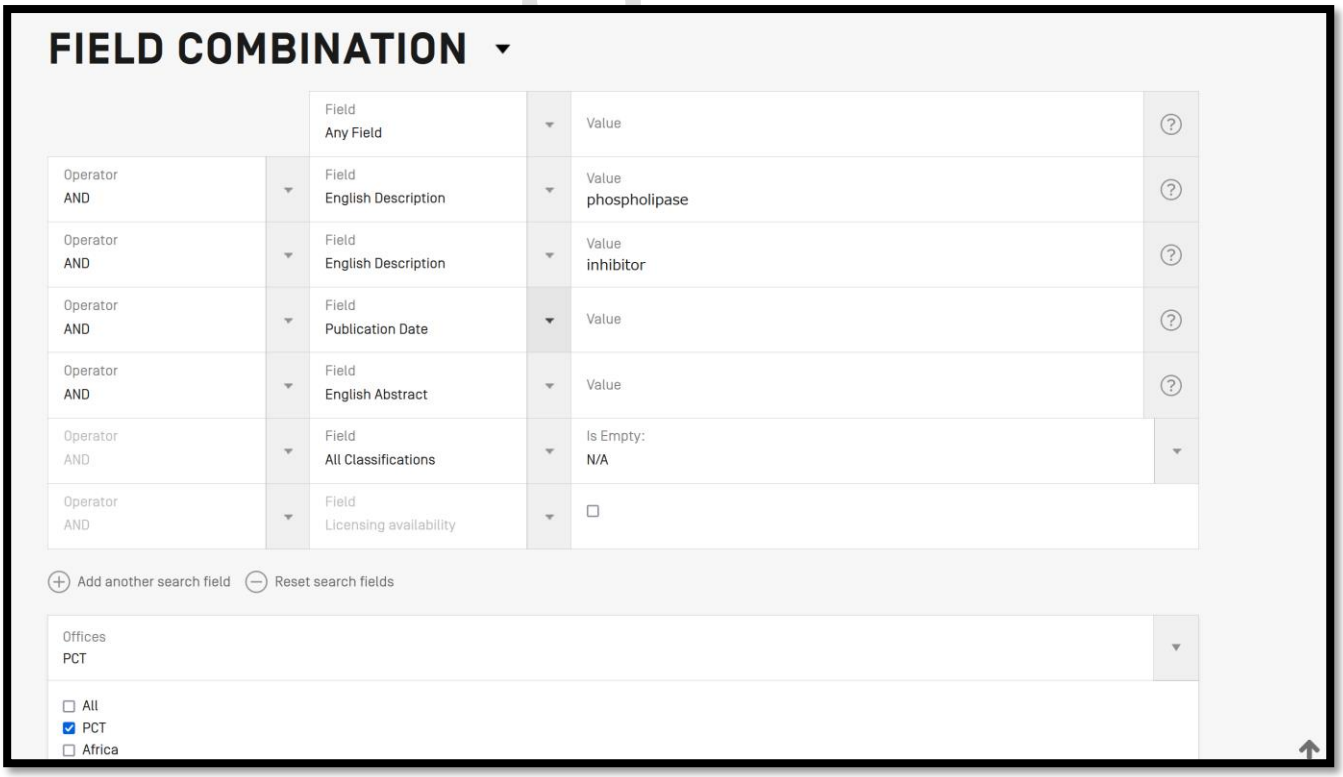
3.3.2.3 STAGE 3: Refining your search query: Trial and error and modification processes

Once you have done an initial search in Stage 2, pick up some hits from the search results and read and investigate them carefully. You may well find some relevant claim languages, search terms, phrases, international patent classification, etc., which may be helpful to refine your search. Once you find some relevant and important patent documents, you can identify enterprise names and other business-related information. Based on such information, you can develop your FtO search further with the internet websites of those enterprises to explore what is going on in the real-world business. It may be valuable to obtain feedback from your colleagues and/or tutors/mentors about your search results.

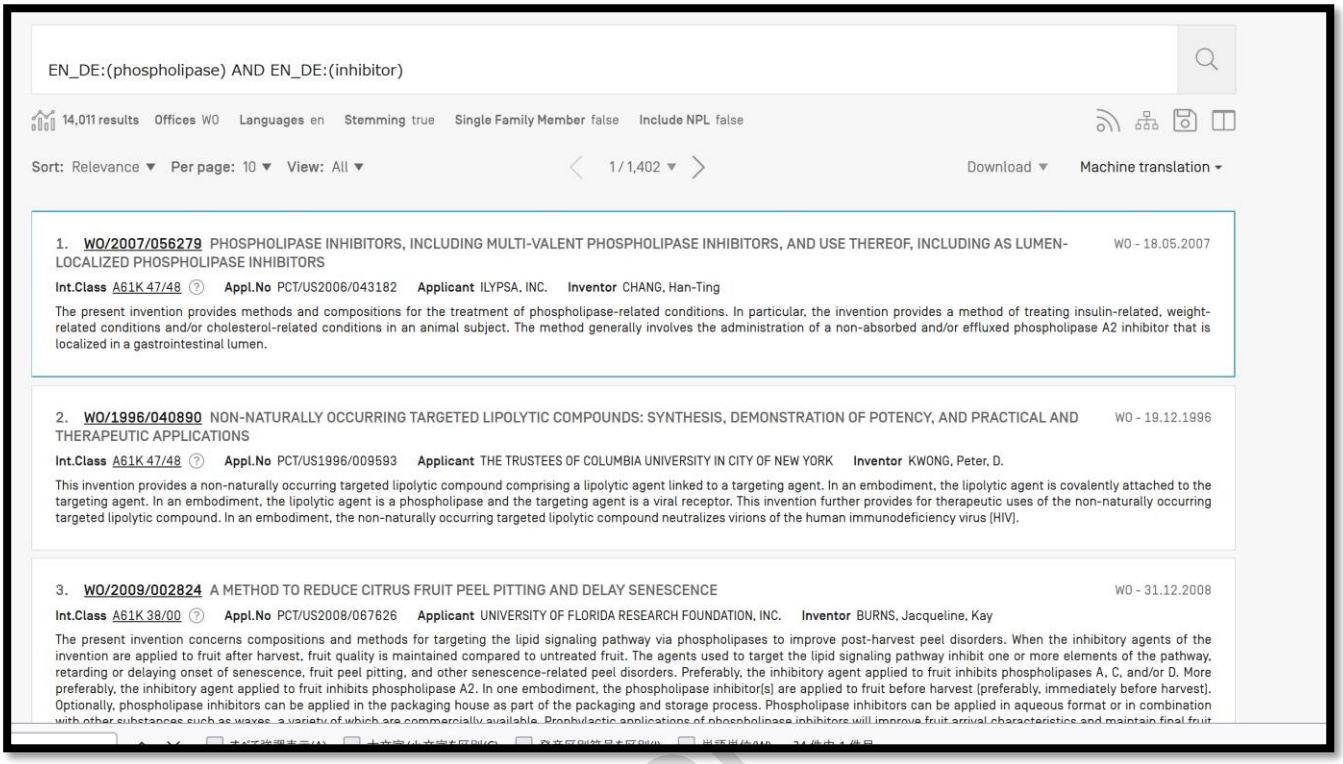
At the next stage, you may wish to conduct searches for actual patents/patent applications relating to your GR target sequence for FtO clearance. For example, you may wish to conduct “phospholipase” AND “inhibitor” as query. At this stage, you may wish to use “Field Combination Searches” as follows:



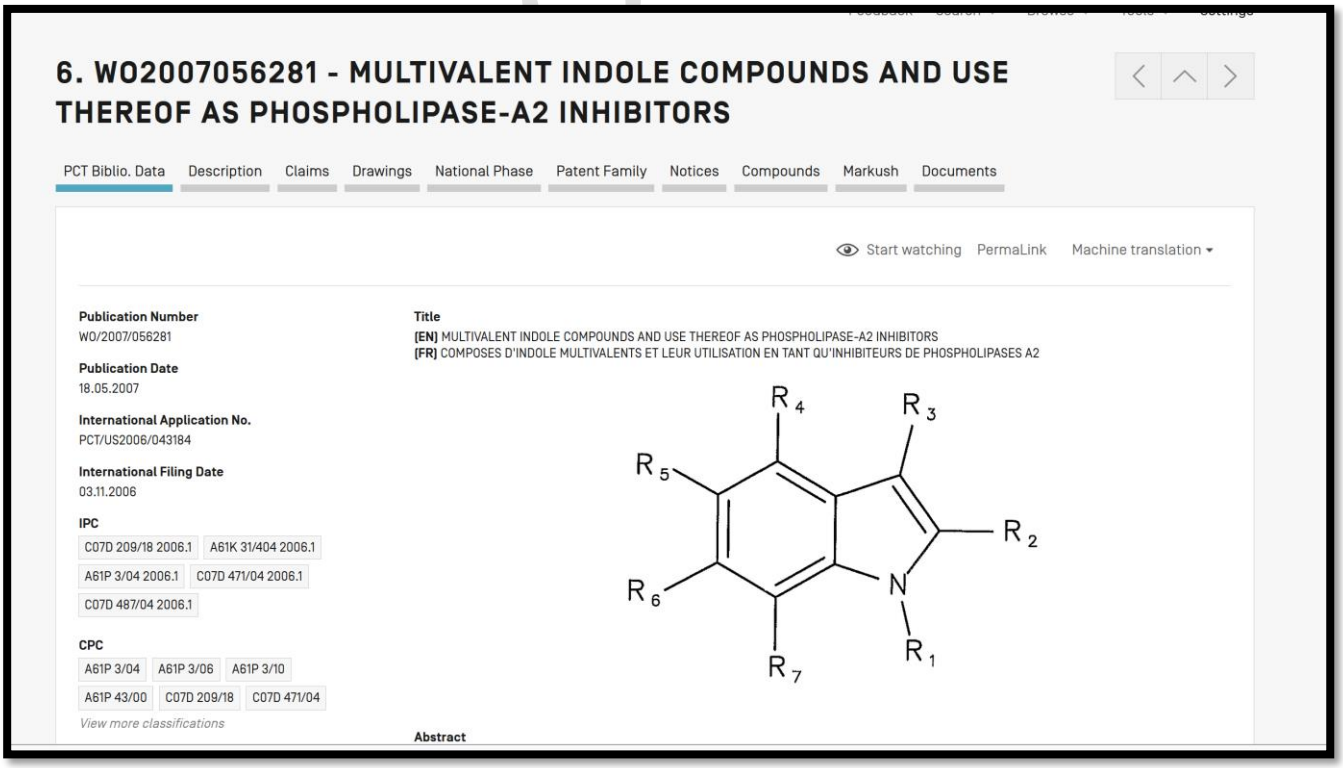
You can then choose your database coverage. Here, “PCT” may be chosen:



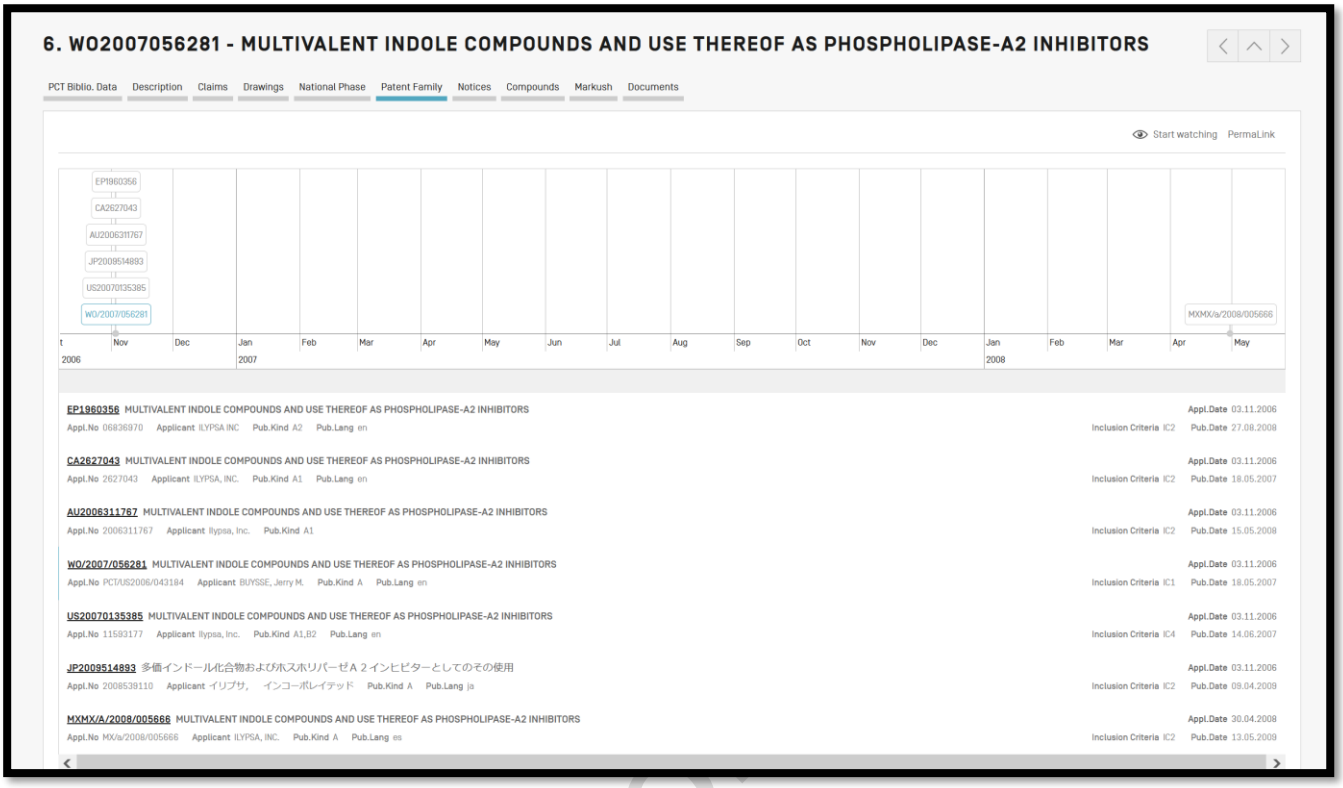
You will then be able to obtain, e.g., the following search results:



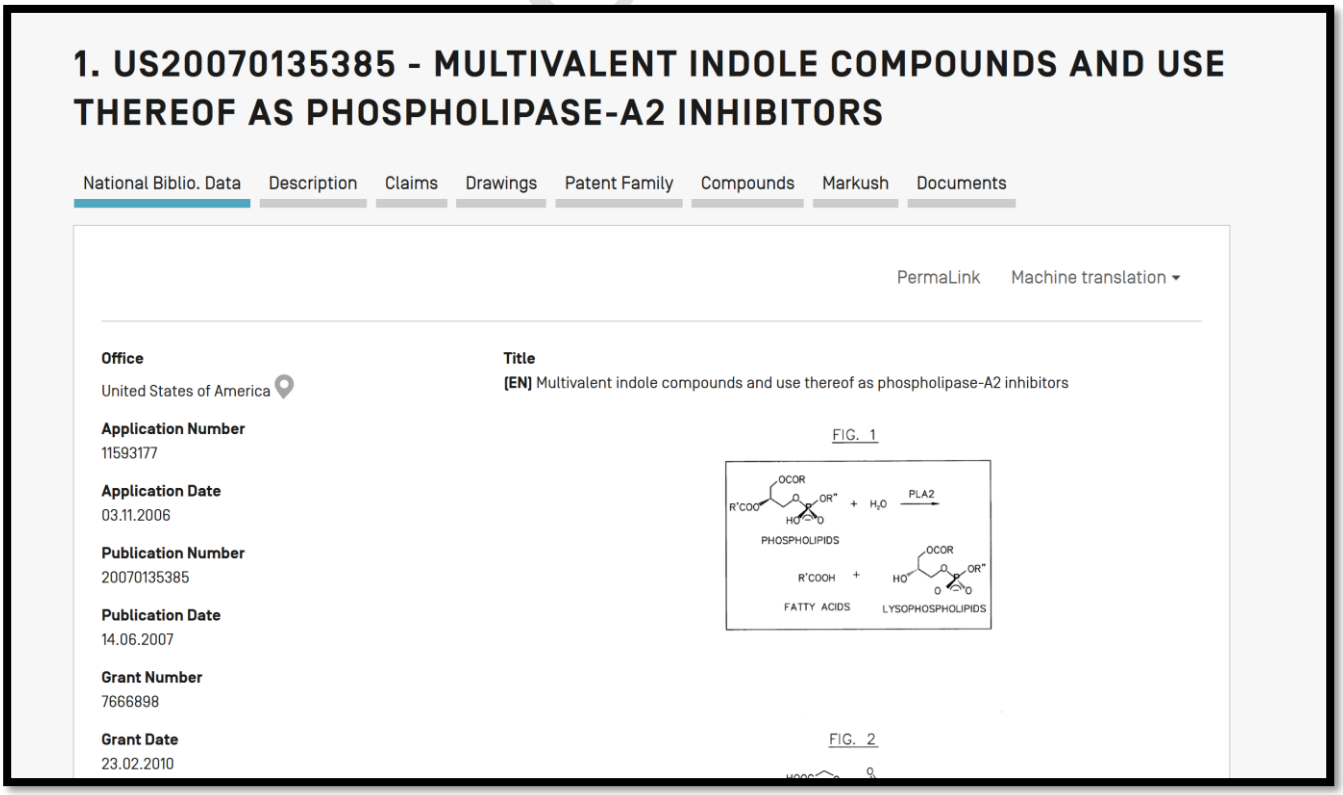
If you click on the third one, you will obtain the following detailed bibliographic information:



If you click on the “Patent Family” function, you will see:

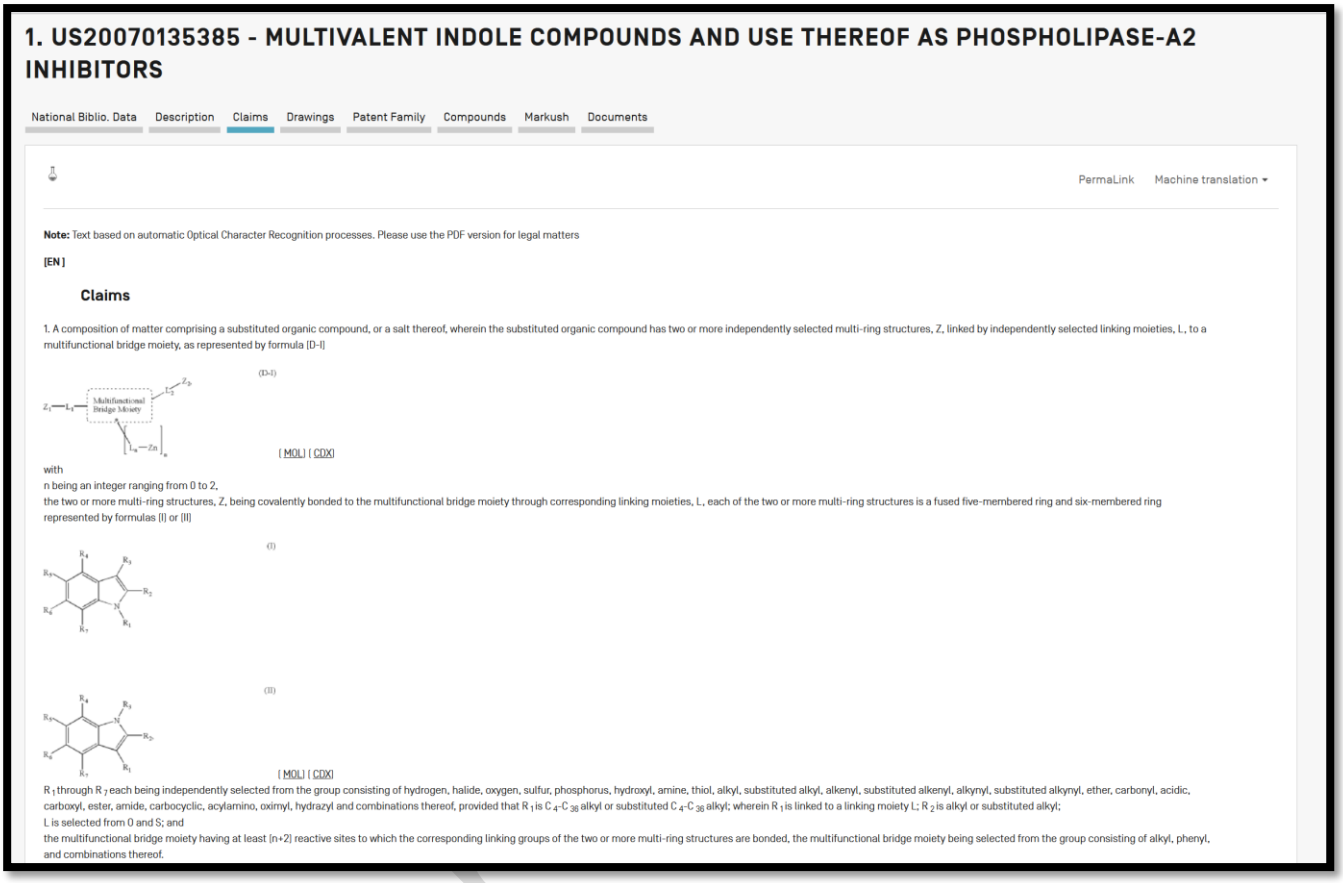


Then, if you click on the U.S. family, you will obtain the following bibliographic details:



In this case, you will know that this U.S. application has been granted as a U.S. patent.

