Global trends in coronavirus research at the time of Covid-19: A general bibliometric approach and content analysis using *SciMAT*

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Abstract

Covid-19 represents the greatest challenge facing mankind today. In December 2019, several cases of pneumonia of unknown etiology were reported from China. This coronavirus infection subsequently identified as Covid-19 aroused worldwide concern. As a result, the scientific community has focused attention on Covid-19, as revealed by recent research reported in literature based on a holistic approach. In this regard, this study conducts a bibliometric analysis of coronavirus research in the literature with an emphasis on Covid-19 disease, using as a reference the publications in the *Web of Science Core Collection* from 1970 to 2020. This research analyzes 12,571 publications from 1970 to (April 18) 2020 by applying advanced bibliometric techniques in *SciMAT* bibliometric analysis software. The current research therefore provides a complete conceptual analysis of the main coronavirus types and strains in the literature by quantifying the main bibliometric performance indicators, identifying the main authors, organizations, countries, sources, and research areas, and evaluating the development of this field. Furthermore, a science map is constructed to understand

the corresponding intellectual structure and main research lines (themes). *SciMAT* thereby offers a complete approach to the field and evaluates the main performance indicators related to coronavirus, with a focus on Covid-19. Finally, this research serves as a framework to strengthen existing research lines and develop new ones, establishing synergistic relationships that were not visible without the maps generated herein.

Keywords

Covid-19; Coronavirus; Pandemics; Virus diseases; Novel coronavirus; Co-word analysis; Strategic intelligence; Mapping analysis; Bibliometric analysis; *SciMAT*.

1.Introduction

In January 2020, the *World Health Organization* (*WHO*) declared the coronavirus 2019-nCoV disease outbreak to be a public health emergency of international concern. On March 11, following an ongoing assessment of the outbreak and the alarming levels of its spread and severity, as well as inaction, the *WHO* declared the Covid-19 disease produced by the new coronavirus to be a pandemic (*WHO*, 2020).

In light of this situation, scientific production on this subject has exhibited strong growth in multiple disciplines. The health crisis caused by Covid-19 has triggered a reaction from the scientific community in the search for solutions to it, leading to an exponential growth in such literature (**Torres-Salinas**, 2020).

The multidisciplinary nature of the research carried out can be seen in the variety of fields involved, ranging from medicine to social sciences, including computer science and information technologies for the detection of behavior, genetic markers, and evolutionary patterns. Research has also been carried out to analyze the implications that geolocalization may have in relation to the privacy of individuals, as well as specific thematic analyses of social networks (**Casero-Ripollés**, 2020; **Lázaro-Rodríguez**; **Herrera-Viedma**, 2020; **Pérez-Dasilva**; **Meso-Ayerdi; Mendiguren-Galdospín**; 2020*;* **Rodríguez-Morales** *et al.*, 2020; **Sahin** *et al.*, 2020; **Thelwall**; **Thelwall**, 2020).

Scientific journals represent one of the main sources of research, projects, and added-value information, providing a new reference point to conduct novel research into Covid-19.

Complete bibliometric analysis thus becomes a key tool to evaluate ongoing actions and research, organizations, countries, sources, and researchers (**Bonilla-Aldana** *et al.*, 2020; **Hossain**, 2020). In this context, the main aim of this paper is to present a bibliometric analysis of coronavirus research with an emphasis on Covid-19 disease, covering authorship, production, and thematic analysis, with the distinction of covering the main and secondary research themes related to coronavirus types and strains, from the first publication in 1970 to the present day.

Thus, the present research focuses on an analysis and description of the development of the research themes about coronavirus and the main related concepts available in the literature using bibliometric techniques and tools. First, the research quantifies the main performance-related indicators: published documents, received citations, journal impact factor (JIF), h-index, most cited articles, most cited authors, and data on the geographic distribution of publications, among others. Next, *SciMAT* is used as a science mapping software tool to analyze the areas of development of scientific knowledge associated with the coronavirus types and strains within a defined time span (**Cobo** *et al.*, 2012; **López-Robles** *et al.*, 2020).

2. Methodology and dataset

Bibliometric techniques and methods represent some of the most common and widely accepted techniques to analyze the output of basic and advanced research. Such methods are increasingly valued as tools for measuring scientific quality, productivity, and evolution (**Garfield**; **Merton**, 1979; **Hirsch**, 2005; **Martínez** *et al.*, 2015; **Moed** *et al.*, 1995; **Moed**, 2009).

2.1. Methodology

In the current research, the bibliometric methodology is combined with performance analysis and science mapping approaches (**Cobo** *et al.*, 2011). Moreover, this methodology can be employed to analyze a field of research, as well as to detect and visualize its conceptual subdomains (particular themes or general thematic areas), along with its thematic evolution. This approach is based on co-word analysis and the h-index (**Callon** *et al.*, 1983; **Garfield**, 1986; **Hirsch**, 2005).

Although various software tools for science mapping analysis exist (**Moral-Muñoz** *et al.*, 2020), *SciMAT* was applied in the current research due to its deduplication process and visualization based on strategic diagrams and thematic areas. The bibliometric methodology used here identifies four phases of analysis within a specified set of periods (**Cobo** *et al.*, 2011; **López-Robles** *et al.*, 2019a; **López-Robles** *et al.*, 2019b):

- Detection of research themes. For each of the periods analyzed, research themes are detected by applying a clustering algorithm (**Coulter** *et al.*, 1998) over a normalized co-word network (**Callon** *et al.*, 1983).
- Visualizing research themes and the thematic network. The detected research themes are classified based on their

centrality and density rank values into a strategic diagram (**Callon** *et al.*, 1991; **He**, 1999). The centrality (c) measures the degree of interaction of a network with other networks, while the density (d) measures the internal strength of the network. By considering both types of measure, a field of research can be visualized as a set of research themes and plotted on a two-dimensional strategic diagram (Fig. 1 (a)). Thereby, the themes can be classified into four categories (**Cobo** *et al.*, 2011):

a. Motor themes (quadrant Q1): The themes within this quadrant are relevant for developing and structuring the research field. They are known as the motor themes of the field, given that they present strong centrality and high density.

b. Highly developed and isolated themes (quadrant Q2): These are strongly related, highly specialized, and peripheral, but they do not have the appropriate background or importance for the field.

c. Emerging or declining themes (quadrant Q3): These themes are relatively weak and exhibit low density and centrality. They mainly represent either emerging or disappearing themes.

d. Basic and transversal themes (quadrant Q4): These themes are relevant for the field of research but are not well developed. This quadrant contains transverse and general basic themes.

- Discovery of thematic areas. The research themes are analyzed using an evolution map (Fig. 1 (b)), which links the themes that maintain a conceptual nexus across consecutive periods.

- Performance analysis. The relative contribution of research themes and thematic areas to the entire field of research is measured quantitatively and qualitatively. This can then be used to identify the most productive and relevant areas within the field.
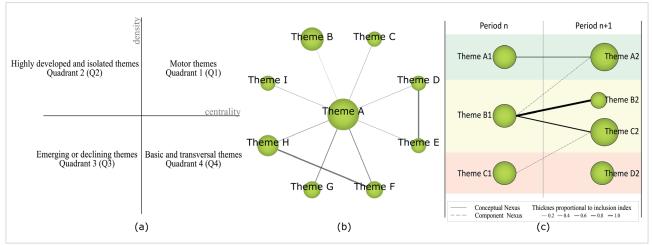

Figure 1. (a) Strategic diagram, (b) thematic network, and (c) thematic evolution

In addition to science mapping analysis, the present research seeks to identify the citation classics, that is, highly cited articles. For this purpose, the concept of H-Classics proposed by **Martínez** *et al.* (2014) was used, which can be defined as follows: "H-Classics of a research area 'A' could be defined as the H-core of 'A' that is composed of the 'H' highly cited papers with more than 'H' citations received" (**Martínez** *et al.*, 2014).