It is important to know that for FtO purposes you will always need to carefully check what are the claims. In PATENTSCOPE, you can see the claims “as filed”:



1. US20070135385 - MULTIVALENT INDOLE COMPOUNDS AND USE THEREOF AS PHOSPHOLIPASE-A2 INHIBITORS

National Biblio. Data | Description | Claims | Drawings | Patent Family | Compounds | Markush | Documents

PermaLink | Machine translation

Note: Text based on automatic Optical Character Recognition processes. Please use the PDF version for legal matters

[EN]

Claims

1. A composition of matter comprising a substituted organic compound, or a salt thereof, wherein the substituted organic compound has two or more independently selected multi-ring structures, Z, linked by independently selected linking moieties, L, to a multifunctional bridge moiety, as represented by formula [D-I]

(D-I)

[MOL] [CDX]

with

n being an integer ranging from 0 to 2,

the two or more multi-ring structures, Z, being covalently bonded to the multifunctional bridge moiety through corresponding linking moieties, L, each of the two or more multi-ring structures is a fused five-membered ring and six-membered ring represented by formulas (I) or (II)

(I)

(II)

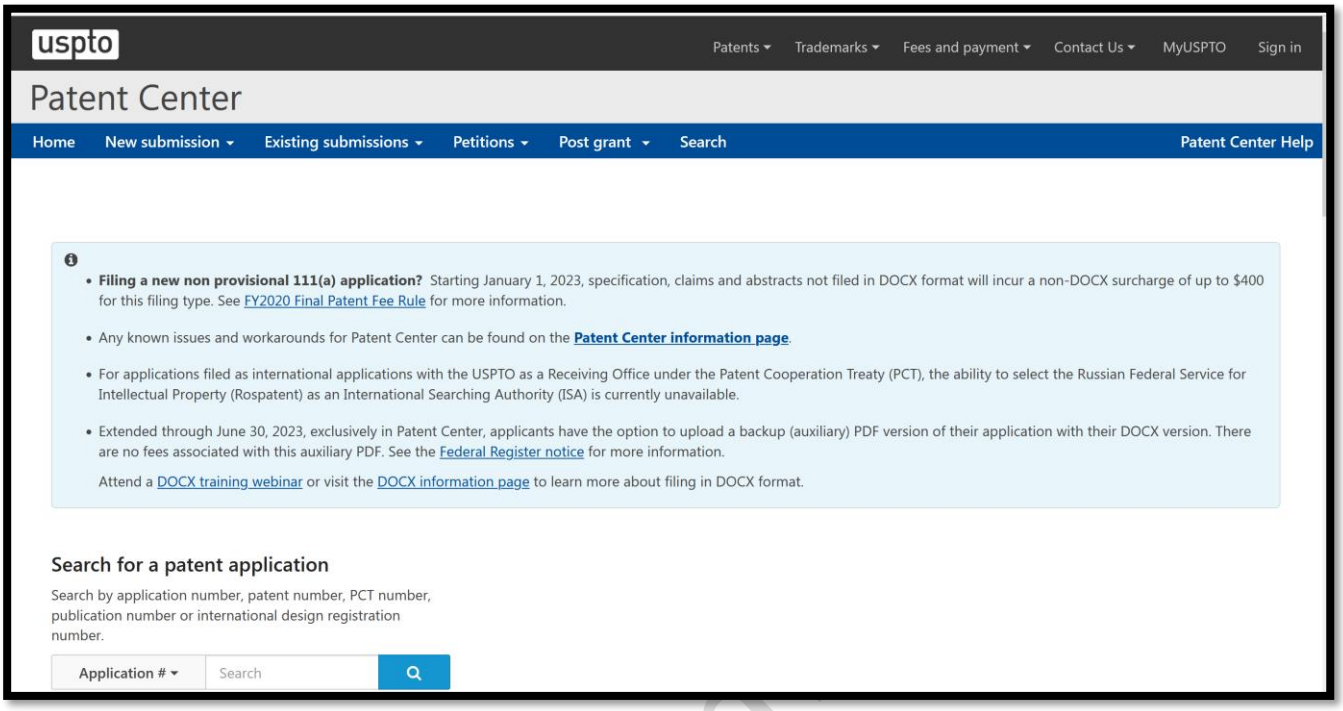
[MOL] [CDX]

R_1 through R_7 each being independently selected from the group consisting of hydrogen, halide, oxygen, sulfur, phosphorus, hydroxyl, amine, thiol, alkyl, substituted alkyl, alkenyl, substituted alkenyl, alkynyl, substituted alkynyl, ether, carbonyl, acidic, carboxyl, ester, amide, carbocyclic, acylamino, oximyl, hydrazyl and combinations thereof, provided that R_1 is C_4-C_{36} alkyl or substituted C_4-C_{36} alkyl; wherein R_1 is linked to a linking moiety L; R_2 is alkyl or substituted alkyl;

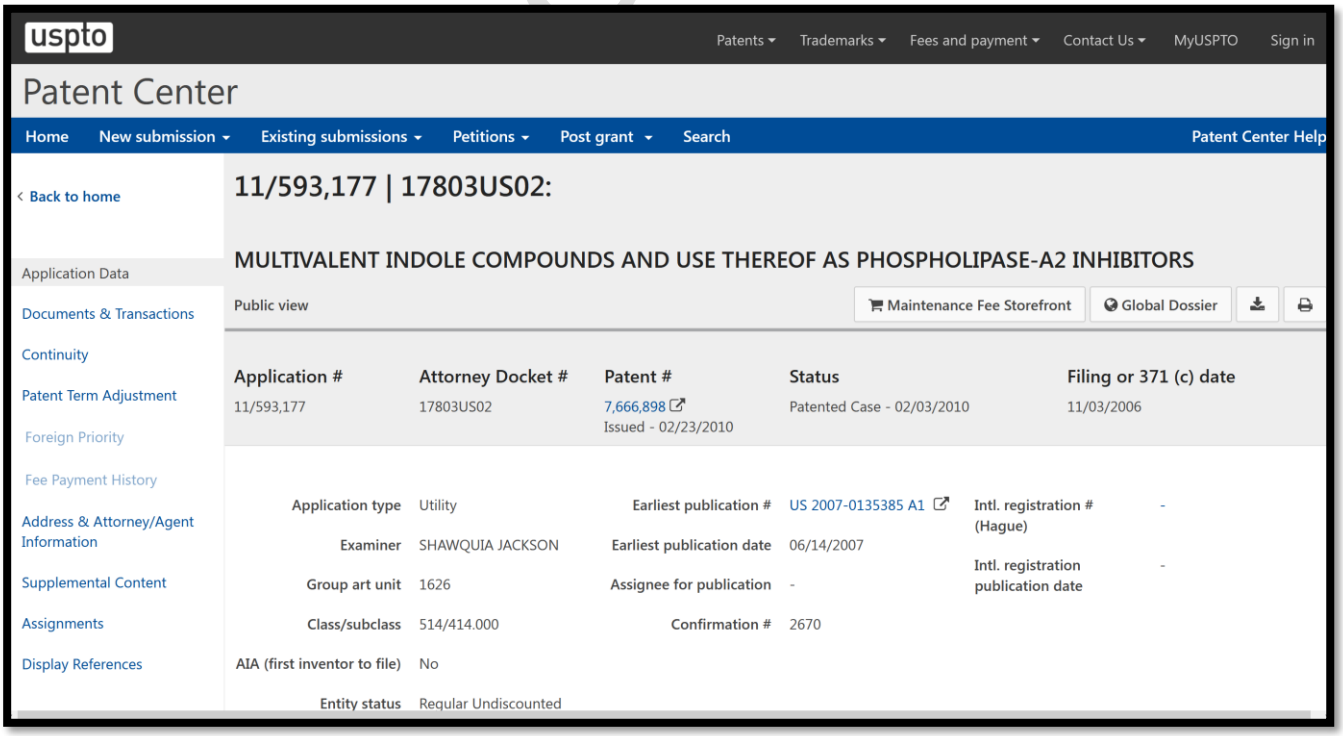
L is selected from O and S; and

the multifunctional bridge moiety having at least (n+2) reactive sites to which the corresponding linking groups of the two or more multi-ring structures are bonded, the multifunctional bridge moiety being selected from the group consisting of alkyl, phenyl, and combinations thereof.

If you know the patent number, you can further search on the national patent office database. In this regard, the USPTO database may be used: https://patentcenter.uspto.gov/

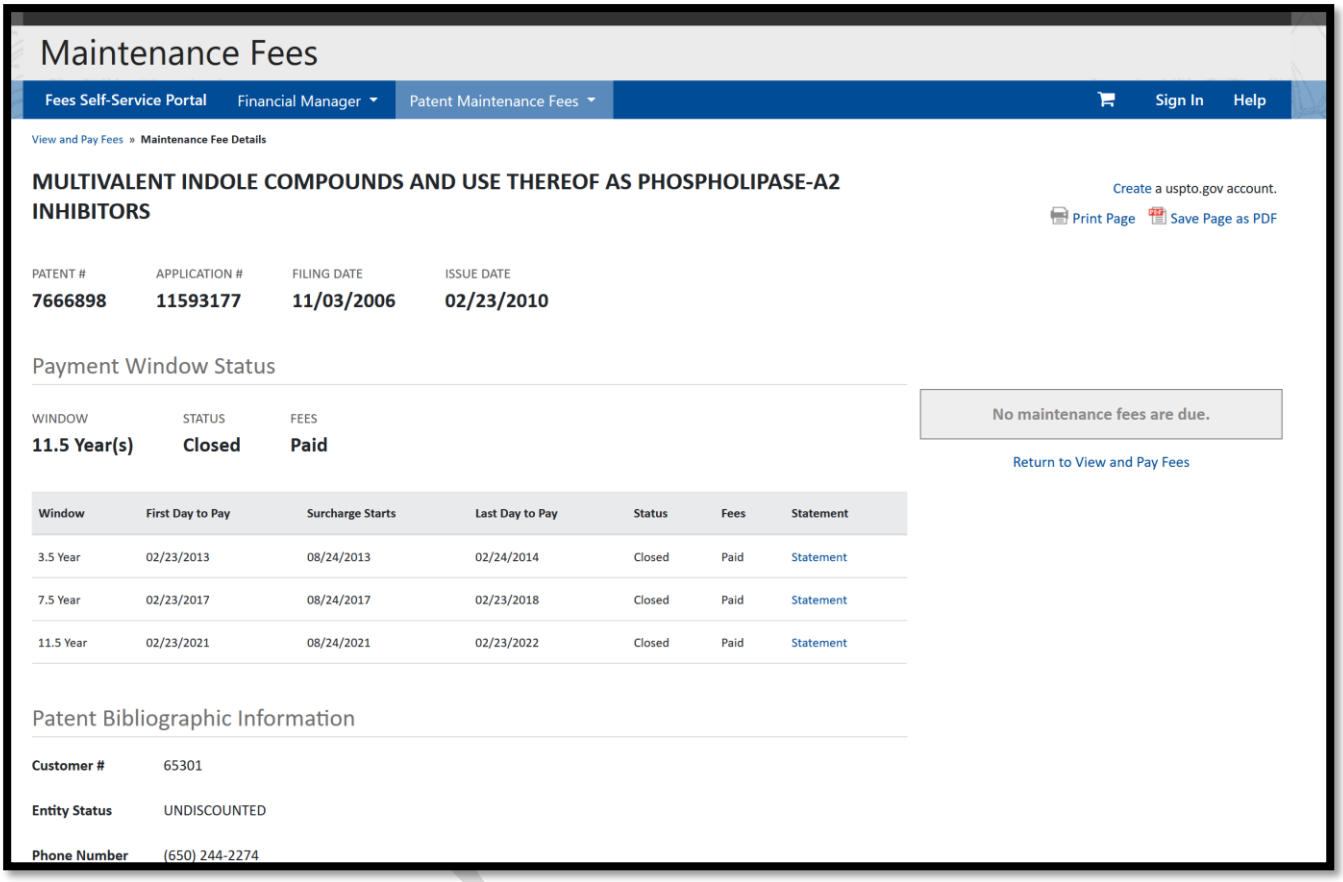


If you input the obtained number and make a search, then you will obtain detailed information on the particular patent. It is important to search for the most updated information, which is usually obtainable from the national patent office.

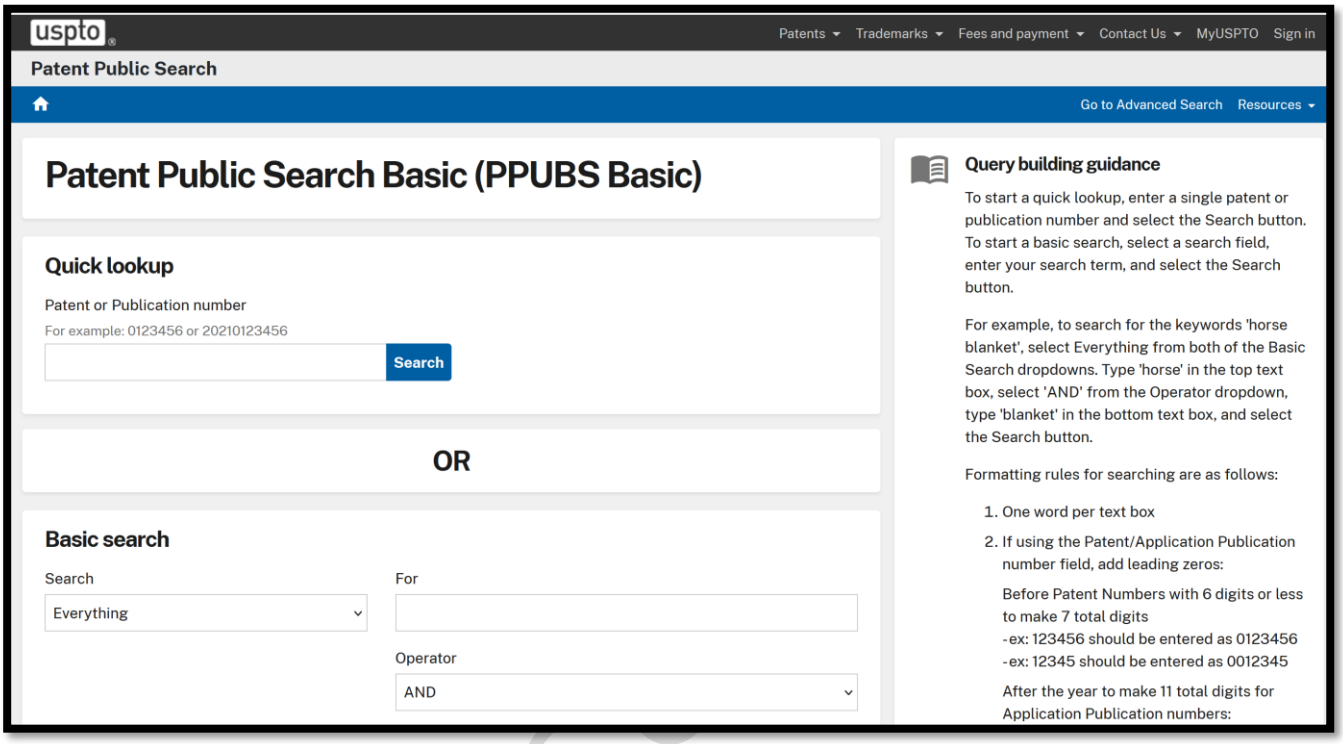


You should check whether the obtained patent is actively in force, or not, by clicking on “Maintenance Fee” Storefront.

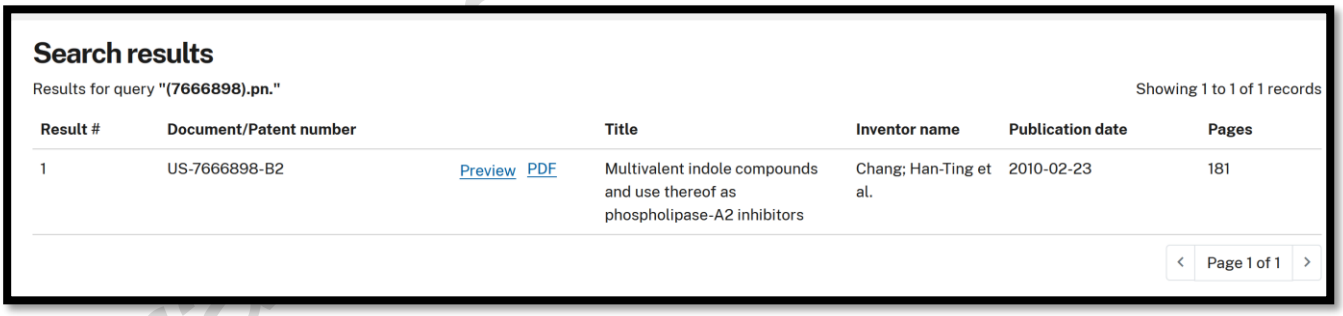
Then you will obtain the following:



Through this, you have verified that the patent at issue is still in force and active. You can also obtain the patent publication and check the claims granted with the function “Patent Public Search”[6].