2.2. Dataset

Publications related to the various types of coronavirus were collected to analyze their bibliometric characteristics and perform science mapping. In this regard, different corpora and queries have been proposed to retrieve articles related to Covid-19 from different databases. In this analysis, we focus on the queries proposed for *Web of Science* (*WoS*), and specially follow the advice suggested in the *ISSI* distribution list. The present study thus focuses on the following concepts: *coronavirus* and *severe acute respiratory syndrome coronavirus.*

As a consequence, the raw data (publications) were collected using the *WoS*, since it is the most important database, covering a wide range of disciplines and thus enabling comparisons across scientific areas. Therefore, the research publications dedicated to the main coronavirus types and themes mentioned above were downloaded from the *Web of Science Core Collection* using the following advanced query:

TS=("Wuhan coronavirus" OR "Wuhan seafood market pneumonia virus" OR "Covid19*" OR "Covid-19*" OR "Covid-2019*" OR "coronavirus disease 2019" OR "SARS-CoV-2" OR "sars2" OR "2019-nCoV" OR "2019 novel coronavirus" OR "severe acute respiratory syndrome coronavirus 2" OR "2019 novel coronavirus infection" OR "coronavirus disease 2019" OR "coronavirus disease-19" OR "novel coronavirus" OR "coronavirus" OR "SARS-CoV-2019" OR "SARS-CoV-19").
Refined by: DOCUMENT TYPES: (ARTICLE OR PROCEEDINGS PAPER OR REVIEW) AND LANGUAGES: (ENGLISH). Timespan: All years. Indexes: SCI-EXPANDED, SSCI, A&HCI, CPCI-S, CPCI-SSH, BKCI-S, BKCI-SSH, ESCI, CCR-EXPANDED, IC.

This query retrieved a total of 12,571 publications from 1970 to 2020. The corpus was further refined and limited to the English language and the following publication types: articles, proceedings, and reviews. The citations of these publications were also used in this work, being collected up to April 18, 2020.

> The growing interest in coronavirus from the scientific community coincided with the SARS disease in 2002 and 2003

After importing this raw data into *SciMAT*, a deduplication process was also applied to improve the data quality, by grouping meanings and concepts that represent the same notion (e.g., "SEVERE-ACUTE-RESPIRATORY-SYNDROME CORONAVIRUS", "SEVERE-ACUTE-RESPIRATORY-SYNDROME-CORONAVIRUS-(SARS-CoV)" and "SARS-CoV" were merged to "SEVERE-ACUTE-RESPIRATORY-SYNDROME-CORONAVIRUS").

As a second step, and to avoid flatness of the data, the whole span of years was split into consecutive periods. While such periods frequently cover the same time spans, given the low number of publications in the early years, the best option was to divide the time span into comparable periods. Therefore, the study period (1970–2020) was split into three consecutive time periods: 1970–1999, 2000–2009, and 2010–2020 with 1,797, 4,129, and 6,645 publications, respectively.

3. Bibliometric analysis of coronavirus research

This section deals with the evolution of the coronavirus in terms of publications, citations, and impact by analyzing the following bibliometric indicators: published documents, received citations, journal impact factors, most cited publications, most cited authors, h-index, research areas, and data on the geographic distribution of publications.

The bibliometric performance analysis is therefore structured into three sections: production and impact of published documents; production and impact of authors, journals, and research areas; and H-Classics analysis.

3.1. Publications and citations

Figure 2 shows the distribution of publications and citations related to coronavirus types and strains per year for the defined periods. Firstly, it should be noted that Figure 2 shows that the values of these indicators have increased over the last year.

Since the appearance of the first publications related to coronavirus in 1970, three milestones in the development of such literature can be observed. The first milestone corresponds to the first 35 years (1970-2005), during which the rate of publications increased, reaching a total of 3,187 (25.11% of the total). This development profile reveals the growing interest in coronavirus within the scientific community and includes the emergence of the SARS disease in 2002 and 2003. In this analysis, the second milestone corresponds to the drop from 2005 to 2011, during which only 3,554 docu-
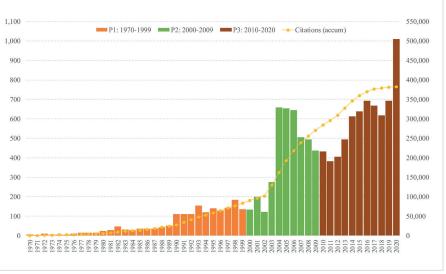

Figure 2. Distribution of publications by year (1970–2020)

ments were published, representing 28.27% of the publications from 1970 to 2020. Finally, the last year (2020) represents the last milestone, during which 1,009 publications (8.03% of the total) were produced in only four months and marking the historical peak in this research field.

Similarly, the distribution of citations shows a positive developmental trend during the period from 1970 to 2020, during which a total of 382,447 citations (including self-citations) were recorded. Finally, *WoS* indicates that the average number of citations per cited article is 40.08. Complementing these data, the first significant increase in citations appears at the beginning of this century, when the number of citations exhibited a higher growth rate. In subsequent years, the average of the citation distribution rose continuously.

Finally, it should be mentioned that the publications during the three stated period generated a total of 83,414, 187,549, and 111,484 citations, respectively. Nonetheless, note that the total number of citations appears to show a downward trend over the past six years, although this is not a real trend. According to **Wang** (2013), the

> The number of publications in the last year (2020) has reached 1,009 (8.03% of the total) in only four months, marking the historical peak in this research field

most cited publications are generally those published in previous years due to the time span between publication and reference. It is estimated that a publication needs between 3 and 7 years to reach its highest number of citations. Furthermore, given the observed pattern of development, it can be assumed that this positive trend will continue.

3.2. Most productive and cited authors, geographic distribution of publications, and research areas

It is also important to determine the most productive and cited authors, along with the research areas and the geographic distribution of publications and organizations, which can support an evaluation of the evolution of the research field. Table 1 shows the most productive authors (with more than 100 publications) and most cited authors (with more than 7,000 citations) during the period from 1970 to 2020.

Because ties were observed for some positions, such authors are listed in alphabetical order.

In addition, Table 1 reveals that, according to *WoS,* seven of the most productive authors are also among those most widely cited: Yuen (201 publications; 16,710 citations), Enjuanes (162; 7,273), Drosten (127; 10,692), Rottier (124; 7,281), Woo (112; 7,292), Chan (111; 11,651), and Snijder (104; 7,888).

In the same way, Table 2 lists the most productive countries (with more than 400 publications) and organizations (with than 190 publications) related to coronavirus research during the period from 1970 to 2020.

Table 1. Most productive authors (1970-2020)

Publications	Author	Citations	Author
201	Yuen	16,710	Yuen
169	Perlman	11,651	Chan
162	Baric; Enjuanes	10,692	Drosten
133	Weiss	10,158	Osterhaus
127	Drosten	10,108	Peiris
124	Rottier	9,516	Guan
112	Woo	8,501	Poon
111	Chan; Saif	7,888	Snijder
105	Lau	7,292	Woo
104	Snijder	7,281	Rottier
-	-	7,273	Enjuanes

Table 2. Most productive countries (1970-2020)

Publications	Country	Publications	Organization
4,513	United States	487	*University of Hong Kong*
2,746	China	373	*Chinese Academy of Sciences*
962	United Kingdom	321	*University of California System*
797	Germany	296	*National Institutes of Health USA; Utrecht University*
712	Netherlands	257	*University of North Carolina*
687	Canada	231	*Centers for Disease Control Prevention USA*
582	Japan	215	*University of Texas System*
491	France	214	*University of North Carolina Chapel Hill*
469	South Korea	195	*University of Pennsylvania*
417	Italy	194	*Chinese University of Hong Kong*
403	Taiwan		

During the period from 1970 to 2020, the USA appears to be the most productive country, with 4,513 publications, followed by the People's Republic of China and the UK with 2,746 and 962 publications, respectively, although countries such as Germany, the Netherlands, Canada, and Japan also recorded significant numbers.

Table 3 shows the most relevant *WoS* subject categories (with more than 400 publications) and research areas (with more than 400 publications) during the period from 1970 to 2020.

Table 3. Most relevant *WoS* subject categories and research areas (1970-2020)

Publications	*WoS* subject categories	Publications	Research areas
4,089	Virology	4,089	Virology
1,731	Veterinary Sciences	1,731	Veterinary Sciences
1,392	Immunology	1,455	Biochemistry Molecular Biology
1,387	Infectious Diseases; Microbiology	1,392	Immunology
1,218	Biochemistry Molecular Biology	1,387	Infectious Diseases; Microbiology
747	Biotechnology Applied Microbiology	747	Biotechnology Applied Microbiology
643	Medicine Research Experimental	643	Research Experimental Medicine
540	Multidisciplinary Sciences	576	Science Technology other Topics
426	Public Environmental Occupational Health	565	Pharmacology Pharmacy
404	Pharmacology Pharmacy	446	General Internal Medicine
		426	Public Environmental Occupational Health

Finally, Table 4 lists the journals with the highest numbers of publications (more than 200), highlighting the diversity of the journals that host the main publications, including subjects from virology to biology.

> During the period from 1970 to 2020, the USA was the most productive country, with 4,513 publications, followed by China and the UK

Table 4. Journals with the highest numbers of publications (1970-2020)

Name	Publications related to coronavirus	Total cites (citable items 2018)	Journal Impact Factor (JIF-2018)	5-Year Impact Factor	Immediacy Index	Impact Factor without Journal Self Cites
Journal of Virology	1,134	88,684 (802)	4.324	4.259	1.185	3.800
Virology	480	25,009 (312)	2.657	3.315	1.026	2.526
Advances in Experimental Medicine and Biology	349	7,609 (394)	0.663	0.778	0.236	0.656
Journal of General Virology	316	18,927 (180)	2.809	2.851	0.728	2.702
Archives of Virology	257	10,715 (447)	2.261	2.134	0.727	2.015
Virus Research	244	9,137 (294)	2.736	2.667	0.916	2.603
Plos One	238	650,727 (17,879)	2.776	3.337	0.388	2.634

Bearing in mind the results presented above, the most relevant authors and publications are analyzed below in terms of citations according to the h-index and H-Classics.

3.3. Citation classics

The H-Classics method (**Martínez** *et al.*, 2014), based on the well-known h-index (**Hirsch**, 2005), serves as an impartial criterion to identify classic papers in any research field. Thus, in this section, the H-Classics method is applied to identify classical papers in the coronavirus research field and thereby the authors, countries, and journals making the greatest contributions.

The search query used in the *WoS Core Collection* database has an h-index of 192. Using this h-index score as a reference, the relevant publications were identified and are listed in Table A.1. In terms of citations, their distribution shows a positive developmental trend. Thus, a total of 72,763 citations (including self-citations) were recorded, and the average number of citations per cited article is 378.97. Thus, the total number of citations and the distribution of the most relevant classic publications from 1970 to 2020 are shown in Figure 3.

Figure 3. Distribution of most relevant publications by year (1970-2020)

Figure 3 shows that there are publications that remain as references after the 7-year period has elapsed, implying that they form part of the core of the coronavirus research field (**Wang**, 2013). Similarly, during the early twenty-first century, the distribution of the most cited articles reached its highest values, in contrast to the fact that this decade showed relatively low productivity.

In addition, Table 5 lists the authors with the highest numbers of publications used as references, and their citations. Twenty-seven authors have five or more publications in the list of most cited articles in recent years. Also, ten authors included in the tables of the most productive and cited authors are included in Table 5.

> The journals with the highest numbers of publications related to coronavirus are: *Journal of Virology*, *Virology*, and *Advances in Experimental Medicine and Biology*

Table 5. Authors with the highest numbers of cited publications.

Publications	Author (Citations)
15	Yuen (7,875)
13	Chan (6,300)
12	Osterhaus (8,044)
11	Peiris (6,437)
10	Guan (6,090)
9	Snijder (3,348)
8	Drosten (5,343); Fouchier (5,403); Gorbalenya (3,058); Poon (5,505)
7	Farzan (2,639); Holmes (2,368); Ziebuhr (2,913)
6	Haagmans (1,992); Lai (2,065); Lau (2,306); Li (2,395); Lim (5,543); Rottier (1,797); Woo (2,306); Zheng (2,912)
5	Choe (2,083); Daszak (2,078); Subbarao (1,390); Thiel (2,278); Tsoi (2,322); Zhang (1,500)

Regarding production by country, the USA accounts for approximately 48.95% (94 publications) of the cited articles, followed by the People's Republic of China (23.43%, 45 publications), the UK (14.58%, 28 publications), and Germany (13.54%, 26 publications). These data strongly agree with the results presented in the tables described above.

Similarly, the most relevant *WoS* subject categories (with more than 10 publications) and research areas (with more than 10 publications) for H-Classics publications are presented in Table 6.

Table 6. *WoS* subject categories and research areas for h-index publications

Publications	*WoS* subject categories	Publications	Research areas
46	Virology	46	Virology
39	Multidisciplinary Sciences	39	Science Technology other Topics
29	Medicine General Internal	30	General Internal Medicine
28	Biochemistry Molecular Biology	29	Biochemistry Molecular Biology
27	Microbiology	27	Microbiology
14	Cell Biology; Infectious Diseases	14	Cell Biology; Infectious Diseases
12	Immunology	12	Immunology

Finally, among the journals listed in Table 4 and the journals identified in this section, only two appear in both sections: *Virology* (with 6 publications) and *Journal of General Virology* (with 5 publications). Furthermore, the most relevant sources within the H-Classics publications are: *Proceedings of The National Academy of Sciences of the United States of America* (16 publications), *Lancet* (15), *Nature* (14), *New England Journal of Medicine* (12), *Science* (9), *Nature Medicine* (6), *Journal of Clinical Microbiology* (5), and *Lancet Infectious Diseases* (5).

4. Science mapping analysis of coronavirus

Next, an overview of the key themes in the main research fields related to coronavirus is provided based on science mapping analysis, being structured into two complementary sections: content analysis of the articles published, and a conceptual evolution map. The former supports the identification of the themes arising in the coronavirus literature, its main types and strains, and its evolution in the literature for each period, whereas the latter shows both the development of these themes and the relationships between them for the entire period of analysis.

4.1. Content analysis

Three strategic diagrams are shown in the following figures to analyze the most important themes within the coronavirus literature for each period. Based on their centrality and density, the research themes have been classified into four categories. Furthermore, in the strategic diagrams, the research themes are represented as spheres whose volume is proportional to the corresponding number of publications.

During the period from 1970 to 1999, sixteen research themes related to coronavirus could be identified, as shown in the strategic diagram and the performance indicators (number of publications, citations achieved, and h-index) of the themes during this period (Figure. 4(a)). Eight research themes are considered to be key because of their contribution to the growth of knowledge about coronavirus (motor themes and basic and transversal themes): BOVINE-CORONAVIRUS, ENDOPLASMIC-RETICULUM, TRANSMISSIBLE-GASTROENTERITIS-VIRUS, LELYSTAD-VIRUS, INFECTIOUS-BRONCHITIS-VIRUS, CORONAVIRUS-JHM, ENTERIC-CORONAVIRUS, and SINDBIS-VIRUS.

Based on the number of citations and h-index, the main research themes directly related to the coronavirus types and strains for this period are as follows: CORONAVIRUS-JHM, ENDOPLASMIC-RETICULUM, INFECTIOUS-BRONCHITIS-VIRUS, TRANSMISSIBLE-GASTROENTERITIS-VIRUS, and ENTERIC-CORONAVIRUS. It is important to mention that the main research themes identified are included in the key themes (motor themes and basic and transversal themes).