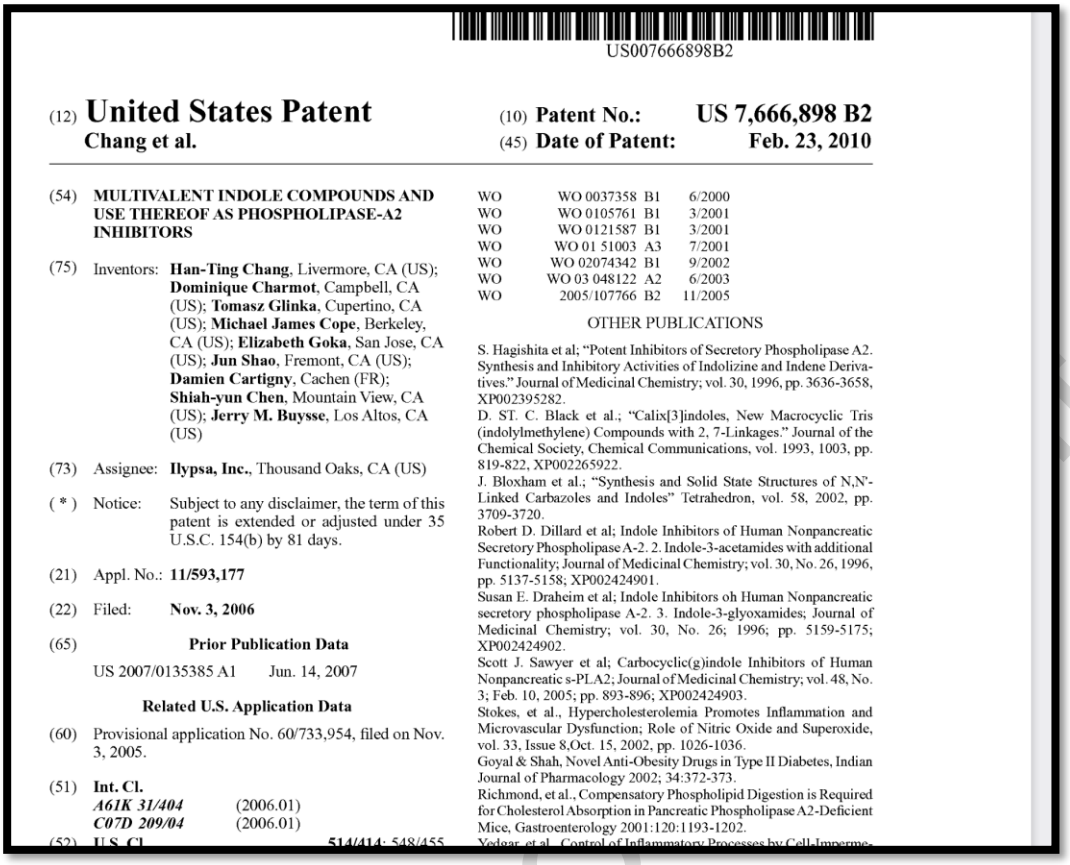


The following is the search result after inputting the patent number:



[6] https://ppubs.uspto.gov/pubwebapp/static/pages/ppubsbasic.html

The patent publication itself has a volume of useful and important information as follows:



US007666898B2

(12) **United States Patent**
Chang et al.

(10) **Patent No.: US 7,666,898 B2**
(45) **Date of Patent: Feb. 23, 2010**

(54) **MULTIVALENT INDOLE COMPOUNDS AND USE THEREOF AS PHOSPHOLIPASE-A2 INHIBITORS**

(75) Inventors: **Han-Ting Chang**, Livermore, CA (US); **Dominique Charmot**, Campbell, CA (US); **Tomasz Glinka**, Cupertino, CA (US); **Michael James Cope**, Berkeley, CA (US); **Elizabeth Goka**, San Jose, CA (US); **Jun Shao**, Fremont, CA (US); **Damien Cartigny**, Cachen (FR); **Shiah-yun Chen**, Mountain View, CA (US); **Jerry M. Buysse**, Los Altos, CA (US)

(73) Assignee: **Ilypsa, Inc.**, Thousand Oaks, CA (US)

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 81 days.

(21) Appl. No.: **11/593,177**

(22) Filed: **Nov. 3, 2006**

(65) **Prior Publication Data**

US 2007/0135385 A1 Jun. 14, 2007

Related U.S. Application Data

(60) Provisional application No. 60/733,954, filed on Nov. 3, 2005.

(51) **Int. Cl.**
A61K 31/404 (2006.01)
C07D 209/04 (2006.01)

(52) **U.S. Cl.** **514/414**; 548/455

WO	WO 0037358	B1	6/2000
WO	WO 0105761	B1	3/2001
WO	WO 0121587	B1	3/2001
WO	WO 01 51003	A3	7/2001
WO	WO 02074342	B1	9/2002
WO	WO 03 048122	A2	6/2003
WO	2005/107766	B2	11/2005

OTHER PUBLICATIONS

S. Hagishita et al; "Potent Inhibitors of Secretory Phospholipase A2. Synthesis and Inhibitory Activities of Indolizine and Indene Derivatives." Journal of Medicinal Chemistry; vol. 30, 1996, pp. 3636-3658, XP002395282.

D. ST. C. Black et al.; "Calix[3]indoles, New Macrocyclic Tris (indolylmethylene) Compounds with 2, 7-Linkages." Journal of the Chemical Society, Chemical Communications, vol. 1993, 1003, pp. 819-822, XP002265922.

J. Bloxham et al.; "Synthesis and Solid State Structures of N,N'-Linked Carbazoles and Indoles" Tetrahedron, vol. 58, 2002, pp. 3709-3720.

Robert D. Dillard et al; Indole Inhibitors of Human Nonpancreatic Secretory Phospholipase A-2. 2. Indole-3-acetamides with additional Functionality; Journal of Medicinal Chemistry; vol. 30, No. 26, 1996, pp. 5137-5158; XP002424901.

Susan E. Draheim et al; Indole Inhibitors oh Human Nonpancreatic secretory phospholipase A-2. 3. Indole-3-glyoxamides; Journal of Medicinal Chemistry; vol. 30, No. 26; 1996; pp. 5159-5175; XP002424902.

Scott J. Sawyer et al; Carbocyclic(g)indole Inhibitors of Human Nonpancreatic s-PLA2; Journal of Medicinal Chemistry; vol. 48, No. 3; Feb. 10, 2005; pp. 893-896; XP002424903.

Stokes, et al., Hypercholesterolemia Promotes Inflammation and Microvascular Dysfunction; Role of Nitric Oxide and Superoxide, vol. 33, Issue 8,Oct. 15, 2002, pp. 1026-1036.

Goyal & Shah, Novel Anti-Obesity Drugs in Type II Diabetes, Indian Journal of Pharmacology 2002; 34:372-373.

Richmond, et al., Compensatory Phospholipid Digestion is Required for Cholesterol Absorption in Pancreatic Phospholipase A2-Deficient Mice, Gastroenterology 2001:120:1193-1202.

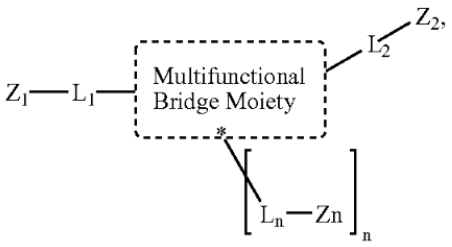
Yedgar, et al. Control of Inflammatory Processes by Cell-Imperme-

The last pages of the publication in the U.S. patent include the claims:

We claim:

1. A composition of matter comprising a substituted organic compound, or a salt thereof, wherein the substituted organic compound has two or more independently selected multi-ring structures, Z, linked by independently selected linking moieties, L, to a multifunctional bridge moiety, as represented by formula (D-I)

(D-I)



with

n being an integer ranging from 0 to 2,

the two or more multi-ring structures, Z, being covalently bonded to the multifunctional bridge moiety through corresponding linking moieties, L, each of the two or more multi-ring structures is a fused five-membered ring and six-membered ring represented by formulas (I) or (II)

The above case includes a chemical compound claim. It thus approaches sequence listing from the chemical side. In a patent/patent application which comes to include sequence listings more from the biological side, typical claims are as follows:

9. WO2010085606 - PROTEIN BIOMARKERS AND THERAPEUTIC TARGETS FOR OSTEOARTHRITIS

PCT Biblio. Data | Description | Claims | National Phase | Patent Family | Notices | Compounds | Documents

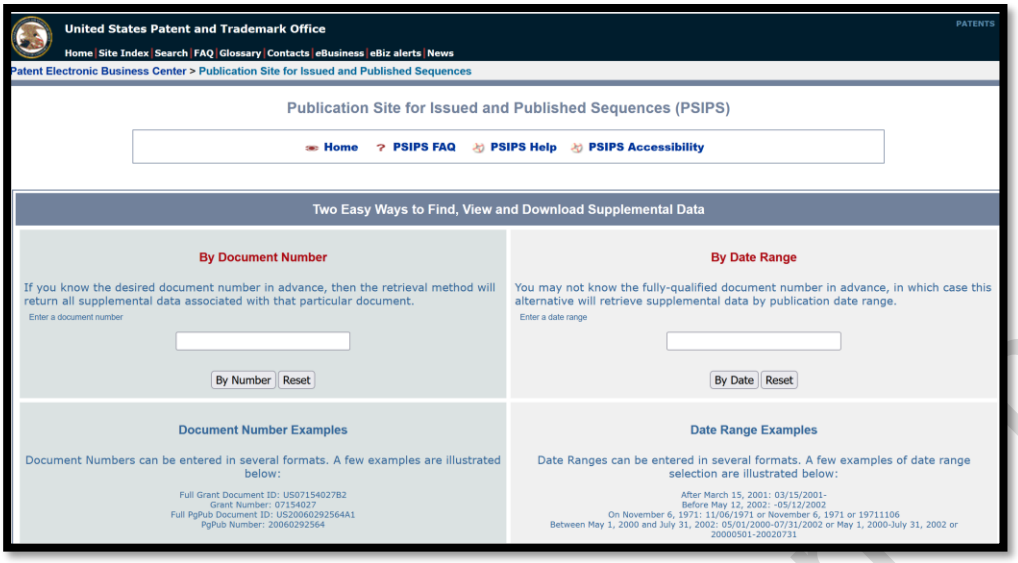
Start watching PermaLink Machine translation

Note: Text based on automatic Optical Character Recognition processes. Please use the PDF version for legal matters

[EN]
Having described the invention, the following is claimed:

1. A method for diagnosing osteoarthritis in a subject, said method comprising steps of: providing a biological sample obtained from the subject; determining, in the biological sample, the level of at least one protein selected from the group consisting of proteins identified in Tables 1-6, to obtain a test protein expression profile; and based on the test protein expression profile obtained, providing an osteoarthritis diagnosis to the subject .

For the purpose of gene sequence searching in the USPTO database, you can use the following function[7]:



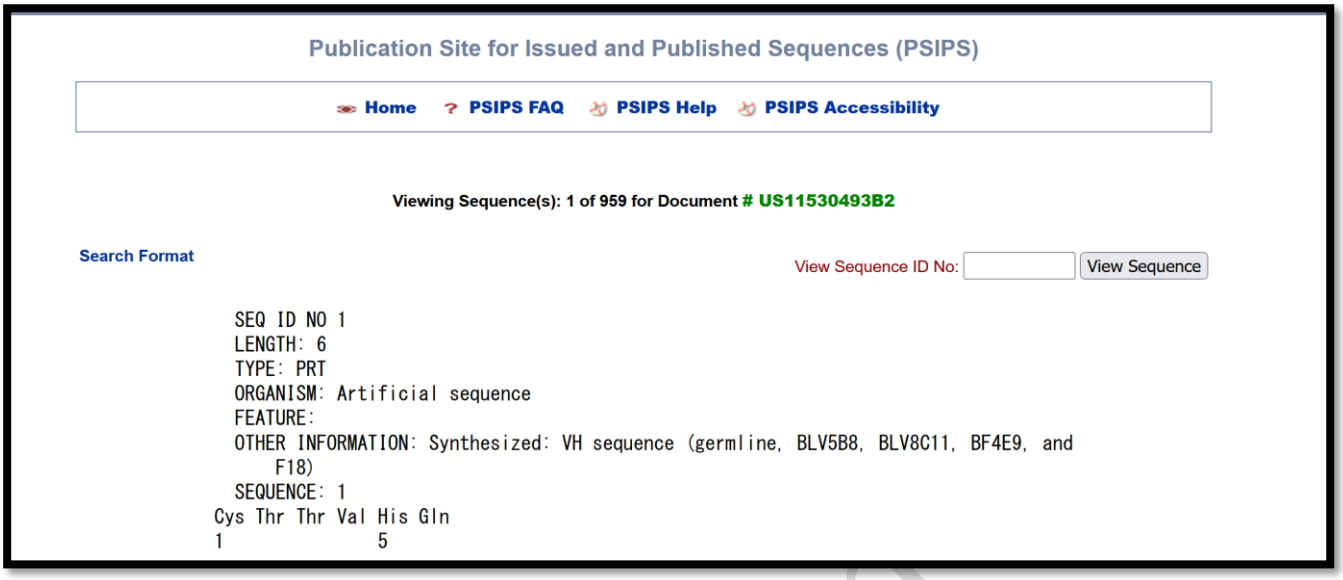
An exemplary result set of a sequence search is as follows:

All Documents Sorted By Date

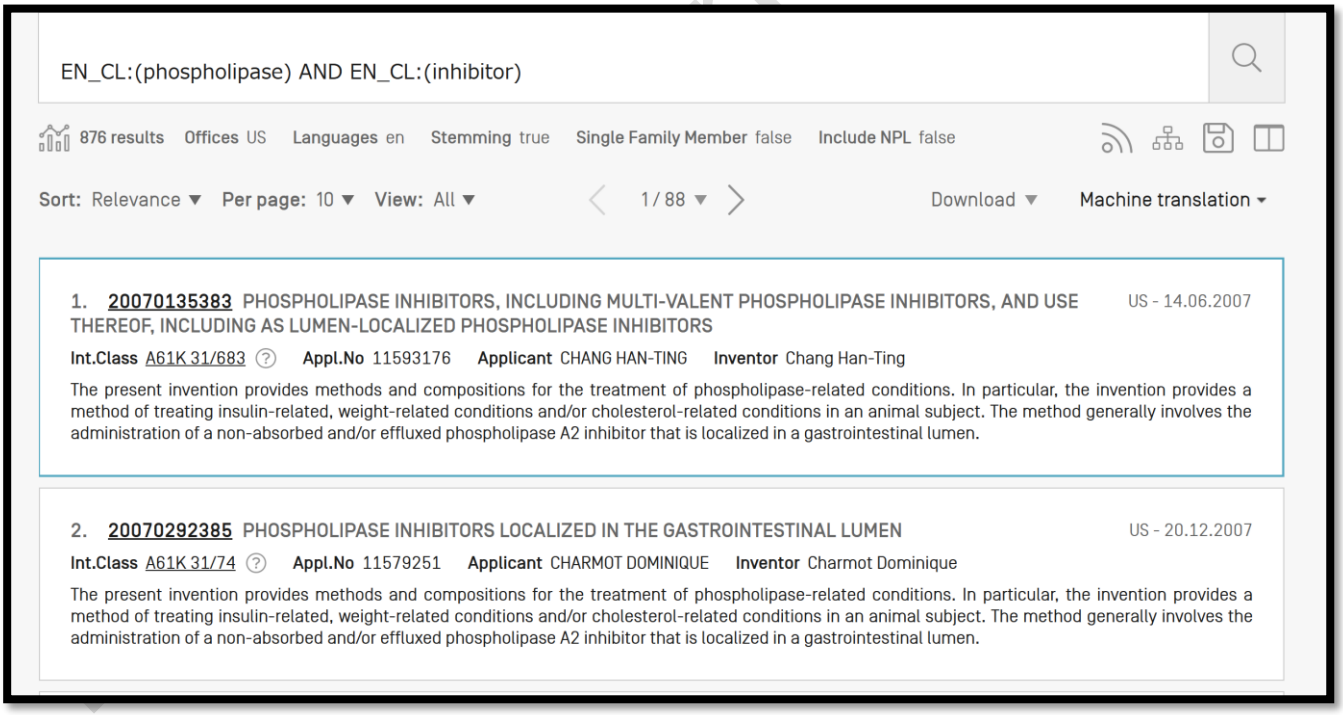
Publication Date	Document Number	Invention Title	Sequences	Tables	Other
20-DEC-22	US11530493B2	Humanized antibodies with ultralong complementary determining regions	959	0	0
20-DEC-22	US11530246B2	Regulated synthetic gene expression systems	380	0	0
20-DEC-22	US11530408B2	Therapeutic compositions	6756	0	0
20-DEC-22	US11530417B2	Drought and heat tolerance in plants	1364	0	0
20-DEC-22	US11530418B2	Polynucleotides and polypeptides for increasing desirable plant qualities	9211	0	0
20-DEC-22	US11530421B2	Self-inactivating endonuclease-encoding nucleic acids and methods of using the same	1135	0	0
15-DEC-22	US20220395544A1	COMPOSITIONS FOR THE TREATMENT OF DISEASE	9223	0	0
15-DEC-22	US20220395562A1	TERMINALLY MODIFIED RNA	5758	0	0
15-DEC-22	US20220396793A1	METHODS AND COMPOSITIONS FOR THE SPECIFIC INHIBITION OF ALPHA-1 ANTITRYPSIN BY DOUBLE-STRANDED RNA	3499	0	0
15-DEC-22	US20220396777A1	PATIENT-MATCHED ORGANOID SYSTEMS FOR STUDYING CANCER	0	6	0

[7] https://seqdata.uspto.gov/

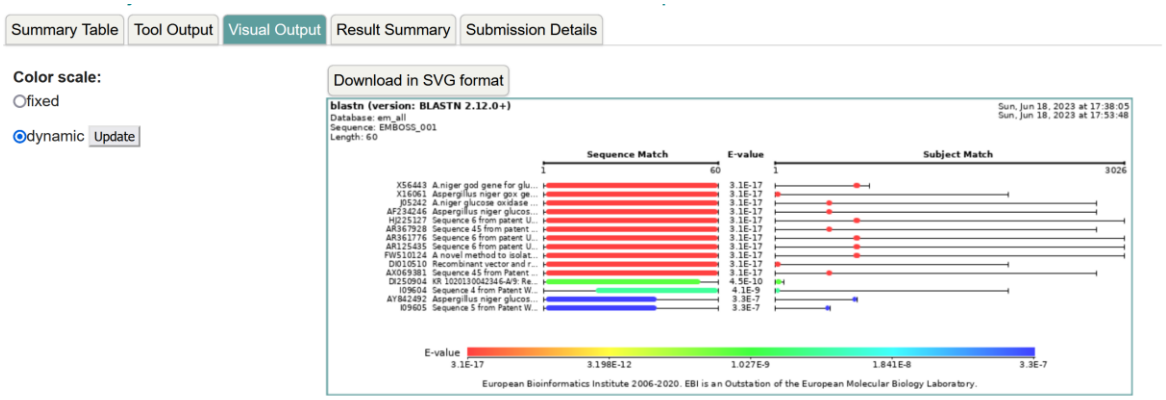
Then you can obtain the actual information on the gene sequence:



In more specific searches, you can refine the search formula to use the “claim” field in the research and specify the country such as “US.”