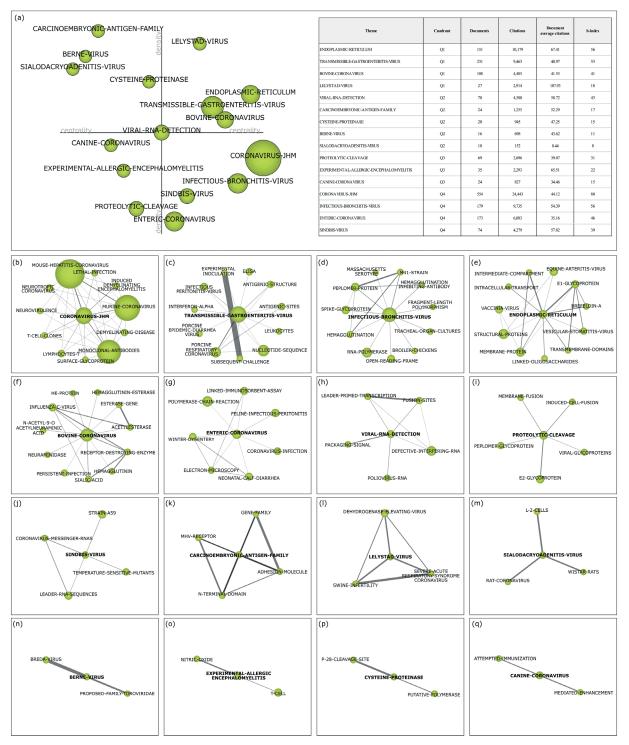| Theme	Cuadrant	Documents	Citations	Document average citations	h-index
ENDOPLASMIC-RETICULUM	Q1	151	10,179	67.41	56
TRANSMISSIBLE-GASTROENTERITIS-VIRUS	Q1	231	9,463	40.97	53
BOVINE-CORONAVIRUS	Q1	108	4,485	41.53	41
LELYSTAD-VIRUS	Q1	27	2,914	107.93	18
VIRAL-RNA-DETECTION	Q2	78	4,580	58.72	43
CARCINOEMBRYONIC-ANTIGEN-FAMILY	Q2	24	1,255	52.29	17
CYSTEINE-PROTEINASE	Q2	20	945	47.25	15
BERNE-VIRUS	Q2	16	698	43.62	11
SIALODACRYOADENITIS-VIRUS	Q2	18	152	8.44	8
PROTEOLYTIC-CLEAVAGE	Q3	69	2,696	39.07	31
EXPERIMENTAL-ALLERGIC-ENCEPHALOMYELITIS	Q3	35	2,293	65.51	22
CANINE-CORONAVIRUS	Q3	24	827	34.46	15
CORONAVIRUS-JHM	Q4	554	24,443	44.12	80
INFECTIOUS-BRONCHITIS-VIRUS	Q4	179	9,735	54.39	56
ENTERIC-CORONAVIRUS	Q4	173	6,083	35.16	46
SINDBIS-VIRUS	Q4	74	4,279	57.82	39

Figure 4. (a) Strategic diagram and performance from 1970 to 1999. Thematic networks, (b) CORONAVIRUS-JHM. (c) TRANSMISSIBLE-GASTROENTERITIS-VIRUS. (d) INFECTIOUS-BRONCHITIS-VIRUS. (e) ENDOPLASMIC-RETICULUM. (f) BOVINE-CORONAVIRUS. (g) ENTERIC-CORONAVIRUS. (h) VIRAL-RNA-DETECTION. (i) PROTEOLYTIC-CLEAVAGE. (j) SINDBIS-VIRUS. (k) CARCINOEMBREYONIC-ANTIGEN-FAMILY. (l) LELYSTAD-VIRUS. (m) SIALODRACRYOADENITIS-VIRUS. (n) BERNE-VIRUS. (o) EXPERIMENTAL-ALLERGIC-ENCEPHALOMYELITIS. (p) CYSTEINE-PROTEINASE. (q) CANINE-CORONAVIRUS.

During the second period, from 2000 to 2009, sixteen research themes related to coronavirus could be identified, as shown in the strategic diagram and the performance indicators (number of publications, citations achieved, and h-index) of the themes in this period (Figure. 5 (a)). Eight research themes are considered to be key because of their contribution to the growth of the knowledge about coronavirus (motor themes and basic and transversal themes): CORONAVIRUS-MAIN-PROTEINASE, HUMAN-METAPNEUMOVIRUS, MOUSE-HEPATITIS-CORONAVIRUS, MONOCLO-NAL-ANTIBODIES, MULTIPLE-SCLEROSIS, POLYMERASE-CHAIN-REACTION, NUCLEOCAPSID-PROTEIN, and TRANSMISSI-BLE-GASTROENTERITIS-CORONAVIRUS.

Based on the number of citations and h-index, the main research themes directly related to cornavirus this period are as follows: MOUSE-HEPATITIS-CORONAVIRUS, MONOCLONAL-ANTIBODIES, NUCLEOCAPSID-PROTEIN, POLYMERA-
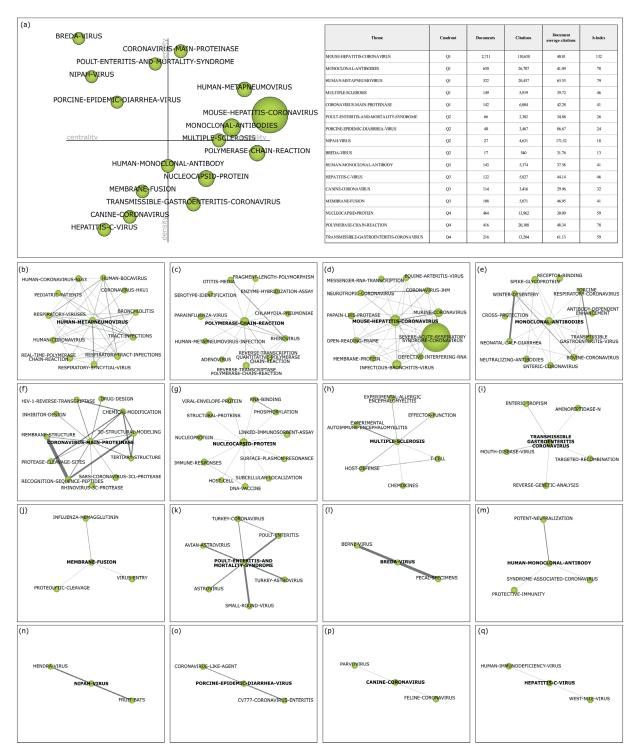
Figure 5. (a) Strategic diagram and performance from 2000 to 2009. Thematic networks. (b) HUMAN-METAPNEUMOVIRUS. (c) POLYMERASE-CHAIN-REACTION. (d) MOUSE-HEPATITIS-CORONAVIRUS. (e) MONOCLONAL-ANTIBODIES. (f) CORONAVIRUS-MAIN-PROTEINASE. (g) NUCLEOCAPSID-PROTEIN. (h) MULTIPLE-SCLEROSIS. (i) GASTROENTERITIS-CORONAVIRUS. (j) MEMBRANE-FUSION. (k) POULT-ENTERITIS-AND-MORTALITY-SINDROME. (l) BREDA-VIRUS. (m) HUMAN-MONOCLONAL-ANTIBODY. (n) NIPAH-VIRUS. (o) PORCINE-EPIDEMIC-DIARRHEA-VIRUS. (p) CANINE-CORONAVIRUS. (q) HEPTITIS-C-VIRUS.

SE-CHAIN-REACTION, and HUMAN-METAPNEUMOVIRUS. As they did in the previous period (1970-1999), the main research themes identified in this period are included in the key themes.

Compared with the previous period, the motor themes retain four themes and incorporate one new theme. Furthermore, CANINE-CORONAVIRUS is the only theme that appears in the first and second period. In this way, the intellectual structure includes themes in all quadrants (motor themes (5), highly developed and isolated themes (4), emerging or declining themes (4), and basic and transversal themes (3)).