For the refinement of the sequence searches, you can use the following output:



In the subject match, you will be able to identify where the matches are found. Then you can classify the results based on the location of matches. You can expand the search with more sequence information as there are too many 100% matches in this case. On the other hand, if the higher matches are not found, then you can shorten your query sequences to improve the hit rate. The literature you have found may be academic literature or patents. In patents, you should look closely at the claims whether the hit sequence is mentioned in the claims to further elaborate and understand the nature of the sequences.

Once you have completed your search, you will obtain a collection of patents/patent applications. You should check whether for FtO purposes that list only contains “active” patents/patent applications, but you also need to check the “dead” date, as in some jurisdictions revival systems are available for potential future infringement.

3.3.2.4 STAGE 4: Analyzing your search results

Then you will undertake the critical step of checking the claims to determine whether your targeted product will fall within the scope of the claims.

Read your search results. Summarize your search results using various analyzing tools. Discuss with your colleagues and/or your tutors/mentors if you are undertaking relevant WIPO TKD training about your results. Prepare a short summary of your results. If you find an important patent document, you should deepen your investigation of the particular case, including a patent family search, analysis of the claims, applicants, inventors and the like.

In principle, you will compare the claim language against your product of interest, usually on an element-by-element basis.

If any one of the claim elements does not satisfy the patented claims (or pending claims in the case of a patent application), then you will not be infringing the patent. However, you must be careful if the difference could be comprised by means of the doctrine of equivalents. So, if you are not confident to exclude the respective claim from the “risk” hits, you should maintain the hit for future review.

In the case of a sequence search, e.g., in the following hit patent case:

(12) **United States Patent**
De Graaff et al.

(10) **Patent No.: US 8,461,320 B2**
(45) **Date of Patent: *Jun. 11, 2013**

(54) **METHOD TO ISOLATE MUTANTS AND TO CLONE THE COMPLEMENTING GENE**

(75) Inventors: **Leendert Hendrik De Graaff**, Oosterbeek (NL); **Henriëtta Catharina Van Den Broeck**, Bennekom (NL); **Jacob Visser**, Wageningen (NL)

(73) Assignee: **DuPont Nutrition Biosciences ApS**, Copenhagen K (DK)

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 828 days.

This patent is subject to a terminal disclaimer.

de Lorenzo et al, Engineering of alkyl- and haloaromatic-responsive gene expression with mini-transposons containing regulated promoters of biodegregadative pathways of *Pseudomonas*, Gene 130:41-46, 1994.*

Scorpione et al., "A New Promoter-Probe Vector for *Saccharomyces cerevisiae* using Fungal Glucoamylase cDNA as the Reporter Gene," *Yeast*, vol. 9, p. 599-605 (1993).

Inouye et al., "Nucleotide Sequence of the Regulatory Gene *xylR* of the TOL plasmid from *Pseudomonas putida," Gene*, vol. 66, No. 2, p. 301-306 (1988).

Kreuzer et al., "Identification and Sequence Analysis of the *Bacillus subtilis* W23 *xylR* Gene and *xyl* Operator," *Journal of Bacteriology*, vol. 171, No. 7, p. 3840-3845 (1989).

Rosenfeld et al., "Cloning and Characterization of the *xyl* genes from *Escherichia coli," Molecular and General Genetics*, vol. 194, p. 410-415 (1984).

You should go to the claims:

The invention claimed is:

1. An isolated nucleic acid molecule comprising nucleotides 1 to 4173 of SEQ ID NO:9.

2. An isolated nucleic acid molecule encoding amino acid residues 1 to 875 of SEQ ID NO: 11.

3. An isolated nucleic acid molecule having at least 96% identity to nucleotides 1 to 4173 of SEQ ID NO:9, wherein said nucleic acid molecule encodes a xylanolytic regulator comprising a zinc finger binding domain, wherein said xylanolytic regulator is capable of binding to one or more of target genes selected from the group consisting of xlnA, xlnB, xlnC, xlnD and axeA.

4. The isolated nucleic acid molecule of claim **3**, wherein said nucleic acid molecule has at least 97% identity to nucleotides 1 to 4173 of SEQ ID NO:9, wherein said nucleic acid molecule encodes a xylanolytic regulator comprising a zinc finger binding domain, wherein said xylanolytic regulator is capable of binding to one or more of target genes selected from the group consisting of xlnA, xlnB, xlnC, xlnD and axeA.

5. The isolated nucleic acid molecule of claim **3**, wherein said nucleic acid molecule has at least 98% identity to nucleotides 1 to 4173 of SEQ ID NO:9, wherein said nucleic acid molecule encodes a xylanolytic regulator comprising a zinc finger binding domain, wherein said xylanolytic regulator is capable of binding to one or more of target genes selected from the group consisting of xlnA, xlnB, xlnC, xlnD and axeA.

Then, you will see that claim 1 reads: An isolated nucleic acid molecule comprising nucleotides 1 to 4173 of SEQ ID NO:9. On the other hand, the hit is derived from SEQ ID NO. 6. Therefore, in this case, you can further analyze whether the claims are really relevant or not.

By doing so, your initial search screening will be completed.

3.3.2.5 STAGE 5: Applying your search results to your objectives

The next phase is the screening of the resulting patents/patent applications. You need to screen the collected patents/patent applications.

Although it is recommended and reasonable to compare the targeted product/service with the claims in force or pending claims (for pending applications) with most updated amendments, it requires a certain amount of effort to collect such most up-to-date information of the collected patents/patent applications, which may amount to as many as several hundreds. Thus, often simply a reasonable screening with abstracts/"published" claims is performed.

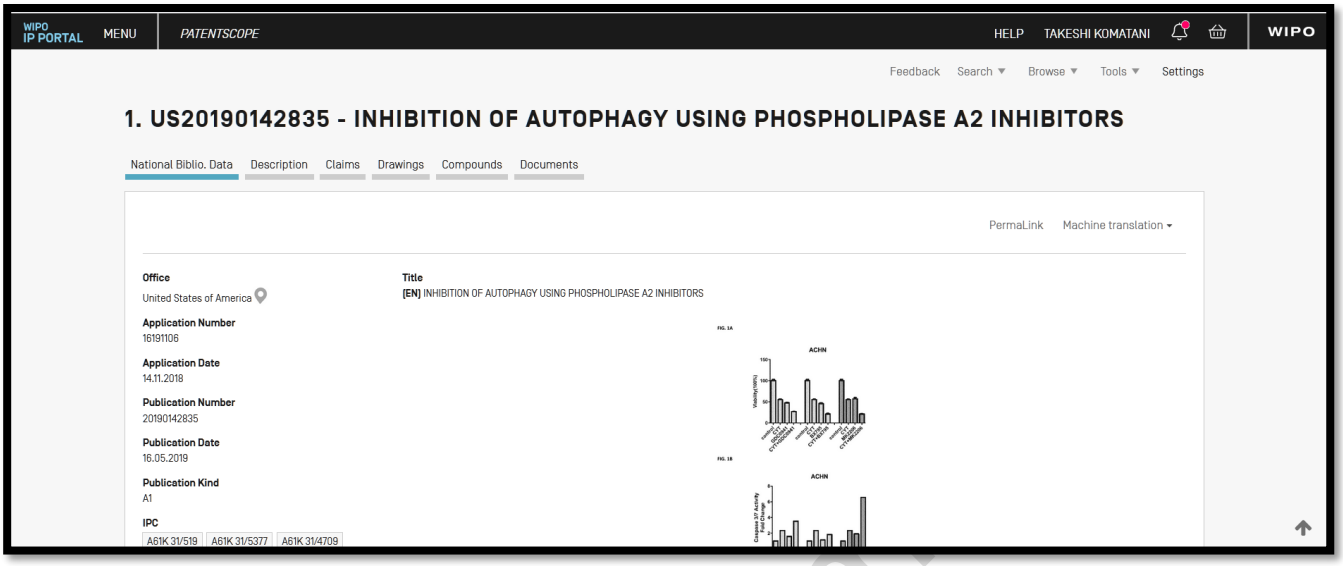
The excel sheet that is obtainable from PATENTSCOPE contains only title in relation to the contents of a patent/patent application, and such a list with abstracts/"published" claims may be obtainable using payable database. So, in this Guide, the excel sheet obtainable from PATENTSCOPE will be used for explanation.

An exemplary excel sheet obtainable from PATENTSCOPE (using "Phospholipase" in English Description, and "inhibitor" and "pharmaceutical" in English Claims) is shown below:

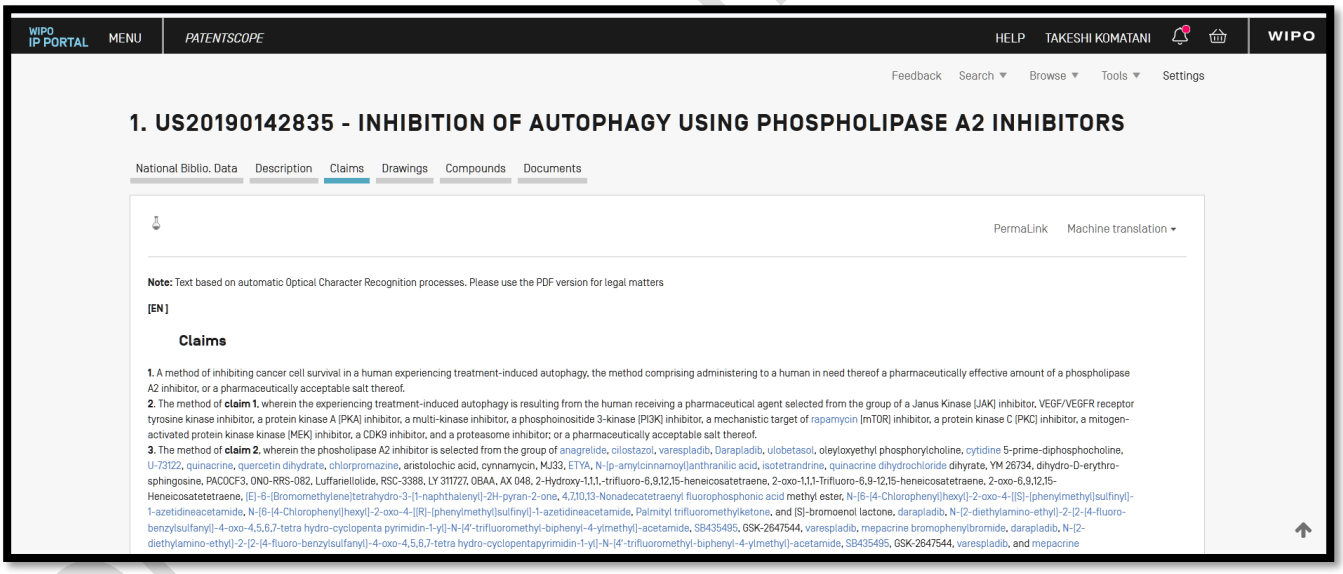
Time:	*25.12.2022 17:43:29*
Query:	*EN_DE:(phospholipase) AND EN_CL:(inhibitor) AND EN_CL:(pharmaceutical) AND DP:([01.01.1997 TO 25.12.2022])*
SortBy:	*Relevance*

Application Id	Application Number	Application Date	Country	Title	I P C
US242148746	16191106	14.11.2018	US	INHIBITION OF AUTOPHAGY USING PHOSPHOLIPASE A2 INHIBITORS	A61K 31/519; A61K 31/5377; A61K 31/4709; A61P 35/00
US332609456	17230840	14.04.2021	US	INHIBITION OF AUTOPHAGY USING PHOSPHOLIPASE A2 INHIBITORS	A61K 31/519; A61K 31/5377; A61K 31/4709; A61P 35/00
WO2005046564	PCT/IL2004/001048	16.11.2004	WO	DIAGNOSIS AND TREATMENT OF LIVER FIBROSIS	A61K 48/00; C07H 21/04; C12Q 1/68
WO2005046565	PCT/IL2004/001049	16.11.2004	WO	DIAGNOSIS AND TREATMENT OF KIDNEY FIBROSIS AND OTHER FIBROTIC DISEASES	C07H 21/04; A01N 43/04; A61K 31/70
US97882831	14103795	11.12.2013	US	METHODS AND COMPOSITIONS OF TREATING HIV INFECTION	C07D 401/04; A61K 45/06; C07D 471/10
AU194176380	2013359311	11.12.2013	AU	Methods and compositions of treating HIV infection	A01N 37/18; A01N 43/40
WO2014093553	PCT/US2013/074496	11.12.2013	WO	METHODS AND COMPOSITIONS OF TREATING HIV INFECTION	A01N 37/18; A01N 43/40
US178303674	15189920	22.06.2016	US	Methods and Compositions for Treating HIV Infection	A61K 31/454; A61K 31/435; A61K 9/00
EP192351016	15717429	25.03.2015	EP	BACTERIAL PHOSPHOLIPASE INHIBITORS AS MODULATOR OF COLONIC BACTERIAL FLORA	A61K 47/55; A61K 47/54; A61P 1/00
WO2015144737	PCT/EP2015/056326	25.03.2015	WO	BACTERIAL PHOSPHOLIPASE INHIBITORS AS MODULATOR OF COLONIC BACTERIAL FLORA	A61K 47/48; A61P 1/00
CA94055033	2425215	10.10.2001	CA	COMPOSITIONS AND METHODS FOR ENHANCING PARACELLULAR PERMEABILITY ACROSS EPITHELIAL AND ENDOTHELIAL BARRIERS	A61K 31/00; A61K 31/353; A61K 31/37; A61K 31/58; A61K 31/685; A61K 45/06
WO2013049773	PCT/US2012/058192	30.09.2012	WO	ANTIVIRAL THERAPIES WITH PHOSPHOLIPASE D INHIBITORS	A61K 31/438
EP152524841	14162028	27.03.2014	EP	Bacterial phospholipase inhibitors as modulator of colonic bacterial flora	A61K 47/48; A61P 1/00
WO1997035588	PCT/US1997/004841	25.03.1997	WO	NOVEL USES OF PHOSPHOLIPASE C INHIBITORS	A61K 31/15; A61K 31/58
US41912776	11637381	12.12.2006	US	Methods of treatment for meconium aspiration syndrome	A61K 31/395; A61K 31/395; A61K 38/43; A61K 38/47; A61K 38/55; A61K 38/55
WO2002005808	PCT/AU2001/000858	13.07.2001	WO	NOVEL METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF DYSMENORRHOEA AND MENSTRUAL SIDE EFFECTS: THE USE OF PHOSPHOLIPASE INHIBITORS	A61K 31/00; A61K 31/192; A61K 31/357; A61K 31/437; A61K 31/675
AU181031871	2001272210	13.07.2001	AU	Novel methods and compositions for the treatment or prevention of dysmenorrhoea and menstrual side effects: the use of phospholipase inhibitors	A61K 31/00; A61K 31/192; A61K 31/195; A61K 31/357; A61K 31/437; A61K 31/675; A61P 15/00; A61P 15/06
WO2022031931	PCT/US2021/044680	05.08.2021	WO	COMPOSITIONS FOR ALTERING A MICROGLIAL CELL, AND METHODS OF USE THEREFORE	A61K 31/5377; A61K 31/405; A61K 31/497
WO2012031763	PCT/EP2011/004532	08.09.2011	WO	USE OF INHIBITORS OF PHOSPHOLIPASE A2 FOR THE TREATMENT OR PREVENTION OF FLAVIVIRUS INFECTION	C12N 9/20; A61K 31/00
US90357294	13819380	08.09.2011	US	USE OF INHIBITORS OF PHOSPHOLIPASE A2 FOR THE TREATMENT OR PREVENTION OF FLAVIVIRUS INFECTION	A61K 31/427; A61K 45/06
US42928304	12092380	03.11.2006	US	INDOLE COMPOUNDS HAVING C4-ACIDIC SUBSTITUENTS AND USE THEREOF AS PHOSPHOLIPASE-A2 INHIBITORS	A61K 31/4353; A61K 31/437; A61K 31/40; A61K 31/40; C07D 209/00; C07D 209/04; C07D 471/00; C07D 471/02
AU194409952	2013359315	11.12.2013	AU	Methods and compositions comprising Akt inhibitors and/or phospholipase D inhibitors	A61K 31/4468

In this excel sheet, you can click on the patent number to see the publication. For example, when you click the first hit, you will obtain this patent:



Further, when you click on the “Claims” tab of the patent, you will obtain the following contents:



In the screening phase, you can remove “apparent noise” by looking at the title columns. For example, in the result list a patent claiming “a computer program for exchanging stocks” is included, and so you can easily remove such hits as apparent noise.

Then you can screen by clicking at the publication number to see the claims of the respective patents/patent applications.

In the first hit, it is claimed as follows:

“**1**. A method of inhibiting cancer cell survival in a human experiencing treatment-induced autophagy, the method comprising administering to a human in need thereof a pharmaceutically effective amount of a phospholipase A2 inhibitor, or a pharmaceutically acceptable salt thereof."

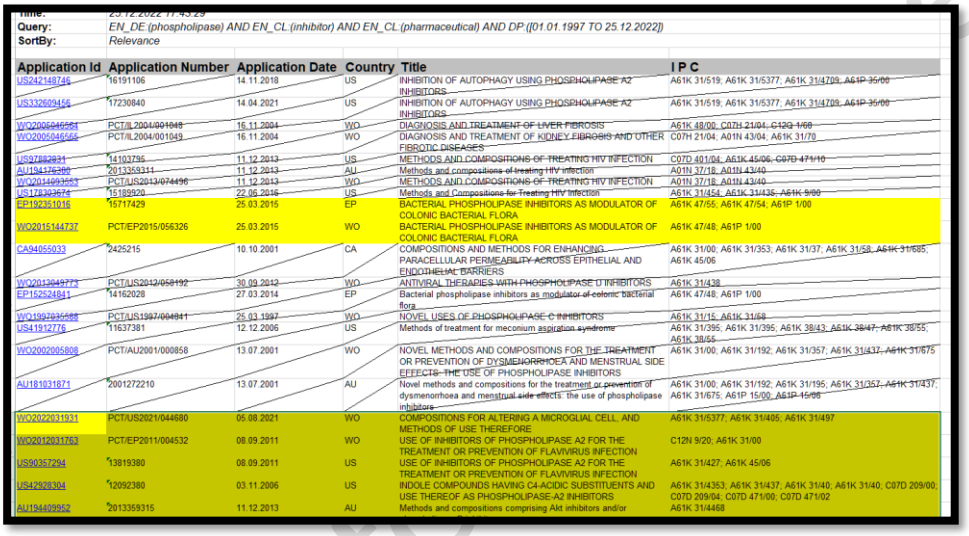
This claim language is in the U.S. format. So, you have to analyze based on the actual subject matter to be affected.

This claim means:

(a) API: a pharmaceutically effective amount of a phospholipase A2 inhibitor, or a pharmaceutically acceptable salt thereof;
(b) targeted indication/use: inhibiting cancer cell survival in a human experiencing treatment-induced autophagy.

In this case, if your targeted product/service is related to an inhibitor of phospholipase C, then this hit can be removed from the hits list, but if your target product/service is related to an inhibitor of phospholipase A2, then you will go to the next parameter to see the use. If your target use is related to cancer, you will maintain this as hit, but if your use is not related to cancer but rather inflammation, then this hit can be removed.

After this screening stage, you can obtain a screened excel sheet as follows:

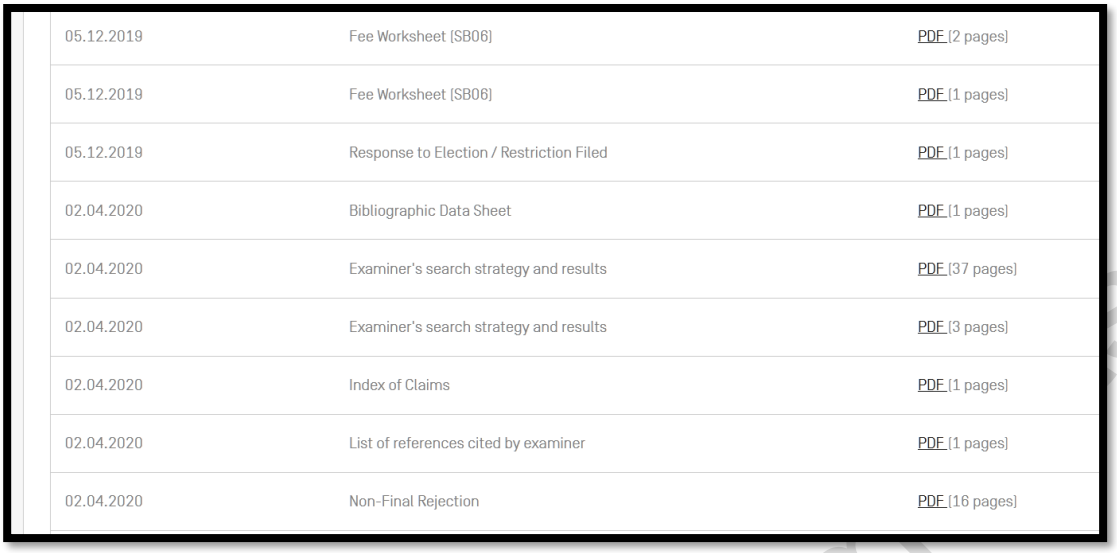


Time: 23.12.2022 17:43:29
Query: EN_DE:(phospholipase) AND EN_CL:(inhibitor) AND EN_CL:(pharmaceutical) AND DP:([01.01.1997 TO 25.12.2022])
SortBy: Relevance

Application Id	Application Number	Application Date	Country	Title	I P C
US242148746	16191106	14.11.2018	US	INHIBITION OF AUTOPHAGY USING PHOSPHOLIPASE A2 INHIBITORS	A61K 31/519; A61K 31/5377; A61K 31/4709; A61P 35/00
US332609456	17230840	14.04.2021	US	INHIBITION OF AUTOPHAGY USING PHOSPHOLIPASE A2 INHIBITORS	A61K 31/519; A61K 31/5377; A61K 31/4709; A61P 35/00
WO2005046565	PCT/IL2004/001048	16.11.2004	WO	DIAGNOSIS AND TREATMENT OF LIVER FIBROSIS	A61K 48/00; C07H 21/04; C12Q 1/68
WO2005046565	PCT/IL2004/001049	16.11.2004	WO	DIAGNOSIS AND TREATMENT OF KIDNEY FIBROSIS AND OTHER FIBROTIC DISEASES	C07H 21/04; A01N 43/04; A61K 31/70
US97882831	14103795	11.12.2013	US	METHODS AND COMPOSITIONS OF TREATING HIV INFECTION	C07D 401/04; A61K 45/06; C07D 471/10
AU194176366	2013359311	11.12.2013	AU	Methods and compositions of treating HIV infection	A01N 37/18; A01N 43/40
WO2014093563	PCT/US2013/074496	11.12.2013	WO	METHODS AND COMPOSITIONS OF TREATING HIV INFECTION	A01N 37/18; A01N 43/40
US17362674	15189920	22.06.2016	US	Methods and Compositions for Treating HIV Infection	A61K 31/454; A61K 31/436; A61K 9/00
EP192351016	15717429	25.03.2015	EP	BACTERIAL PHOSPHOLIPASE INHIBITORS AS MODULATOR OF COLONIC BACTERIAL FLORA	A61K 47/55; A61K 47/54; A61P 1/00
WO2015144737	PCT/EP2015/056326	25.03.2015	WO	BACTERIAL PHOSPHOLIPASE INHIBITORS AS MODULATOR OF COLONIC BACTERIAL FLORA	A61K 47/48; A61P 1/00
CA94055033	2425215	10.10.2001	CA	COMPOSITIONS AND METHODS FOR ENHANCING PARACELLULAR PERMEABILITY ACROSS EPITHELIAL AND ENDOTHELIAL BARRIERS	A61K 31/00; A61K 31/353; A61K 31/37; A61K 31/58; A61K 31/685; A61K 45/06
WO2013049773	PCT/US2012/058192	30.09.2012	WO	ANTIVIRAL THERAPIES WITH PHOSPHOLIPASE D INHIBITORS	A61K 31/438
EP152524841	14162028	27.03.2014	EP	Bacterial phospholipase inhibitors as modulator of colonic bacterial flora	A61K 47/48; A61P 1/00
WO1997035583	PCT/US1997/004841	25.03.1997	WO	NOVEL USES OF PHOSPHOLIPASE C INHIBITORS	A61K 31/15; A61K 31/58
US41912776	11637381	12.12.2006	US	Methods of treatment for meconium aspiration syndrome	A61K 31/395; A61K 31/395; A61K 38/43; A61K 38/47; A61K 38/55; A61K 38/55
WO2002005808	PCT/AU2001/000858	13.07.2001	WO	NOVEL METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF DYSMENORRHOEA AND MENSTRUAL SIDE EFFECTS, THE USE OF PHOSPHOLIPASE INHIBITORS	A61K 31/00; A61K 31/192; A61K 31/357; A61K 31/437; A61K 31/675
AU181031871	2001272210	13.07.2001	AU	Novel methods and compositions for the treatment or prevention of dysmenorrhoea and menstrual side effects, the use of phospholipase inhibitors	A61K 31/00; A61K 31/192; A61K 31/195; A61K 31/357; A61K 31/437; A61K 31/675; A61P 15/00; A61P 15/06
WO2022031931	PCT/US2021/044680	05.08.2021	WO	COMPOSITIONS FOR ALTERING A MICROGLIAL CELL, AND METHODS OF USE THEREFORE	A61K 31/5377; A61K 31/405; A61K 31/497
WO2012031763	PCT/EP2011/004532	08.09.2011	WO	USE OF INHIBITORS OF PHOSPHOLIPASE A2 FOR THE TREATMENT OR PREVENTION OF FLAVIVIRUS INFECTION	C12N 9/20; A61K 31/00
US90357294	13819380	08.09.2011	US	USE OF INHIBITORS OF PHOSPHOLIPASE A2 FOR THE TREATMENT OR PREVENTION OF FLAVIVIRUS INFECTION	A61K 31/427; A61K 45/06
US42928304	12092380	03.11.2006	US	INDOLE COMPOUNDS HAVING C4-ACIDIC SUBSTITUENTS AND USE THEREOF AS PHOSPHOLIPASE-A2 INHIBITORS	A61K 31/4363; A61K 31/437; A61K 31/40; A61K 31/40; C07D 209/00; C07D 209/04; C07D 471/00; C07D 471/02
AU194409952	2013359315	11.12.2013	AU	Methods and compositions comprising Akt inhibitors and/or	A61K 31/4468

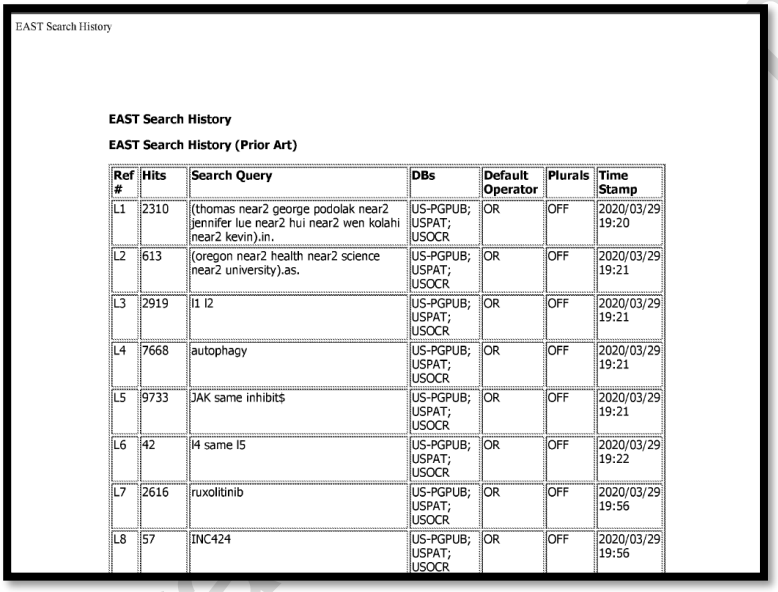
You can refine your search if you feel that your list is not appropriate. You may wish to look at a search strategy in your hits. For example, in the first patent, when you click “Document” you

will see several documents, and in the documents, you will find “Examiner's search strategy and results”:



05.12.2019	Fee Worksheet (SB06)	PDF (2 pages)
05.12.2019	Fee Worksheet (SB06)	PDF (1 pages)
05.12.2019	Response to Election / Restriction Filed	PDF (1 pages)
02.04.2020	Bibliographic Data Sheet	PDF (1 pages)
02.04.2020	Examiner's search strategy and results	PDF (37 pages)
02.04.2020	Examiner's search strategy and results	PDF (3 pages)
02.04.2020	Index of Claims	PDF (1 pages)
02.04.2020	List of references cited by examiner	PDF (1 pages)
02.04.2020	Non-Final Rejection	PDF (16 pages)

And you will obtain a document as follows:



EAST Search History

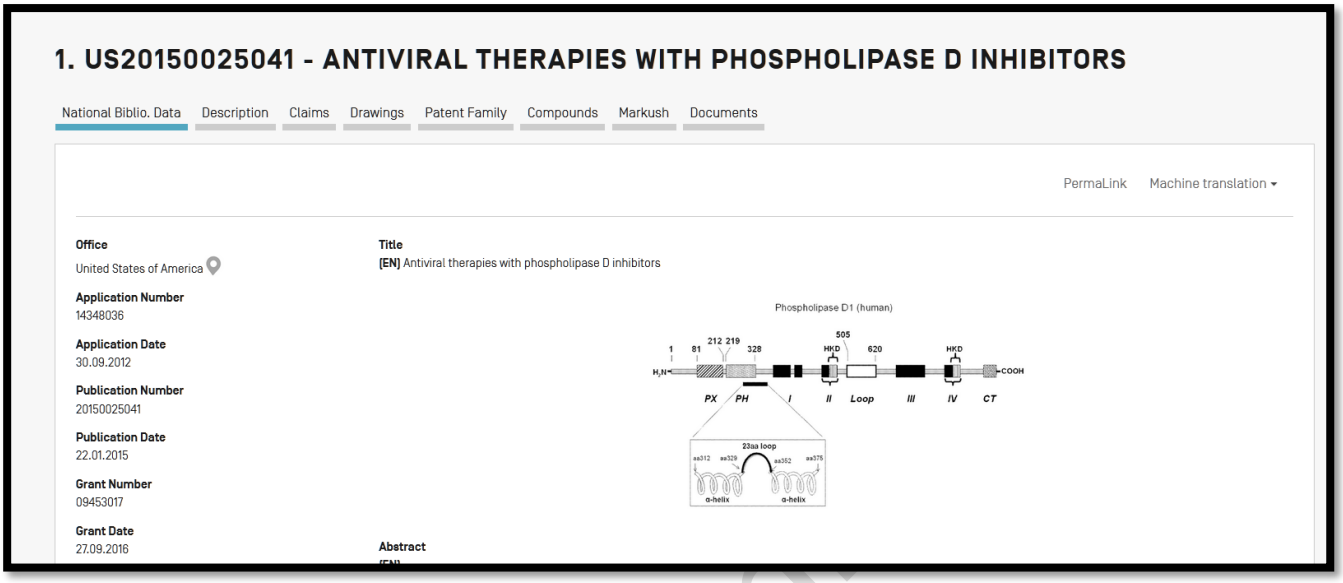
EAST Search History

EAST Search History (Prior Art)

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2310	(thomas near2 george podolak near2 jennifer lue near2 hui near2 wen kolahi near2 kevin).in.	US-PGPUB; USPAT; USOCR	OR	OFF	2020/03/29 19:20
L2	613	(oregon near2 health near2 science near2 university).as.	US-PGPUB; USPAT; USOCR	OR	OFF	2020/03/29 19:21
L3	2919	l1 l2	US-PGPUB; USPAT; USOCR	OR	OFF	2020/03/29 19:21
L4	7668	autophagy	US-PGPUB; USPAT; USOCR	OR	OFF	2020/03/29 19:21
L5	9733	JAK same inhibit$	US-PGPUB; USPAT; USOCR	OR	OFF	2020/03/29 19:21
L6	42	l4 same l5	US-PGPUB; USPAT; USOCR	OR	OFF	2020/03/29 19:22
L7	2616	ruxolitinib	US-PGPUB; USPAT; USOCR	OR	OFF	2020/03/29 19:56
L8	57	INC424	US-PGPUB; USPAT; USOCR	OR	OFF	2020/03/29 19:56

In the next step of your sequence search exercise, you need to analyze the hits for the patented claims.

For example, in the exemplary list, you will obtain the following hit:



1. US20150025041 - ANTIVIRAL THERAPIES WITH PHOSPHOLIPASE D INHIBITORS

National Biblio. Data | Description | Claims | Drawings | Patent Family | Compounds | Markush | Documents

PermaLink | Machine translation

Office
United States of America

Application Number
14348036

Application Date
30.09.2012

Publication Number
20150025041

Publication Date
22.01.2015

Grant Number
09453017

Grant Date
27.09.2016

Title
(EN) Antiviral therapies with phospholipase D inhibitors

Phospholipase D1 (human)

1 81 212 219 328 505 620 HKD HKD COOH

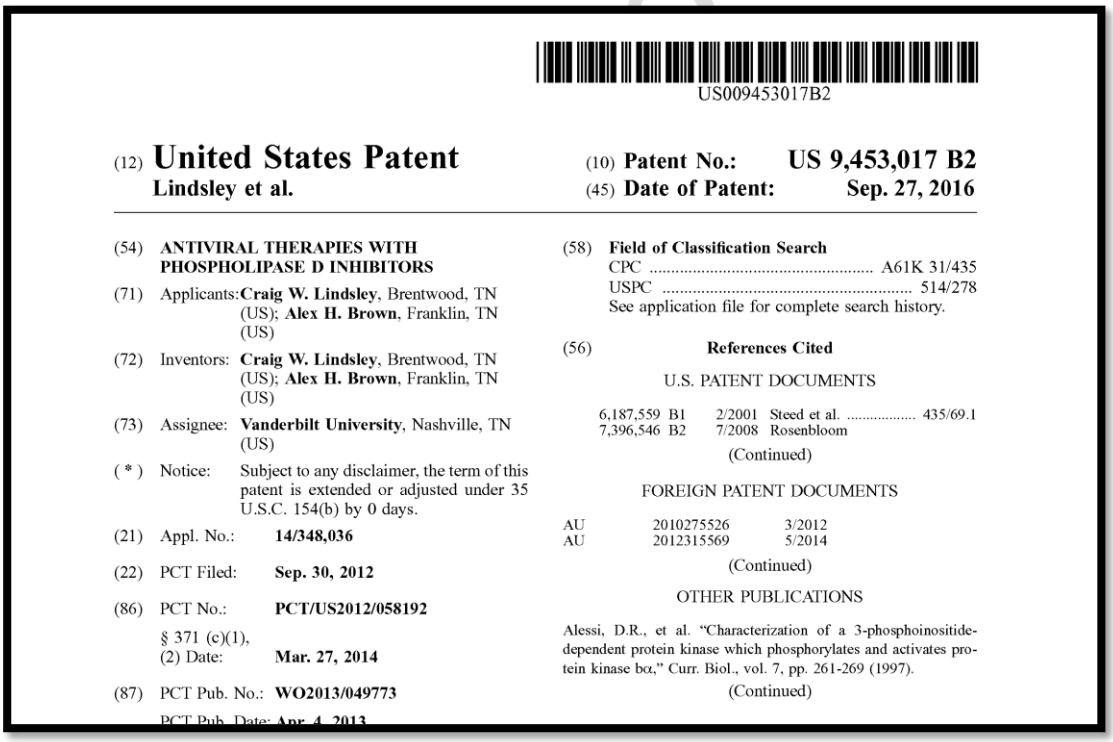
PX PH I II Loop III IV CT

23aa loop

α-helix α-helix

Abstract

You can obtain an issued patent using the method described above:



US009453017B2

(12) **United States Patent**
Lindsley et al.

(10) **Patent No.: US 9,453,017 B2**
(45) **Date of Patent: Sep. 27, 2016**

(54) **ANTIVIRAL THERAPIES WITH PHOSPHOLIPASE D INHIBITORS**

(71) Applicants: **Craig W. Lindsley**, Brentwood, TN (US); **Alex H. Brown**, Franklin, TN (US)

(72) Inventors: **Craig W. Lindsley**, Brentwood, TN (US); **Alex H. Brown**, Franklin, TN (US)

(73) Assignee: **Vanderbilt University**, Nashville, TN (US)

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

(21) Appl. No.: **14/348,036**

(22) PCT Filed: **Sep. 30, 2012**

(86) PCT No.: **PCT/US2012/058192**
§ 371 (c)(1),
(2) Date: **Mar. 27, 2014**

(87) PCT Pub. No.: **WO2013/049773**
PCT Pub. Date: **Apr. 4, 2013**

(58) **Field of Classification Search**
CPC A61K 31/435
USPC 514/278
See application file for complete search history.

(56) **References Cited**

U.S. PATENT DOCUMENTS

6,187,559 B1 2/2001 Steed et al. 435/69.1
7,396,546 B2 7/2008 Rosenbloom
(Continued)

FOREIGN PATENT DOCUMENTS

AU 2010275526 3/2012
AU 2012315569 5/2014
(Continued)

OTHER PUBLICATIONS

Alessi, D.R., et al. "Characterization of a 3-phosphoinositide-dependent protein kinase which phosphorylates and activates protein kinase bα," Curr. Biol., vol. 7, pp. 261-269 (1997).
(Continued)

In the obtained patent, the claims appear as described for our illustrative example below:

invention. Other embodiments of the invention will be apparent to those skilled in the art from consideration of the specification and practice of the invention disclosed herein. It is intended that the specification and examples be considered as exemplary only, with a true scope and spirit of the invention being indicated by the following claims.