Finally, during the third period (2010 to 2020), sixteen research themes related to the coronavirus could be identified, as shown in the strategic diagram and the performance indicators (number of publications, citations achieved, and h-index) of the themes in this period (Figure. 6 (a)). In this regard, eight research themes are considered to be key because
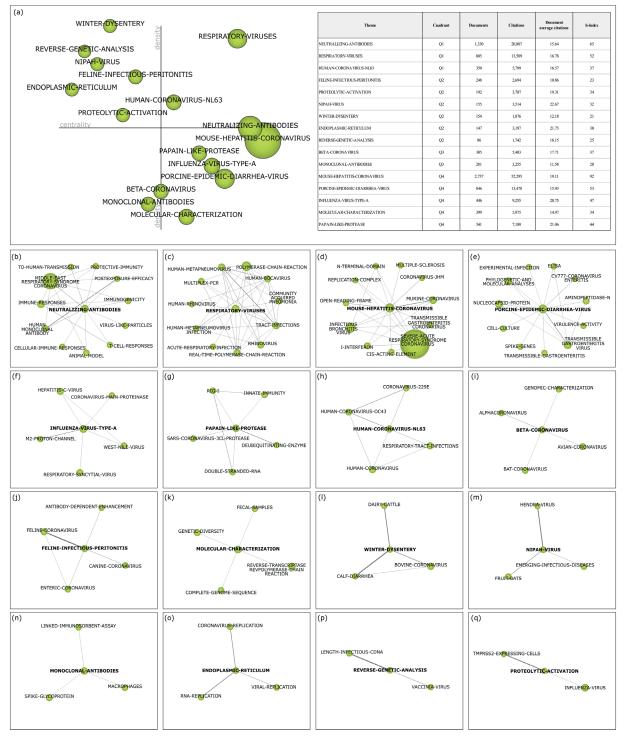
Figure 6. (a) Strategic diagram and performance from 2010 to 2020. Thematic networks. (b) NEUTRALIZING-ANTIBODIES. (c) RESPIRATORY-VIRUSES. (d) MOUSE-HEPATITIS-CORONAVIRUS. (e) PORCINE-EPIDEMIC-DIARRHEA-VIRUS. (f) INFLUENZA-VIRUS-TYPE-A. (g) PAPAIN-LIKE-PROTEASE. (h) HUMAN-CORONAVIRUS-NL63. (i) BETA-CORONAVIRUS. (j) FELINE-INFECTIOUS-PERITONITIS. (k) MOLECULAR-CHARACTERIZATION. (l) WINTER-DYSENTERY. (m) NIPAH-VIRUS. (n) MONOCLONAL-ANTIBODIES. (o) ENDOPLASMIC-RETICULUM. (p) REVERSE-GENETIC-ANALYSIS. (q) PROTOELYTIC-ACTIVATION.

of their contribution to the growth of knowledge about coronavirus (motor themes and basic and transversal themes): RESPIRATORY-VIRUSES, NEUTRALIZING-ANTIBODIES, HUMAN-CORONAVIRUS-NL63, MOUSE-HEPATITIS-CORONAVIRUS, PORCINE-EPIDEMIC-DIARRHEA-VIRUS, PAPAIN-LIKE-PROTEASE, INFLUENZA-VIRUS-TYPE-A, and MOLECULAR-CHARAC-TERIZATION.

Based on the number of citations and h-index, the main research themes directly related to cornavirus this period are as follows: MOUSE-HEPATITIS-CORONAVIRUS, NEUTRALIZING-ANTIBODIES, PORCINE-EPIDEMIC-DIARRHEA-VIRUS, RES-PIRATORY-VIRUSES, and INFLUENZA-VIRUS-TYPE-A. In the period from 2010 to 2020, as in the previous period, the main research themes identified are included in the key themes.

Compared with the previous period, the motor themes retain three and lose two. Furthermore, ENDOPLASMIC-RE-TICULUM, MOUSE-HEPATITIS-CORONAVIRUS, NUCLEOCAPSID-PROTEIN, PORCINE-EPIDEMIC-DIARRHEA-VIRUS, and NI-

PAH-VIRUS are the themes that appear in the first, second, and third periods. In this way, the intellectual structure includes themes in all four quadrants (motor themes (3), highly developed and isolated themes (6), emerging or declining themes (2), and basic and transversal themes (5)).

Finally, taking into account the strategic diagrams shown in Figures 4, 5, and 6, Table 7 summarizes the main research themes developed and their performance according to the number of publications from 1970 to 2020.

Table 7. Principal research themes related to coronavirus from 1970 to 2020

Theme	P1: 1969-1999	P2: 2000-2009	P3: 2010-2020
CORONAVIRUS-JHM	Q4 (554 | 24,443 | 80)		
TRANSMISSIBLE-GASTROENTERITIS-VIRUS	Q1 (231 | 9,463 | 53)		
INFECTIOUS-BRONCHITIS-VIRUS	Q4 (179 | 9,735 | 56)		
ENTERIC-CORONAVIRUS	Q4 (173 | 6,083 | 46)		
ENDOPLASMIC-RETICULUM	Q1 (151 | 10,179 | 56)		Q2 (147 | 3,197 | 30)
BOVINE-CORONAVIRUS	Q1 (108 | 4,485 | 41)		
PROTEOLYTIC-CLEAVAGE	Q3 (69 | 2,696 | 31)		
VIRAL-RNA-DETECTION	Q2 (78 | 4,580 | 43)		
SINDBIS-VIRUS	Q4 (74 | 4,279 | 39)		
EXPERIMENTAL-ALLERGIC-ENCEPHALOMYELITIS	Q3 (35 | 2,293 | 22)		
LELYSTAD-VIRUS	Q1 (27 | 2,914 | 18)		
CANINE-CORONAVIRUS	Q3 (24 | 827 | 15)	Q3 (114 | 3,416 | 32)	
CARCINOEMBRYONIC-ANTIGEN-FAMILY	Q2 (24 | 1,255 | 17)		
CYSTEINE-PROTEINASE	Q2 (20 | 945 | 15)		
SIALODACRYOADENITIS-VIRUS	Q2 (18 | 152 | 8)		
BERNE-VIRUS	Q2 (16 | 698 | 11)		
MOUSE-HEPATITIS-CORONAVIRUS		Q1 (2,711 | 110,638 | 132)	Q4 (2,737 | 52,295 | 92)
MONOCLONAL-ANTIBODIES		Q1 (650 | 26,707 | 78)	Q3 (281 | 3,255 | 28)
NUCLEOCAPSID-PROTEIN		Q4 (464 | 13,962 | 59)	
POLYMERASE-CHAIN-REACTION		Q4 (416 | 20,108 | 78)	
HUMAN-METAPNEUMOVIRUS		Q1 (322 | 20,457 | 79)	
TRANSMISSIBLE-GASTROENTERITIS-CORONAVIRUS		Q4 (216 | 13,204 | 59)	
MULTIPLE-SCLEROSIS		Q1 (149 | 5,919 | 46)	
HUMAN-MONOCLONAL-ANTIBODY		Q3 (143 | 5,374 | 41)	
CORONAVIRUS-MAIN-PROTEINASE		Q1 (142 | 6,004 | 41)	
HEPATITIS-C-VIRUS		Q3 (132 | 5,827 | 46)	
MEMBRANE-FUSION		Q3 (108 | 5,071 | 41)	
POULT-ENTERITIS-AND-MORTALITY-SYNDROME		Q2 (66 | 2,302 | 26)	
PORCINE-EPIDEMIC-DIARRHEA-VIRUS		Q2 (40 | 3,467 | 24)	Q4 (846 | 13,478 | 53)
NIPAH-VIRUS		Q2 (27 | 4,631 | 18)	Q2 (155 | 3,514 | 32)
BREDA-VIRUS		Q2 (17 | 540 | 13)	
NEUTRALIZING-ANTIBODIES			Q1 (1,330 | 20,807 | 65)
RESPIRATORY-VIRUSES			Q1 (805 | 13,509 | 52)
INFLUENZA-VIRUS-TYPE-A			Q4 (446 | 9,255 | 47)
MOLECULAR-CHARACTERIZATION			Q4 (399 | 5,975 | 34)
HUMAN-CORONAVIRUS-NL63			Q1 (350 | 5,799 | 37)
PAPAIN-LIKE-PROTEASE			Q4 (341 | 7,180 | 44)
BETA-CORONAVIRUS			Q3 (305 | 5,403 | 37)
FELINE-INFECTIOUS-PERITONITIS			Q2 (248 | 2,694 | 23)
PROTEOLYTIC-ACTIVATION			Q2 (192 | 3,707 | 34)
WINTER-DYSENTERY			Q2 (154 | 1,876 | 21)
REVERSE-GENETIC-ANALYSIS			Q2 (96 | 1,742 | 25)

4.2. Conceptual evolution map

The themes detected in each period can be jointly analyzed by means of their conceptual evolution, that is, discovering the shared terms and how they evolve through time. Thus, using as input the themes of the three consecutive time periods, a second analysis focusing on the conceptual evolution was carried out.