What is claimed is:

1. A method for treating a subject comprising the step of co-administering an effective amount of a combination of two or more therapeutic agents to the subject;

wherein the subject has been diagnosed with a need for treatment of an influenza infection prior to the administering step; and

wherein the combination of two or more therapeutic agents comprises:

(a) an phospholipase D inhibitor; and

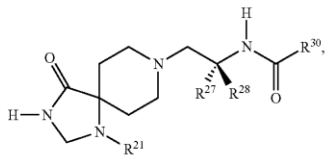
(b) one or more therapeutic agents selected from:

(i) a viral protein M2 ion channel inhibitor,

(ii) a neuraminidase inhibitor, and

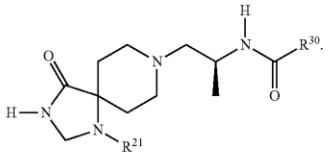
(iii) a nucleoside analog selected from ribavirin, viramidine, 6-fluoro-3-hydroxy-2-pyrazinecarboxamide, 2'-deoxy-2'-fluoroguanosine, pyrazofurin, carbodine, and cyclopenenyl cytosine;

wherein the phospholipase D inhibitor is a compound having a structure represented by a formula:

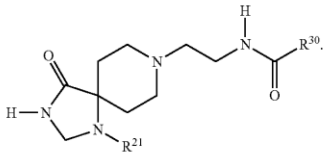


Wherein R^{21} is a phenyl or halophenyl; each of R^{27} and R^{28} is, independently, a hydrogen or a C1 to C6 alkyl; R^{30} is an optionally substituted organic residue selected from aryl and heteroaryl, wherein the organic residue is up to C16,

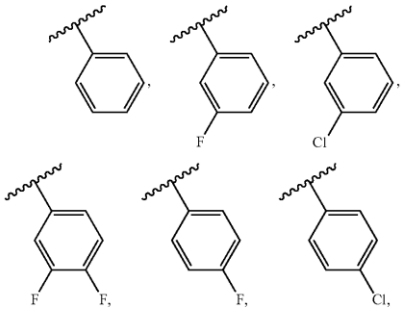
or a pharmaceutically acceptable salt thereof.



12. The method of claim **1**, the compound has the structure represented by a formula:



13. The method of claim **1**, wherein R^{21} is selected from:

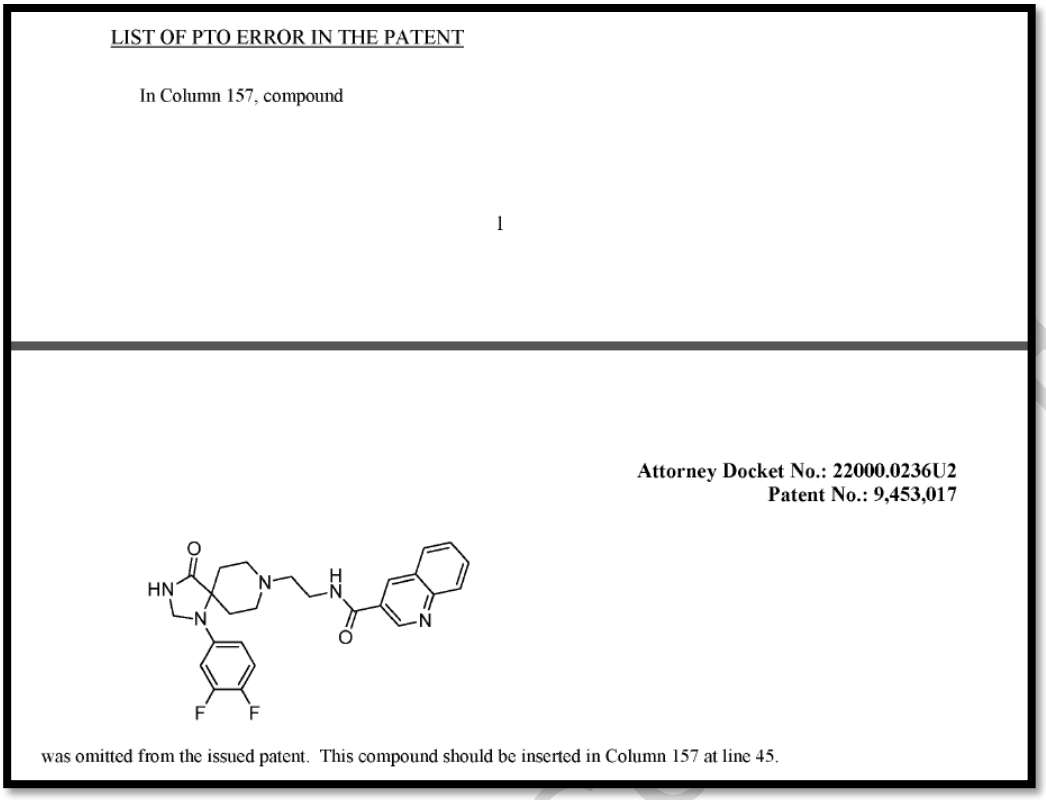


and

In this case, these published claims have been corrected as mentioned below:

23.08.2016	Foreign Reference	PDF (79 pages)
23.08.2016	Information Disclosure Statement (IDS) Form (SB08)	PDF (2 pages)
23.08.2016	Request for Continued Examination(RCE) Not Entered	PDF (3 pages)
23.08.2016	Transmittal Letter	PDF (2 pages)
01.09.2016	List of References cited by applicant and considered by examiner	PDF (2 pages)
01.09.2016	Notice of Allowance and Fees Due (PTOL-85)	PDF (2 pages)
02.09.2016	Fee Worksheet (SB06)	PDF (2 pages)
07.09.2016	Issue Notification	PDF (1 pages)
11.11.2016	Electronic Filing System(EFS) Acknowledgment Receipt	PDF (2 pages)
11.11.2016	Request for Certificate of Correction	PDF (3 pages)
03.01.2017	Certificate of Correction - Post Issue Communication	PDF (1 pages)

In this case, the claim is corrected and thus you should refer to this correction in order to properly analyze the infringement:



LIST OF PTO ERROR IN THE PATENT

In Column 157, compound

1

Attorney Docket No.: 22000.0236U2
Patent No.: 9,453,017

was omitted from the issued patent. This compound should be inserted in Column 157 at line 45.

As mentioned above, FtO is of constantly moving and evolving scope. For example, this correction is directed to the claims, so, in order to have an appropriate search, "current" information should be considered, including the most updated information as exemplified above.

In this screening stage of phase 5 of your sequence searches, you can distinguish several stages:

- first, you can do a "cursory" screening by only looking at abstracts and/or independent claims, and,
- second, you can conduct a "secondary" screening to identify "real" hits to continue for further and final analysis.

After the "secondary" screening and your "deep" analysis of the hits, you have completed stage 5 of your FtO search and can go on to stage 6 regarding the limitations of your search results.

3.3.2.6 STAGE 6: Recognizing the limitations of your search results

As the FtO clearance searches eventually require professional legal opinions, this Guide only provides preliminary searches so that you may obtain a general sense and feel of infringement/non-infringement for your particular project or target sequence. So, it lies in the nature of this search, which you are performing, that you should recognize limitations of your search results. As mentioned, to recognize the limits of this Guide and your introductory searches, it is necessary to obtain a professional opinion by a patent lawyer to rest assured that you have accurately analyzed your FtO for your project.

3.3.2.7 STAGE 7: Finalizing your search: preparing reports

In the final stage, you will usually obtain several to dozens of hits. At this stage, you will do your literal infringement analysis and your indirect infringement/doctrine of equivalents search. This is rather professional analysis to be conducted by a patent lawyer with extensive IP management expertise. Therefore, this is not covered in this introductory Guide.

3.3.3 Technology trends searches

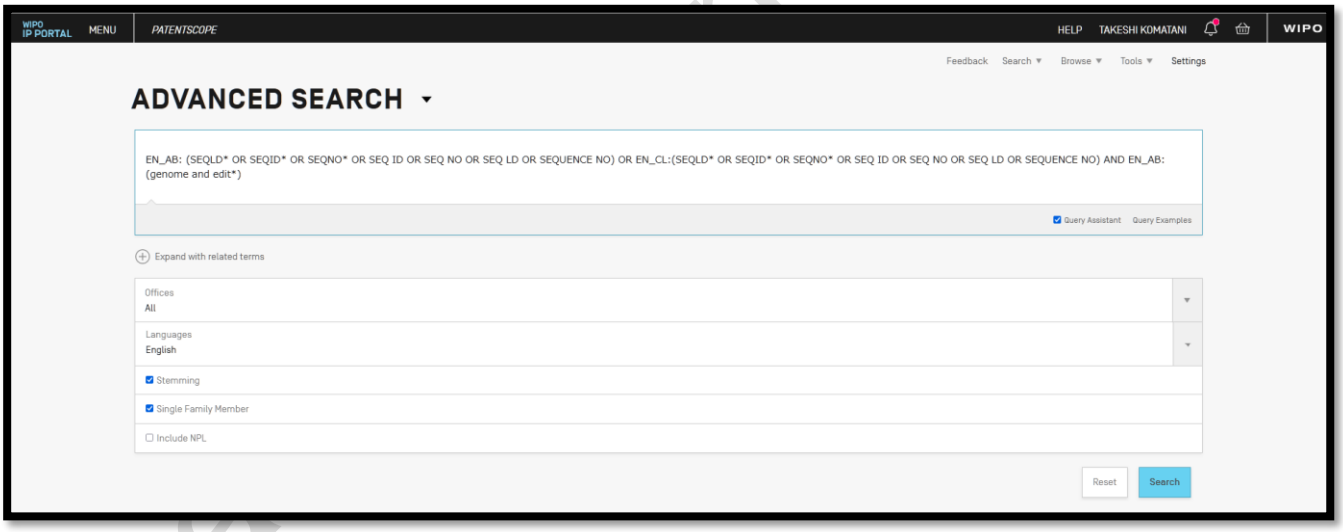
Besides prior art/patentability searches and FtO searches concerning the GR sequences of your interest, you can also elucidate technology trends by conducting patent and non-patent sequence searches. This section will briefly explain technology trends searches by conducting a search for a major technology trend in GRs which includes sequence related information.

3.3.3.1 STAGE 1: Defining objectives of your search

In order to illustrate technology trend searches, here we will use an example from a major life science technology trend for the utilization of GRs, namely genome editing with sequence listing information included.

3.3.3.2 STAGE 2: Building your initial query building blocks

In this function, you may wish to use the “Advanced Search” function:



Here, an exemplary search query string to identify a collection of patent literature having sequence information in the documents with genome editing can be drafted, namely: “EN_AB: (SEQLD* OR SEQID* OR SEQNO* OR SEQ ID OR SEQ NO OR SEQ LD OR SEQUENCE NO) OR EN_CL:(SEQLD* OR SEQID* OR SEQNO* OR SEQ ID OR SEQ NO OR SEQ LD OR SEQUENCE NO) AND EN_DE:(genome and edit*)”.

From use of this search query string, you will obtain an error message as the number of hits exceed the limitation, however, that does not need to be a reason for concern at this stage.

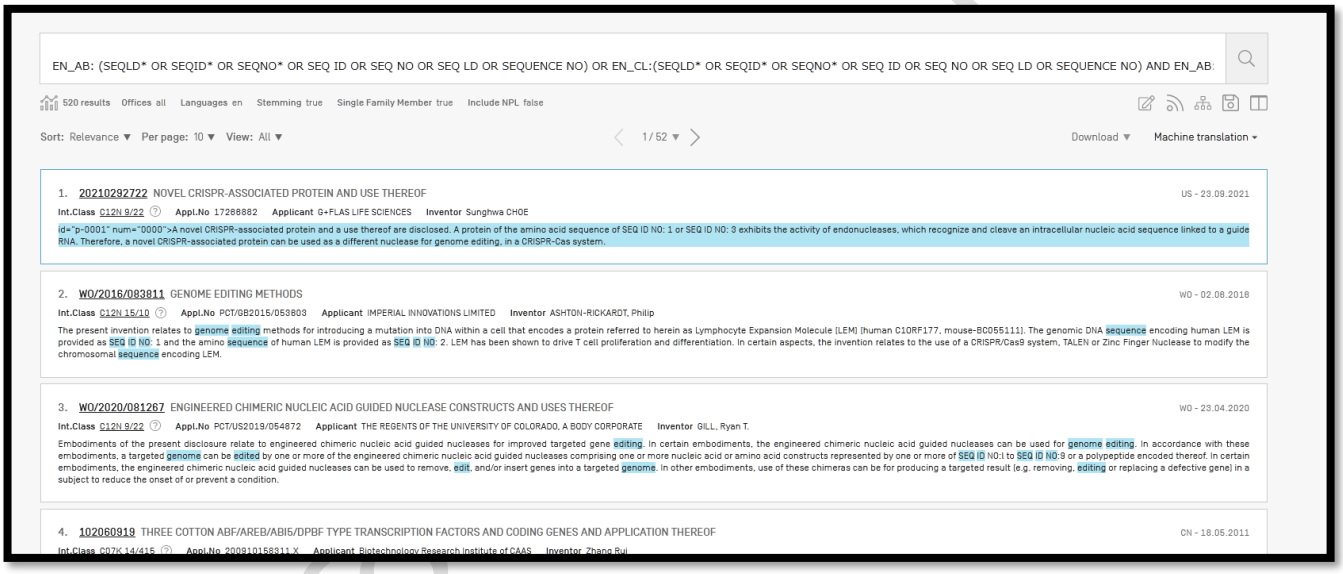
3.3.3.3 STAGE 3: Refining your search query: Trial and error and modification processes

Once you have done an initial search, pick up some hits from the search results, and read and investigate them closely. You may well find some relevant claim language, search terms, phrases, international patent classification categories, etc., which may be helpful to refine your search. Once you find some relevant and important patent documents, you can identify

enterprise names and other business-related information, through which you can apply your familiarity with the relevant business sector. Based on such information, you can develop your search within the internet websites of those enterprises to explore what is going on in the real world business context. Be sure to discuss your initial impressions with your colleagues and, if you are undertaking a WIPO training course, discuss them with your tutor/mentor, to refine your results.

In this context, you can rewrite the above-identified exemplary formula to collect patent literature containing sequence information in the documents with genome editing inventions to limit the second parameter from Description to Abstract: EN_AB: (SEQLD* OR SEQID* OR SEQNO* OR SEQ ID OR SEQ NO OR SEQ LD OR SEQUENCE NO) OR EN_CL:(SEQLD* OR SEQID* OR SEQNO* OR SEQ ID OR SEQ NO OR SEQ LD OR SEQUENCE NO) AND EN_AB:(genome and edit*)

Then you will obtain the following results:

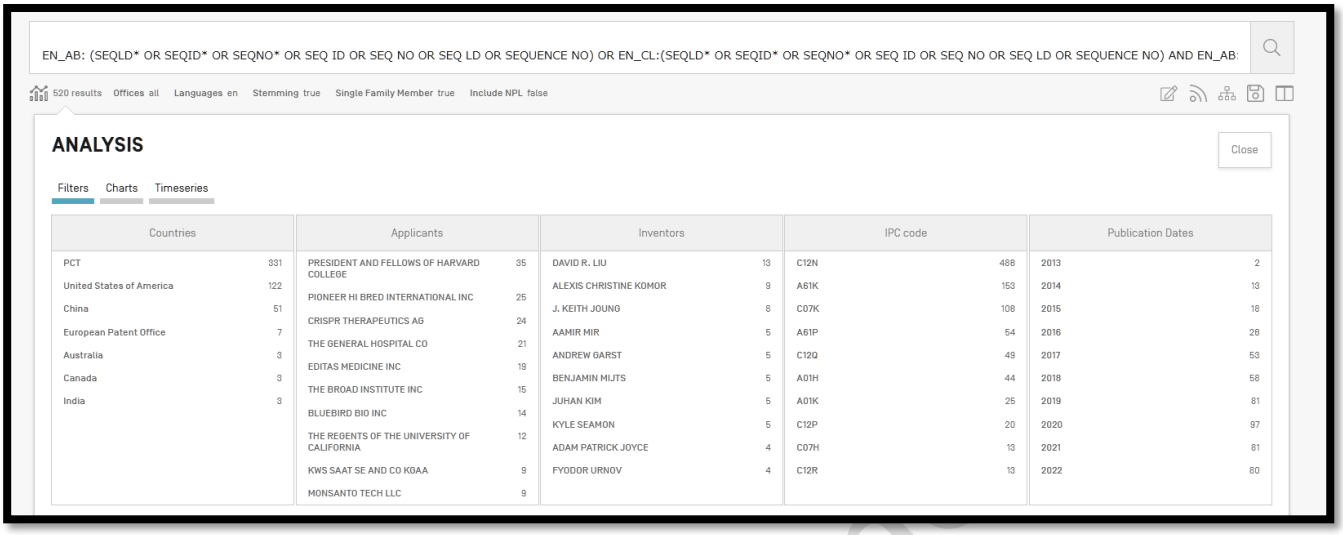


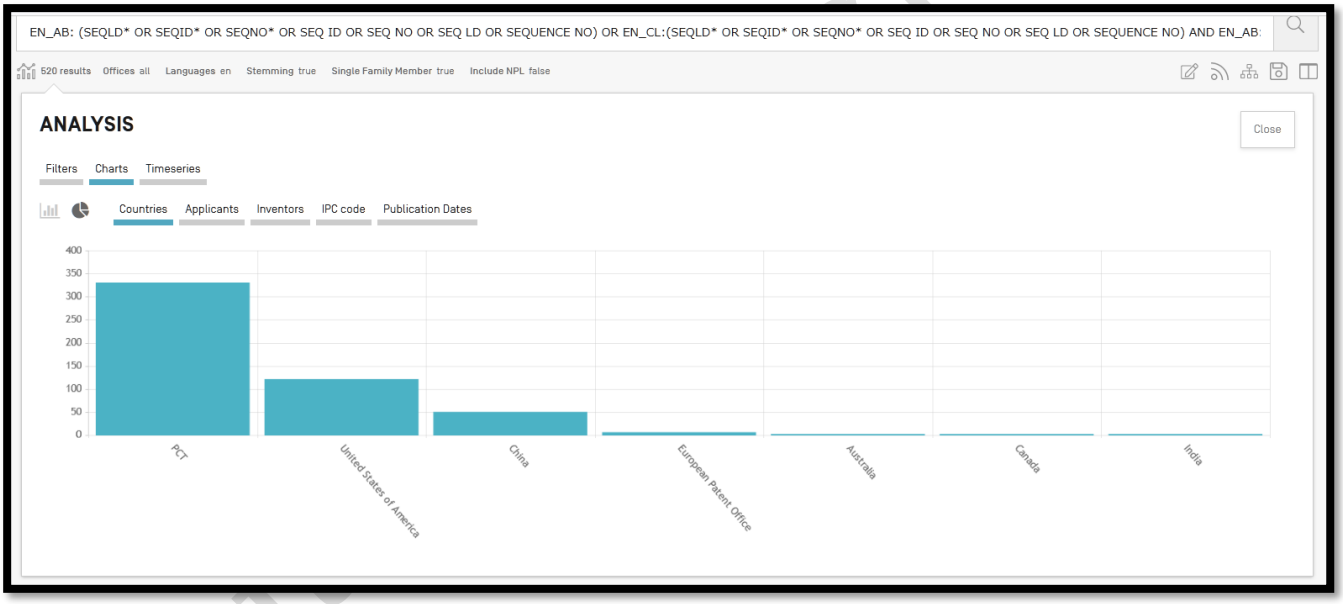
3.3.3.4 Analysis:

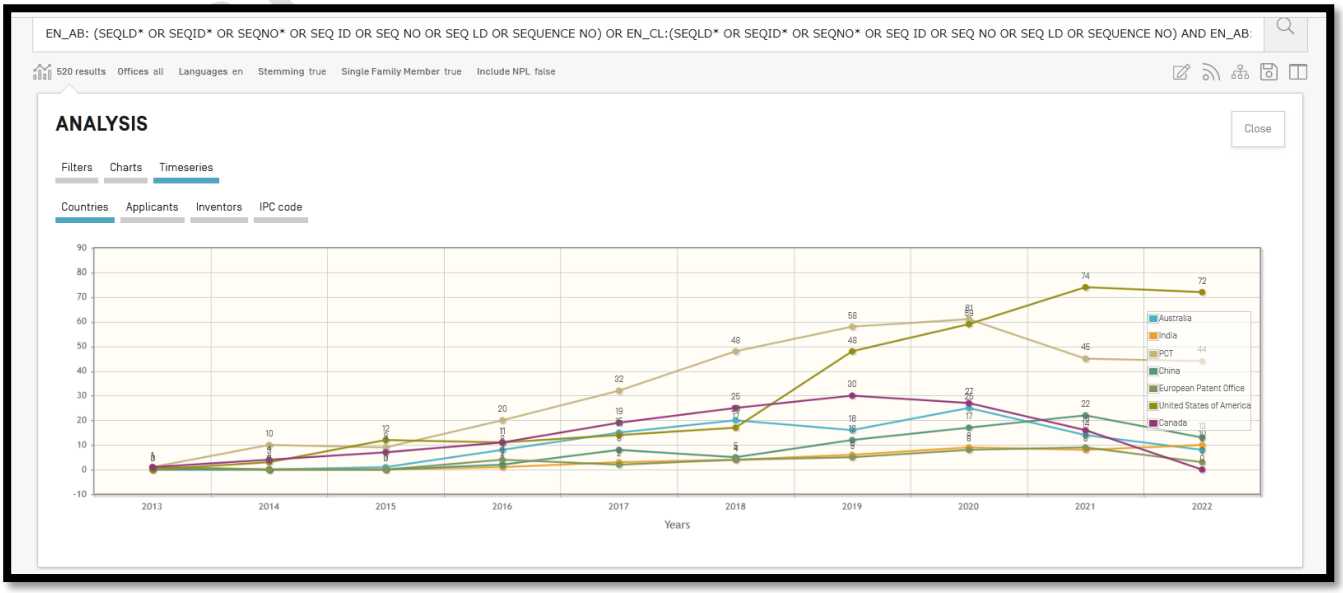
For technology trend searches, you can use the standard PATENTSCOPE functions to conduct your analysis. PATENTSCOPE offers beautiful, automated technology trend analysis functions, which can give you a fast overview of the trends reflected in your search results.

Click on the “Analysis”-button in PATENTSCOPE:

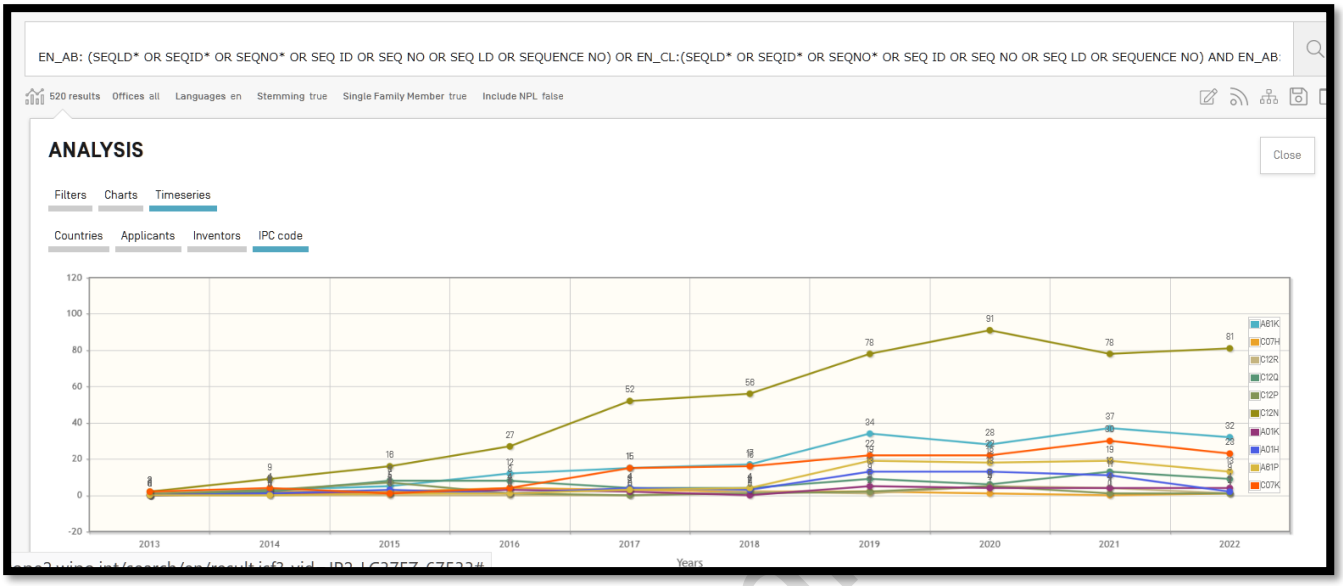
And then PATENTSCOPE will display the results obtainable by the unique PATENTSCOPE Analysis functions:

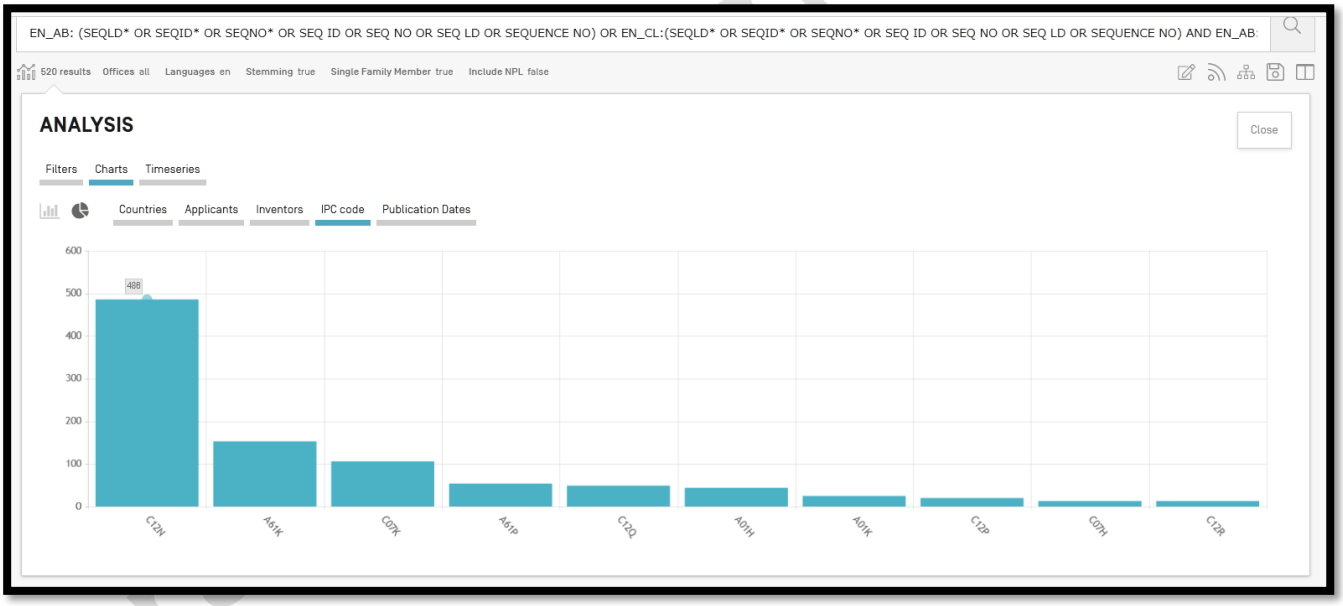




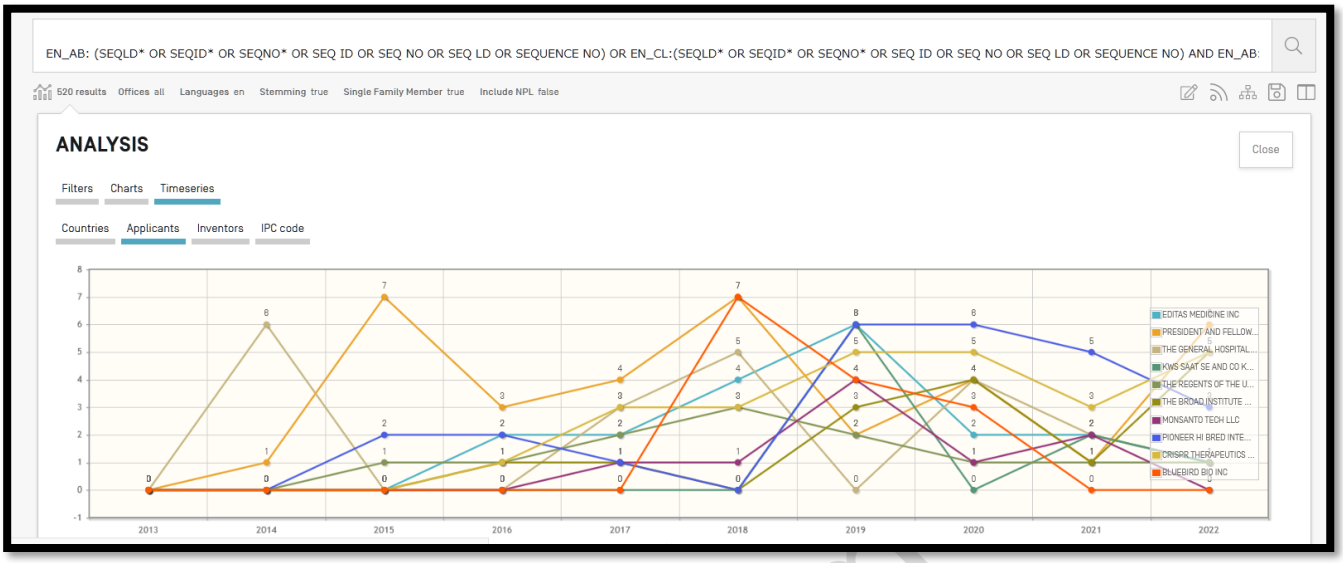


You can conduct further refined searches by zooming in on specific genome editing technologies, such as CRISPR Cas9 or your own favorite alternative CRISPR Cas system applications (Cas 12, Cas 13, Cas3 or CasMINI). Furthermore, you can conduct refined analyses by IPC classes, applicants, inventors, and the like. For example:

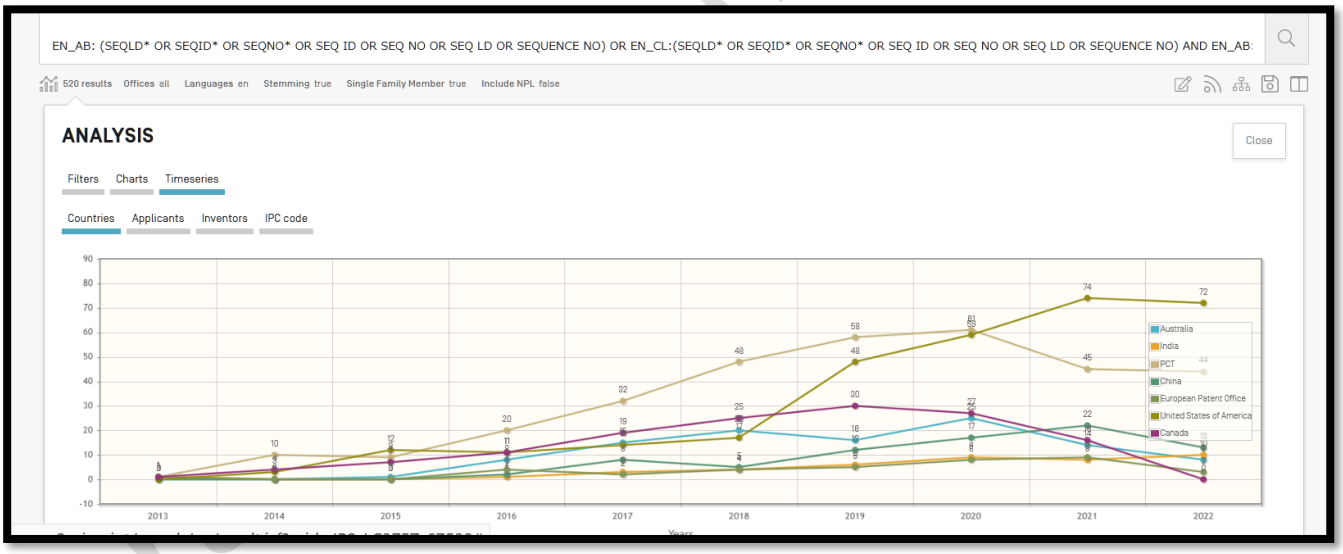




In the IPC analysis, you will see some technology trends by subsections of the technologies and also over-time tendencies and trends in genome editing:



As regards the trends by countries, you can see some trends over time and sometimes you can find which countries/applicants are active these days or in the past in your field of genome editing:



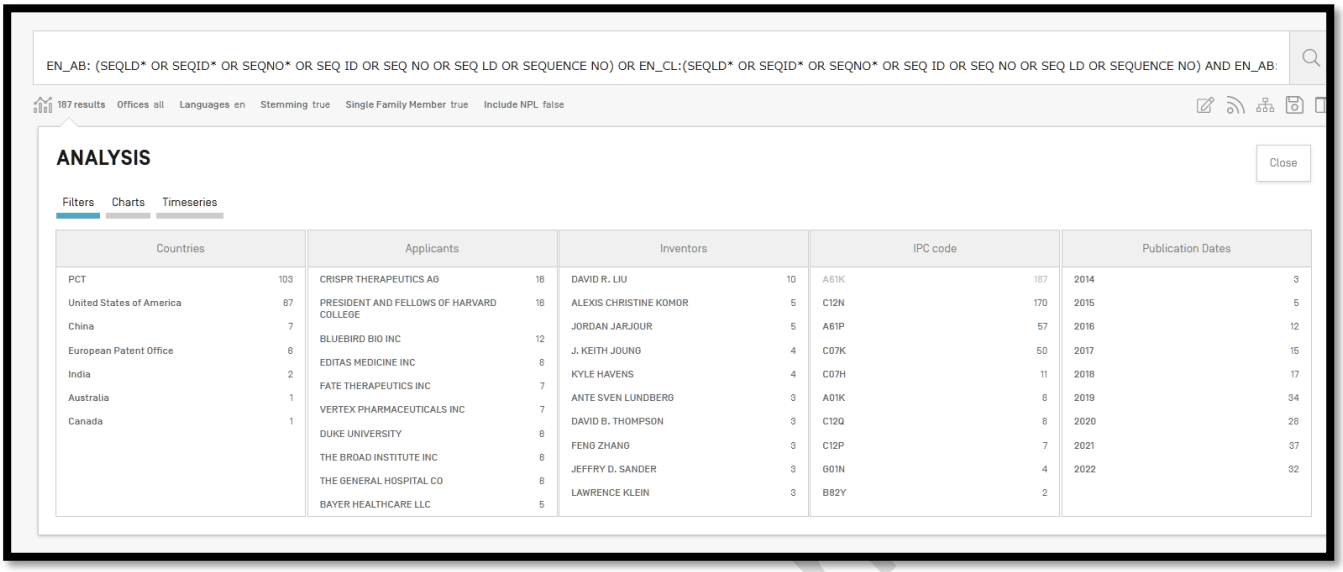
In any event, please also take your time to do as follows:

- Read your search results.
- Summarize your search results using various analyzing tools.
- Discuss with your colleagues and/or instructors about your results.
- Prepare a short summary of your results.

If you find an important patent document, you should deepen your investigation of the particular case, including patent family search, analysis of the claims, applicants and inventors, and the like.

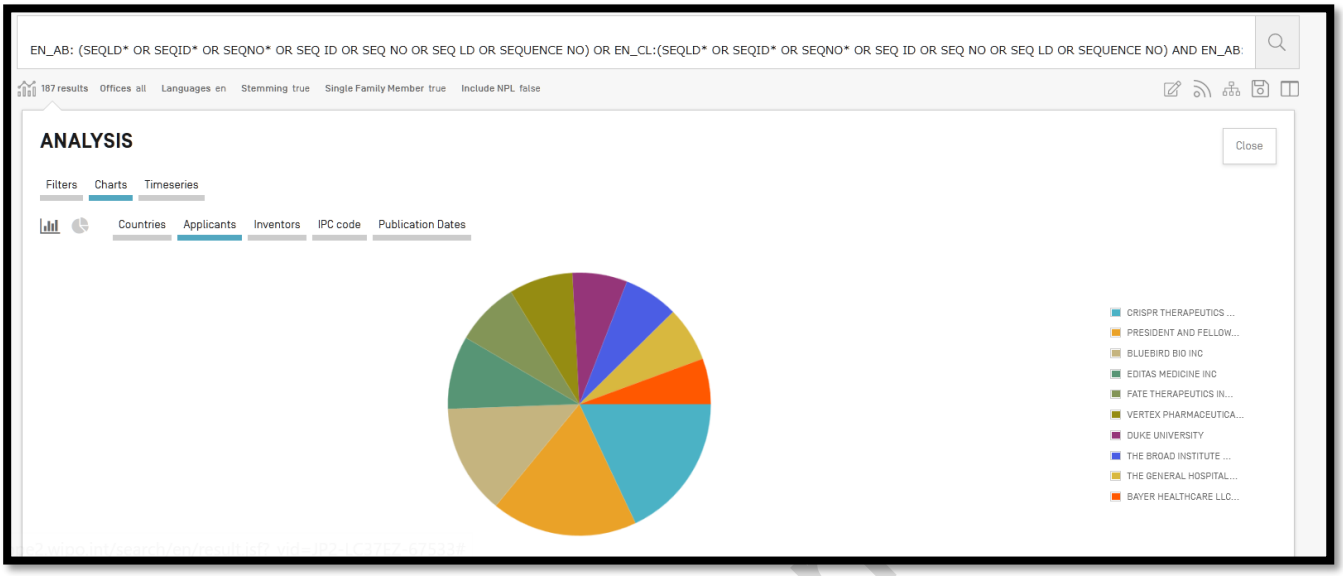
3.3.3.5 STAGE 5: Applying your search results to your objectives

If you want to further deepen your sequence search results, you can use a Filter function:



To focus your results, you can click on a particular IPC code for further analysis:

For sharing your results with your colleagues and your tutor/mentor, keep in mind that you can also change your expression style as below to bring out different dimensions of and perspectives on the technology trends you are trying to assess and portray:



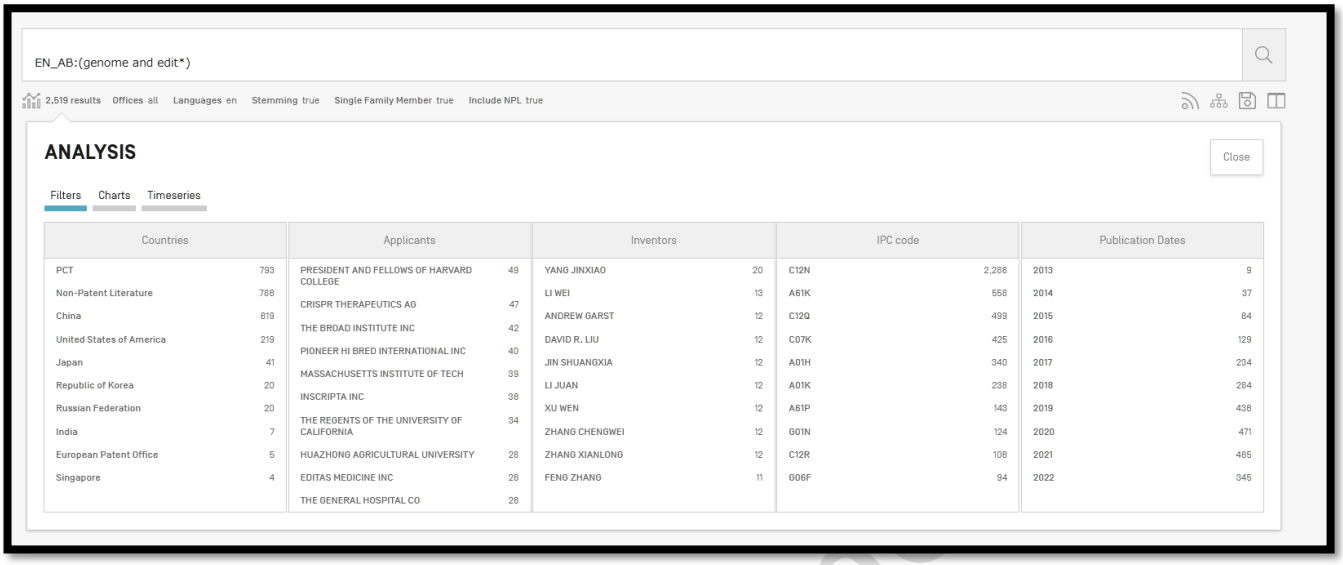
Watching technology trends: The key insights and value added from technology trend searches come when you conduct them repeatedly over time and in regular intervals. This will truly give you an insight into what the trends and tendencies are surrounding your sequence and technology of interest.