Hence, two thematic areas were identified: *virus and coronavirus complementary research* and *virus and coronavirus types and strains.* These thematic areas consolidate the main themes and research areas related to coronavirus. Figure 7 shows the conceptual evolution map and lists the key performance indicators for each thematic area.

Virus and coronavirus types and strains (pink area) is the most representative thematic area within the conceptual evolution map (Figure 7). It accounts for 11,029 publications, 333,082 of the total citations, and 132 publications highly cited according to the h-index. In terms of structure and thematic composition, it contains motor themes, highly developed and isolated themes, and basic and transversal themes in all the periods, but it covers all the quadrants in the last period. This thematic area covers themes related to BERNE-VIRUS, BETA-CORONAVIRUS, BOVINE-CORONAVIRUS, BREDA-VIRUS, CANINE-CORONAVIRUS, CORONAVIRUS-JHM, ENTERIC-CORONAVIRUS, FELINE-INFECTIOUS-PERITONITIS, HEPATITIS-C-VIRUS, HUMAN-CORONAVIRUS-NL63, HUMAN-METAPNEUMOVIRUS, INFECTIOUS-BRONCHITIS-VIRUS, INFLUENZA-VIRUS-TYPE-A, LELYSTAD-VIRUS, MOUSE-HEPATITIS-CORONAVIRUS, NIPAH-VIRUS, PORCINE-EPIDEMIC-DIARRHEA-VIRUS, RESPIRATORY-VIRUSES, SIALODACRYOADENITIS-VIRUS, SINDBIS-VIRUS, TRANSMISSIBLE-GASTROENTERITIS-CORONAVIRUS, TRANSMISSIBLE-GASTROENTERITIS-VIRUS, and WINTER-DYSENTERY.

Name	Documents	Citations	Document average citations	h-index
Virus and coronavirus complementary research (green area)	5,301	153,258	36.84	78
Virus and coronavirus types and strains (pink area)	11,029	333,082	42.61	132

Figure 7. Evolution of thematic areas (1970–2020)

Virus and coronavirus complementary research (green area) is the second thematic area within the map in terms of number of publications. It has 5,301 publications, 153,258 citations, and 78 highly cited publications according to the h-index. This thematic area contains the motor themes, highly developed and isolated themes, and emerging or declining themes in all the periods, but it covers all the quadrants in the last period. Regarding its thematic composition, this thematic area covers

> The development of coronavirus research will mainly support the following areas: virology, veterinary sciences, biochemistry, molecular biology, immunology, infectious diseases, microbiology, biotechnology, and applied microbiology

themes related to CARCINOEMBRYONIC-ANTIGEN-FAMILY, CORONAVIRUS-MAIN-PROTEINASE, CYSTEINE-PROTEINASE, ENDOPLASMIC-RETICULUM, EXPERIMENTAL-ALLERGIC-ENCEPHALOMYELITIS, HUMAN-MONOCLONAL-ANTIBODY, MEMBRANE-FUSION, MOLECULAR-CHARACTERIZATION, MONOCLONAL-ANTIBODIES, MULTIPLE-SCLEROSIS NEUTRALIZING-ANTIBODIES, NUCLEOCAPSID-PROTEIN, PAPAIN-LIKE-PROTEASE, POLYMERASE-CHAIN-REACTION, POULT-ENTERITIS-AND-MORTALITY-SYNDROME, PROTEOLYTIC-ACTIVATION, PROTEOLYTIC-CLEAVAGE, REVERSE-GENETIC-ANALYSIS, and VIRAL-RNA-DETECTION.

Therefore, it is important to emphasize that all the thematic areas include themes from the motor themes, highly developed and isolated themes, and basic and transversal themes and present a growing pattern in the last period. This growth can be considered to reflect the growing interest in coronavirus research within the scientific and business community.

However, according to the bibliometric methodology implemented by *SciMAT* as described herein, the evolution maps can be used to reveal the pattern of development within the field throughout the periods analyzed based on the interaction between the graphical elements. Therefore, the size of the spheres is proportional to the number of publications associated with each theme, while the colored areas represent the clusters of themes pertaining to the same thematic area. Moreover, the solid line represents the thematic link between the different areas, while the dotted line indicates that related thematic areas share some keywords. Furthermore, the thickness of the lines is proportional to the rate of inclusion (**Cobo** *et al.*, 2012). The conceptual evolution and thematic areas identified are shown in Figure 7.

5. Conclusions

The current analysis represents the first bibliometric study on coronavirus types and strains since the first publication in 1970 to the present day, with an emphasis on Covid-19 disease and using *SciMAT*. It therefore focuses on an analysis and description of the development of the research themes about coronavirus and the main related concepts available in the literature using bibliometric techniques and tools. It establishes a holistic approach to identify new research that supports the interest of the scientific community.

In terms of bibliometric volume, more than 12,571 original research publications have been processed and analyzed. The size of this literature related to research on coronavirus, its main types and strains, and complementary themes has shown a noteworthy increase over the past 50 years (1970-2020). Given the large volume of publications and citations received and the current global disease, it is expected that such interest will continue to grow and serve as a support to different knowledge areas such as virology, veterinary sciences, biochemistry, molecular biology, immunology, infectious diseases, microbiology, biotechnology, applied microbiology, experimental medical research, pharmacology, pharmacy, and public, environmental, and occupational health, among others.

Accordingly, coronavirus research published during the period from 1970 to 2020 includes papers coauthored by 35,359 researchers from 462 organizations and 145 different countries. The publications analyzed have received more than 382,447 citations (including self-citations) according to *Web of Science Core Collection*. The most productive authors are Yuen, Perlman, Baric, Enjuanes, Weiss, Drosten, Rottier, Woo, Chan, Saif, Lau, and Snijder, and the most cited are Yuen, Chan, Drosten, Osterhaus, Peiris, Guan, Poon, Snijder, Woo, Rottier, and Enjuanes. The correspondence between the most productive and most cited authors reflects the balance and quality of the publications analyzed.

Moreover, the most productive countries are the USA, China, the UK, Germany, the Netherlands, Canada, Japan, France, South Korea, Italy, and Taiwan. Furthermore, the most productive organizations are *University of Hong Kong*, *Chinese Academy of Sciences*, *University of California System*, *National Institutes of Health* (USA), *Utrecht University*, *University of North Carolina*, *Centers for Disease Control and Prevention* (*USA*), *University of Texas System*, *University of North Carolina Chapel Hill*, *University of Pennsylvania,* and *Chinese University of Hong Kong*. As with the previous point, the most productive countries and most productive organizations reflect the position of the main agents in this field.

In this regard, the number of core publications related to coronavirus research identified by using the h-index and H-classics is 192. In terms of citations, their citation distribution reveals a positive developmental trend, with a total of 72,763 citations (including self-citations) being recorded and the average number of citations per cited article being 378.97.

In addition, based on the results of the bibliometric analysis, this research provides a visual overview of the development and structure of the main types and strains of coronavirus and related themes over the past 50 years (1970-2020).

The intellectual structure of coronavirus research and its main themes described in the literature are arranged into two

thematic areas: *virus and coronavirus complementary research* and *virus and coronavirus types and strains.* These thematic areas support a visualization of coronavirus types and strains, with its main components covering aspects from the identification and characterization of the virus to its evolution and solutions.

The research themes within these thematic areas that are considered to be key because of their contribution to the growth of the field are BOVINE-CORONAVIRUS, CORONAVIRUS-JHM, CORONAVIRUS-MAIN-PROTEINASE, ENDOPLASMIC-RETICULUM, ENTERIC-CORONAVIRUS, HUMAN-CORONAVIRUS-NL63, HUMAN-METAPNEUMOVIRUS, INFECTIOUS-BRONCHITIS-VIRUS, INFLUENZA-VIRUS-TYPE-A, LELYSTAD-VIRUS, MOLECULAR-CHARACTERIZATION, MONOCLONAL-ANTIBODIES, MOUSE-HEPATITIS-CORONAVIRUS, MULTIPLE-SCLEROSIS, NEUTRALIZING-ANTIBODIES, NUCLEOCAPSID-PROTEIN, PAPAIN-LIKE-PROTEASE, POLYMERASE-CHAIN-REACTION, PORCINE-EPIDEMIC-DIARRHEA-VIRUS, RESPIRATORY-VIRUSES, SINDBIS-VIRUS, and TRANSMISSIBLE-GASTROENTERITIS-VIRUS.