For completing and updating your technology trend searches you then need to pick up search results and create further graphical displays. For this you can use additional tools to analyze your search results, focusing on specific companies/institutions/innovators. For example, you can compare company A and B to see specific technology trends.

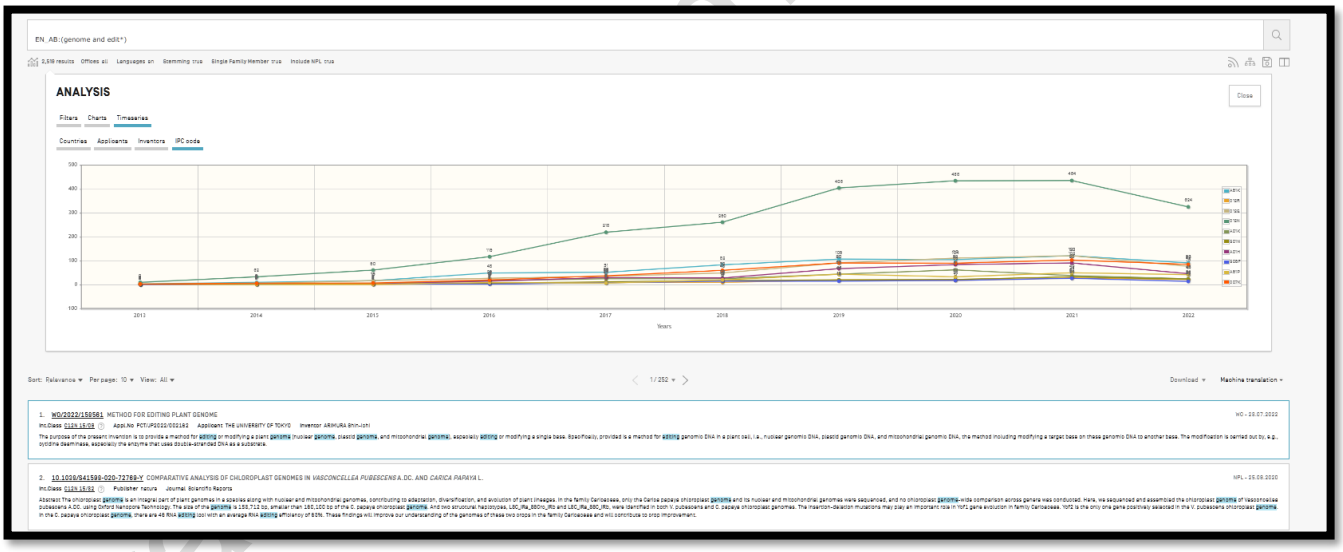
3.3.3.6 STAGE 6: Recognizing the limitations of your search results

In the technology trends, you may also include non-patent literature. In this case, you need to recognize the limitations of your search results: the “SEQ ID” query can be removed as this will not function in non-patent literature.

Here you can use simply “genome edit*” as a search query.



In a search including non-patent literature, the IPC code filter is useful as non-patent literature can also have this information:



3.3.3.7 STAGE 7: Finalizing your search: preparing reports

By conducting several searches as exemplified above, you can prepare some reports on technology trends. Some representative technology trends reports are available at WIPO websites: https://www.wipo.int/publications/en/details.jsp?id=4541

3.3.4 Market analysis/searches

3.3.4.1 STAGE 1: Defining objectives of your search

Market information may be obtained from an organization or a private sector service provider. For instance, the International Federation of Pharmaceutical Manufacturers and Traders (IFPMA) publishes “IFPMA - Facts And Figures 2022”, so this kind of information can be referred to. See: https://www.ifpma.org/resource-centre/facts-and-figures-2022-the-pharmaceutical-industry-and-global-health/

Furthermore, other information may be combined to formulate your market search. Patent landscape searches can be found from WIPO with respect to general overviews for specific markets: https://www.wipo.int/patentscope/en/programs/patent_landscapes/

For example, COVID-19 related patent landscapes may be obtained at:
https://www.wipo.int/patentscope/en/programs/patent_landscapes/news/2022/news_0001.html

This report is formulated in the context of the COVID-19 situation, where "since the start of the COVID-19 pandemic there have been remarkable research and innovation efforts to fight the SARS-COV-2 virus and the related disease. This patent landscape report provides early observations on the patenting activity which took place in the field of COVID-19 vaccines and therapeutics and compares results with clinical trial data for related candidate vaccines and drugs".

3.3.4.2 STAGE 2: Building your initial query building blocks

A market search can be conducted upon obtaining technology trends or combining the technology trends and information of market information reports.

3.3.4.3 STAGE 3: Refining your search query: Trial and error and modification processes

Market searches can be refined upon having obtained technology trends or having combined the technology trends and market information.

3.3.4.4 STAGE 4: Analyzing your search results

Market searches can be analyzed upon obtaining initial analysis results referring to your technology trends and the market information you were able to collect.

3.3.4.5 STAGE 5: Applying your search results to your objectives

Market searches can be analyzed vis-à-vis your search objectives in view of the market information you gathered. Watching technology trends on the marketplace, you need to pick up search results and create further graphical displays, using additional tools to analyze search results. You can focus on specific companies/institutions/innovators, e.g., by comparing company A and B to see specific technology trends.

3.3.4.6 STAGE 6: Recognizing the limitations of your search results

Market analysis has its own limitations as patent information has its own limitations, and thus market analysis should not be considered an exhaustive basis for making your business and market entry decisions. It is important that your information basis be comprehensive and to recognize that market analysis is a tool to obtain additional information.

3.3.4.7 STAGE 7: Finalizing your search: preparing reports

Your market analysis may be summarized as a report. Some of WIPO's representative market analysis reports can be found at:
https://www.wipo.int/meetings/en/doc_details.jsp?doc_id=376752

3.4 SUBMITTING YOUR SEQUENCES FOR TECHNICAL PUBLIC DISCLOSURE

If you decide to disclose your sequences and wish to ensure legal certainty for your technical public disclosures, this is not automatic through a simple upload of your sequence(s) to an average or random public databases. In order to ensure that your technical public disclosure does create legal certainty on the prior art status of your sequence, you can approach your sequence submission in the following two stages with the following considerations:

3.4.1 Optional STAGE A: Deciding and preparing possible prior art submissions and technical public disclosures

An effective technical public disclosure for IP purposes does not just mean to disclosure the nucleotide sequence or amino acid sequence itself and then it is done. Rather, an effective technical public disclosure includes the comprehensive, precise, coordinated, and inter-connected disclosure of three layers of information about your sequence:

- biological sequence,
- biological function(s) of the sequence, and
- technical use(s) of the biological function(s) of the sequence.

In your disclosure you might wish to ensure that you have well documented and included all these three layers for the effective disclosure of your sequence.

Prior to undertaking any such disclosure, it is of paramount importance to consider multiple IP strategic considerations *before* you disclose any of the layers. These crucial *advance* considerations include careful strategizing, timing, versioning of your sequence submissions from a business strategy, IP management strategy, commercial and research strategy perspective. This Guide does ***not*** cover these business and IP strategy dimensions. To learn more about these considerations, please refer to the other components of the WIPO Toolkit for Rights Management in GRs and Data, in particular (i) the Strategy Tool for Improved Use of GRs and GR Data as IP Assets; and (ii) the GRs and GR Data Licensing Tools.

However, before implementing your disclosure, please carefully work through at minimum the following considerations:

- meeting your business model, business strategy and IP objectives;
- your IP strategy considerations and IP portfolio management strategy;
- the timing of your disclosure; and
- the version management of your disclosure of the sequence.

Only after you have worked through all these strategic considerations and practical preparations, you may proceed to implementing your technical public disclosure.

3.4.2 Optional STAGE B: Implementing your possible prior art submission and technical public disclosures

Once you have decided on the strategic and practical aspects of your technical public disclosure, you may implement your sequence submission, while choosing among a variety of options. These include among other things the sequence data repository through which you want to submit and disclose your sequence(s), and the mode of upload (web-in upload, programmatic upload, client-based upload, etc.), the mode of submission (direct or indirect) and its phasing (immediate or delayed release dates).

You may wish to implement the submission, *inter alia*, to any of the following sequence data repositories or a combination thereof:

- The Lens
- EPO
- JPO/DDBJ
- USPTO

For the mode of submission, you may undertake your sequence submissions directly to those repositories or with various supporting functions of various WIPO services and platforms, such as:

- WIPO INSPIRE
- TISCs

Since sequence submissions are highly specific, depending on the system and modalities of submission that you chose to implement them, the technical details for the submission are not listed in this Guide, but can be found as part of the detailed technical documentation available on the websites of the respective repositories or submission support services.

3.4.3 Review of key databases and data repositories for searches and submissions related to GRs and GR data

3.4.3.1 Some representative databases

- Patentscope
- The Lens
- INSDC
- EPO
- USPTO
- ENA
- JPO/DDBJ

WIPO's work on IP, GRs and GR data that pertains to nucleotide sequence data is consistent with, and has wherever possible been developed in coordination with, the INSDC. This is because INSDC is a long-standing foundational initiative on nucleotide sequence data, which covers the full spectrum of raw reads, through alignments and assemblies to functional annotation, enriched with contextual information relating to samples and experimental configurations. INSDC operates between the world's major nucleotide sequence database providers, DDBJ, European Bioinformatics Institute (EBI) EMBL and NCBI.

These data repositories are relevant for you in the following circumstances: if you have decided (a) not to patent potential resulting inventions or (b) not to maintain those sequence data or related information or know-how as a trade secret or protected undisclosed information, and if you are opting for technical public disclosure of the sequence data as your preferred rights management option. In this context, an option is to upload the resulting data into INSDC sequence databases, in order to make the data as widely available as possible and for them to be searchable by other researchers and innovators as well as recognized by patent examiners for purposes of search and examination.

3.4.3.2 Uploading to INSDC databases

By using the WIPO suite of rights management tools for GRs and GR data to manage your nucleotide sequence listings, you can control and undertake certain aspects of your practical rights management work for your sequence listings yourself. One rights management option in this regard is the technical public disclosure of the sequence data. As for nucleotide sequence databases for disclosing your nucleotide sequence listings, an option is the nucleotide sequence databases of INSDC.

With the TK Division's rights management tools for IP and GRs, you can bring your sequence data automatically into compatible format for you to be able to upload it to INSDC member databases. This requires multiple work steps, and you can undertake them for your own nucleotide sequence data with the resources available at the one-stop service tile for IP Rights Management in GRs and Data on the TK Division's webpage.

For full details of how to submit data to the INSDC databases, please see the practical instructions for technical public disclosure in the Subject Guide which forms part of the wider WIPO Toolkit for Rights Management in GRs and Data, and the links to INSDC on the IP Rights Management in GRs and Data service tile. Please select the upload instructions of a collaborating partner database, GenBank, the European Nucleotide Archive (ENA) or DDBJ, and consult the DDBJ/ENA/GenBank Feature Table Definition for submitting your data to INSDC partners. The overall goal of the Feature Table design is to provide an extensive vocabulary for describing features in a flexible framework for manipulating them. The Feature Table documentation represents the shared rules that allow INSDC databases to exchange data on a daily basis.

The range of features to be represented is diverse, including regions which:

* perform a biological function,
* affect or are the result of the expression of a biological function,
* interact with other molecules,
* affect replication of a sequence,
* affect or are the result of recombination of different sequences,
* are a recognizable repeated unit,
* have secondary or tertiary structure,
* exhibit variation or have been revised or corrected.

Access to INSDC databases is free-of-charge, unrestricted and open to any member of the public. This enables you and other researchers and innovators to access data, plan their experiments and analyze their results together with existing data. As original scientific contributions, data deposits form part of the scientific record and are citable in the literature. You can also correct and update your deposited data anytime. Moreover, many scientific journals demand a database accession number as a condition of publication of an article.

Additional resources, tools, and references: If you have decided (a) not to patent potential inventions resulting from the use of a sequence and (b) not to maintain that nucleotide sequence or related information or know-how as trade secrets or under protection of undisclosed information, you can opt to make a technical public disclosure. You can use the one-stop IP Rights Management in GRs and Data service tile for references to the steps of a legally certain technical public disclosure. If you decide to make a technical public disclosure, an option is to submit your data to the INSDC databases. To submit and upload your data to INSDC participating databases, please see the Feature Table of INSDC and the upload instructions of the INSDC database providers.

4 WIPO TRAINING AND MENTORING RESOURCES AND SERVICES

4.1 THE WIPO TOOLKIT FOR RIGHTS MANAGEMENT IN GRS AND DATA

The tools and services provided by the WIPO Traditional Knowledge Division under this Toolkit include customized information, practical tools and training related to the management of IP in GRs and data in the life sciences. The WIPO Toolkit for Rights Management in GRs and Data provides a one-stop source for cross-cutting products and services, including practical tools and information on how to protect and manage trade secrets, patents, technological protection measures, effective public disclosures and regulatory compliance for GRs and GR data in the life sciences. They include the WIPO IP Guide for GRs and Genetic Sequence Data; the Guide on IP Issues in Access and Benefit-sharing Agreements; the WIPO Online Database on GRs Contracts and the present Guide. Other information resources available on related subjects include the WIPO DL-427 Executive Course on IP and GRs in the Life Sciences;[8] the WIPO-UNEP Study on the Role of IP Rights in the Sharing of Benefits Arising from the Use of Biological Resources and Associated Traditional Knowledge and the INSDC Submission Standards.

4.2 WIPO INSPIRE

WIPO INSPIRE is a global reference for innovation, helping innovators and entrepreneurs make informed decisions at critical junctures throughout the innovation cycle. WIPO INSPIRE integrates expert and social content on patent databases, patent registers, patent analytics, technology transfer, and institutional IP policies, providing a unique blend of information and knowledge on resources, tools, and good practices in these areas.

- *Innovators*: Innovators must take into account prior research and patenting activity in their area of work to ensure that they allocate their resources efficiently and can benefit from a birds-eye view of developments and trends in these areas. Their work can generate value for themselves and society if supportive institutional frameworks are in place.
- *Entrepreneurs*: Entrepreneurs must have a clear picture of the technology and competitive landscape in which they intend to launch new products and services and minimize the risk of infringing patent rights of others. They are essential partners in technology transfer, transforming IP into tangible benefits for the public.
- *TISCs*: Technology and Innovation Support Centers (TISCs) provide a wide range of services to innovators and entrepreneurs, including in patent search, freedom-to-operate analysis, patent analytics, and technology transfer and IP rights management.
- *Patent Information Professionals*: Patent information professionals support innovators and entrepreneurs to identify patent documents relevant to their research and

[8] For participants and alumni of the WIPO DL-427 Executive Course, the WIPO BRIDGE platform is a tailor-made platform that facilitates training, mentoring, rights management information support and match-making services, which are delivered as part of a wider and coherent "TKD customer journey", for example, to facilitate the development, technology transfer and commercialization to bring GRs and GR data to the market. Throughout these service processes, as a matter of principle, the platform does not store any confidential or proprietary data. It is a training, information and mentoring platform. The platform provides personalized rights management information support services through customized law and prior art trackers, which address the unique features of GRs and GR data and the unique IP needs of GR innovators in the life sciences. For example, it makes available an automated prior art tracker for Patentscope through which users can retrieve or submit sequence data and sequence-related information from and to Patentscope. As user you can set your personalized "prior art tracker," through which you can submit or retrieve sequence data and sequence-related technical information for your own search queries and submissions on a regular and personalized basis for your favourite genes, genomic locations or proteins. These rights management information support services are available free-of-charge on WIPO BRIDGE.

business interests and gain an overview over complex relationships between technologies, individuals, and organizations.

- *Patent attorneys*: Patent attorneys and agents can help innovators and entrepreneurs assess the patentability of inventions they have developed and determine the legal status of patent rights that may intersect with products and services they intend to commercialize, allowing them to draft stronger patent applications and diminish the risk of patent infringement.

5 CONCLUSION

This tool has provided you with an introduction to the GR sequence search and submissions for GR innovators and stakeholders in developing and developed countries and among IPLCs. It does not provide an exhaustive tool and it provides no legal advice, but it provides you with a first starting point for familiarizing yourself with the practices of sequence search and submission. The actual familiarization, however, comes only through practice and experience. We therefore wish you good practice and enjoyment in conducting your searches and submissions.

ANNEX

List of Relevant Existing Databases

- WIPO Patentscope
- WIPO INSPIRE
- The International Nucleotide Sequence Database Collaboration (INSDC)
- Genbank at the National Center for Biotechnology Information (NCBI)
- The European Nucleotide Archive (ENA) at the European Molecular Biology Laboratory (EMBL)
- The DNA Data Bank of Japan (DDBJ) at the National Institute of Genetics (NIG)
- The Universal Protein Resource (Uniprot) at EMBL, the Swiss Institute of Bioinformatics (SIB) and the Protein Information Resource (PIR)
- The Lens of the Center for Applied Molecular Biology in Agriculture (CAMBIA)