> We identified the following themes that will attract interest from the scientific community: human coronavirus, genetic analysis, neutralizing antibodies, and social and economic effects of coronavirus disease, among others

After analyzing these lines of research and their evolution, this study finds that the development of coronavirus research will mainly support the following areas: virology, veterinary sciences, biochemistry, molecular biology, immunology, infectious diseases, microbiology, biotechnology, applied microbiology, experimental medical research, pharmacology, pharmacy, general medicine, and public and environmental occupational health.

In addition, the present study identified the following themes that will attract interest from the scientific community in the future: human coronavirus, genetic analysis, neutralizing antibodies, molecular characterization, coronavirus main proteinase, proteolytic activation, social and economic effects of coronavirus disease, and new research methods in fields related to the coronavirus, among others.

Finally, future work is necessary to provide a more in-depth examination of coronavirus research considering a multidisciplinary approach.

6. Annexes

Table A.1 H-Classics of coronavirus

Rank	Title (Year, First author)	Citations
1	A novel coronavirus associated with severe acute respiratory syndrome (2003, Ksiazek, T. G.)	1,932
2	Identification of a novel coronavirus in patients with severe acute respiratory syndrome (2003, Drosten, C.)	1,826
3	Characterization of a novel coronavirus associated with severe acute respiratory syndrome (2003, Ksiazek, T. G.)	1,510
4	Coronavirus as a possible cause of severe acute respiratory syndrome (2003, Lim, W.)	1,482
5	Isolation of a novel coronavirus from a man with pneumonia in Saudi Arabia (2012, Osterhaus, A. D. M. E.)	1,389
6	Community study of role of viral-infections in exacerbations of asthma in 9-11 year-old children (1995, Johnston, S. L.)	1,337
7	The genome sequence of the SARS-associated coronavirus (2003, Marra, M. A.)	1,303
8	Cloning of a human parvovirus by molecular screening of respiratory tract samples (2005, Tammi, M. T.)	1,038
9	Angiotensin-converting enzyme 2 is a functional receptor for the SARS coronavirus (2003, Li, W. H.)	1,034
10	Psychological stress and susceptibility to the common cold (1991, Tyrrell, D. A. J.)	1,011
11	Isolation and characterization of viruses related to the SARS coronavirus from animals in Southern China (2003, Lim, W.)	934
12	Bats are natural reservoirs of SARS-like coronaviruses (2005, Li, W. D.)	890
13	Clinical progression and viral load in a community outbreak of coronavirus-associated SARS pneumonia: a prospective study (2003, Peiris, J. S. M.)	875
14	Regulation and cellular roles of ubiquitin-specific deubiquitinating enzymes (2009, Reyes-Turcu, F. E.)	791
15	Identification of a new human coronavirus (2004, van der Hoek, L.)	771
16	Unique and conserved features of genome and proteome of SARS-coronavirus, an early split-off from the coronavirus group 2 lineage (2003, Poon, L. L. M.)	686
17	Identification of severe acute respiratory syndrome in Canada (2003, Brunham, R. C.)	685
18	Bats: Important reservoir hosts of emerging viruses (2006, Calisher, C. H.)	679
19	Severe acute respiratory syndrome coronavirus-like virus in Chinese horseshoe bats (2005, Chan, K. H.)	666
20	Characterization and complete genome sequence of a novel coronavirus, coronavirus HKU1, from patients with pneumonia (2005, Peiris, J. S. M.)	660
21	Structural bioinformatics and its impact to biomedical science (2004, Chou, K. C.)	636
22	Lelystad virus, the causative agent of porcine epidemic abortion and respiratory syndrome (pears), is related to ldv and eav (1993, Meulenberg, J. J. M.)	609

23	Transmission dynamics and control of severe acute respiratory syndrome (2003, Lipsitch, M.)	584
24	Hospital outbreak of Middle East respiratory syndrome coronavirus (2013, Assiri, A.)	566
25	The molecular biology of coronaviruses (1997, Lai, M. M. C.)	551
26	Human infections with the emerging avian influenza A H7N9 virus from wet market poultry: clinical analysis and characterisation of viral genome (2013, Chan, K. H.)	550
27	Isolation and direct characterization of resident microglial cells from the normal and inflamed central-nervous-system (1991, Sedgwick, J. D.)	536
28	Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China (2020, Huang, C. L.)	529
29	Newly discovered coronavirus as the primary cause of severe acute respiratory syndrome (2003, Lim, W.)	504
30	Dipeptidyl peptidase 4 is a functional receptor for the emerging human coronavirus-EMC (2013, Osterhaus, A. D. M. E.)	499
31	RNA recombination in animal and plant-viruses (1992, Lai, M. M. C.)	497
32	Identification of a novel polyomavirus from patients with acute respiratory tract infections (2007, Gaynor, A. M.)	496
33	Porcine reproductive and respiratory syndrome virus comparison: Divergent evolution on two continents (1999, Nelsen, C. J.)	495
34	From carbohydrate leads to glycomimetic drugs (2009, Ernst, B.)	486
35	Current concepts: The severe acute respiratory syndrome (2003, Osterhaus, A. D. M. E.)	483
36	Coronavirus main proteinase (3CL(pro)) structure: Basis for design of anti-SARS drugs (2003, Ziebuhr, J.)	477
37	Virus-encoded proteinases and proteolytic processing in the Nidovirales (2000, Snijder, E. J.)	469
38	Characterization of an efficient coronavirus ribosomal frameshifting signal - requirement for an RNA pseudoknot (1989, Brierley, I.)	469
39	Human aminopeptidase-n is a receptor for human coronavirus-229e (1992, Yeager, C. L.)	460
40	Structures and mechanisms of viral membrane fusion proteins: Multiple variations on a common theme (2008, White, J. M.)	450
41	Aminopeptidase-n is a major receptor for the enteropathogenic coronavirus TGEV (1992, Delmas, B.)	427
42	Viruses and bacteria in the etiology of the common cold (1998, Makela, M. J.)	426
43	Lung pathology of fatal severe acute respiratory syndrome (2003, Lim, W.)	418
44	Angiotensin-converting enzyme 2 protects from severe acute lung failure (2005, Slutsky, A. S.)	405
45	Autoimmunity to myelin oligodendrocyte glycoprotein in rats mimics the spectrum of multiple sclerosis pathology (1998, Storch, M. K.)	398
46	Human bocavirus and acute wheezing in children (2007, Allander, T.)	396
47	An efficient method to make human monoclonal antibodies from memory B cells: potent neutralization of SARS coronavirus (2004, Becker, S.)	390
48	Mechanisms and enzymes involved in SARS coronavirus genome expression (2003, Rabenau, H.)	389
49	Impacts of bioinformatics to medicinal chemistry (2015, Chou, K. C.)	387
50	The coronavirus spike protein is a class I virus fusion protein: Structural and functional characterization of the fusion core complex (2003, Bosch, B. J.)	387
51	Epidemiological, demographic, and clinical characteristics of 47 cases of Middle East respiratory syndrome coronavirus disease from Saudi Arabia: a descriptive study (2013, Assiri, A.)	386
52	2′-O methylation of the viral mRNA cap evades host restriction by IFIT family members (2010, Thiel, V.)	380
53	Factors that make an infectious disease outbreak controllable (2004, Fraser, C.)	378
54	Coronavirus avian infectious bronchitis virus (2007, Cavanagh, D.)	376
55	Genomic characterization of a newly discovered coronavirus associated with acute respiratory distress syndrome in humans (2012, Osterhaus, A. D. M. E.)	372
56	Pseudo amino acid composition and its applications in bioinformatics, proteomics and system biology (2009, Chou, K. C.)	365
57	Glycyrrhizin, an active component of liquorice roots, and replication of SARS-associated coronavirus (2003, Rabenau, H.)	365
58	Nidovirales: Evolving the largest RNA virus genome (2006, Snijder, E. J.)	358
59	Network theory and SARS: predicting outbreak diversity (2005, Brunham, R. C.)	358
60	Severe acute respiratory syndrome (2004, Peiris, J. S. M.)	358
61	Middle East respiratory syndrome coronavirus neutralising serum antibodies in dromedary camels: a comparative serological study (2013, Osterhaus, A. D. M. E.)	353
62	Contamination, disinfection, and cross-colonization: Are hospital surfaces reservoirs for nosocomial infection? (2004, Hota, B.)	351
63	Equine arteritis virus is not a togavirus but belongs to the coronaviruslike superfamily (1991, Denboon, J. A.)	343
64	Emergence of Porcine epidemic diarrhea virus in the United States: clinical signs, lesions, and viral genomic sequences (2013, Stevenson, G. W.)	341
65	A previously undescribed coronavirus associated with respiratory disease in humans (2004, Fouchier, R. A. M.)	340

66	Discovery of seven novel mammalian and avian coronaviruses in the genus deltacoronavirus supports bat coronaviruses as the gene source of alphacoronavirus and betacoronavirus and avian coronaviruses as the gene source of gammacoronavirus and deltacoronavirus (2012, Chan, K. H.)	339
67	The crystal structures of severe acute respiratory syndrome virus main protease and its complex with an inhibitor (2003, Anand, K.)	338
68	Porcine epidemic diarrhoea virus: a comprehensive review of molecular epidemiology, diagnosis, and vaccines (2012, Song, D.)	337
69	A novel coronavirus from patients with pneumonia in China, 2019 (2020, Li, X. W.)	330
70	Structure of SARS coronavirus spike receptor-binding domain complexed with receptor (2005, Li, W. H.)	329
71	Binding mechanism of coronavirus main proteinase with ligands and its implication to drug design against SARS (2003, Chou, K. C.)	329
72	Rhinovirus and respiratory syncytial virus in wheezing children requiring emergency care - IgE and eosinophil analyses (1999, Rakes, C. P.)	326
73	A DNA vaccine induces SARS coronavirus neutralization and protective immunity in mice (2004, Huang, Y.)	325
74	Ribose 2′-O-methylation provides a molecular signature for the distinction of self and non-self mRNA dependent on the RNA sensor Mda5 (2011, Thiel, V.)	324
75	Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor (2013, Ge, X. Y.)	323
76	The molecular biology of coronaviruses (2006, Masters, P. S.)	323
77	Emerging roles of cysteine cathepsins in disease and their potential as drug targets (2007, Vasiljeva, O.)	319
78	Cross-species virus transmission and the emergence of new epidemic diseases (2008, Calisher, C. H.)	313
79	Characterization of proteins encoded by orf-2 to orf-7 of lelystad-virus (1995, Meulenberg, J. J. M.)	312
80	Viral discovery and sequence recovery using DNA microarrays (2003, Ksiazek, T. G.)	308
81	Evidence for camel-to-human transmission of MERS coronavirus (2014, Azhar, E. I.)	307
82	Inhibitors of cathepsin L prevent severe acute respiratory syndrome coronavirus entry (2005, Simmons, G.)	306
83	Completion of the sequence of the genome of the coronavirus avian infectious-bronchitis virus (1987, Boursnell, M. E. G.)	306
84	SARS-coronavirus replication is supported by a reticulovesicular network of modified endoplasmic reticulum (2008, Snijder, E. J.)	305
85	Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study (2020, Zhang, L.)	304
86	Epidemic dynamics at the human-animal interface (2009, Lloyd-Smith, J. O.)	298
87	Coronaviruses post-SARS: update on replication and pathogenesis (2009, Perlman, S.)	297
88	Middle East respiratory syndrome coronavirus in dromedary camels: an outbreak investigation (2014, Osterhaus, A. D. M. E.)	295
89	Using siRNA in prophylactic and therapeutic regimens against SARS coronavirus in rhesus macaque (2005, Zheng, B. J.)	295
90	Rhinovirus-induced wheezing in infancy-the first sign of childhood asthma? (2003, Kotaniemi-Syrjanen, A.)	294
91	Predicting linear B-cell epitopes using string kernels (2008, El-Manzalawy, Y.)	293
92	A crucial role of angiotensin converting enzyme 2 (ACE2) in SARS coronavirus-induced lung injury (2005, Slutsky, A. S.)	293
93	The complete sequence (22 kilobases) of murine coronavirus gene-1 encoding the putative proteases and rna-polymerase (1991, Lai, M. M. C.)	293
94	A 193-amino acid fragment of the SARS coronavirus S protein efficiently binds angiotensin-converting enzyme 2 (2004, Li, W. H.)	289
95	Molecular evolution of the SARS coronavirus during the course of the SARS epidemic in China (2004, Hu, Z. H.)	288
96	Tissue distribution of ACE2 protein, the functional receptor for SARS coronavirus. A first step in understanding SARS pathogenesis (2004, Hamming, I.)	287
97	Middle East respiratory syndrome coronavirus in bats, Saudi Arabia (2013, Memish, Z. A.)	286
98	Receptor for mouse hepatitis-virus is a member of the carcinoembryonic antigen family of glycoproteins (1991, Williams, R. K.)	281
99	Cloning of the mouse hepatitis-virus (MHV) receptor - expression in human and hamster-cell lines confers susceptibility to MHV (1991, Williams, R. K.)	275
100	SARS virus infection of cats and ferrets (2003, Lim, W.)	273
101	Nucleocapsid-independent assembly of coronavirus-like particles by co-expression of viral envelope protein genes (1996, Rottier, P. J. M.)	273
102	Potent neutralization of severe acute respiratory syndrome (SARS) coronavirus by a human mAb to S1 protein that blocks receptor association (2004, Bellini, W. J.)	272
103	Comparative full-length genome sequence analysis of 14 SARS coronavirus isolates and common mutations associated with putative origins of infection (2003, Ruan, Y. J.)	272
104	Virus glycosylation: role in virulence and immune interactions (2007, Vigerust, D. J.)	271

105	Putative papain-related thiol proteases of positive-strand RNA viruses - identification of rubivirus and aphthovirus proteases and delineation of a novel conserved domain associated with proteases of rubivirus, alpha- and coronaviruses (1991, Lai, M. M. C.)	268
106	Zoonoses 3 prediction and prevention of the next pandemic zoonosis (2012, Daszak, P.)	266
107	Pathogenicity of antigenic variants of murine coronavirus JHM selected with monoclonal-antibodies (1986, Fleming, J. O.)	266
108	Cross-host evolution of severe acute respiratory syndrome coronavirus in palm civet and human (2005, Tong, S. X.)	264
109	Coronavirus spike proteins in viral entry and pathogenesis (2001, Gallagher, T. M.)	264
110	Incubation periods of acute respiratory viral infections: a systematic review (2009, Perl, T. M.)	262
111	RNA replication of mouse hepatitis virus takes place at double-membrane vesicles (2002, Gosert, R.)	261
112	Clinical characteristics of 138 hospitalized patients with 2019 novel coronavirus-infected pneumonia in Wuhan, China (2020, Cheng, Z. S.)	260
113	Database resources of the National Center for Biotechnology Information: update (2004, Wheeler, D. L.)	260
114	Epidemiology and cause of severe acute respiratory syndrome (SARS) in Guangdong, People's Republic of China, in February, 2003 (2003, Peiris, J. S. M.)	255
115	Origin, evolution, and genotyping of emergent porcine epidemic diarrhea virus strains in the United States (2013, Huang, Y. W.)	252
116	Evidence of human coronavirus HKU1 and human bocavirus in Australian children (2006, Sloots, T. P.)	252
117	Coronavirus-organization, replication and expression of genome (1990, Lai, M. M. C.)	252
118	The association of newly identified respiratory viruses with lower respiratory tract infections in Korean children, 2000-2005 (2006, Choi, E. H.)	251
119	Virus maturation by budding (1998, Opstelten, D. J. E.)	251
120	Coronavirus pathogenesis and the emerging pathogen severe acute respiratory syndrome coronavirus (2005, Weiss, S. R.)	250
121	Development of a respiratory virus panel test for detection of twenty human respiratory viruses by use of multiplex PCR and a fluid microbead-based assay (2007, Mahony, J.)	247
122	Middle East respiratory syndrome (2015, Perlman, S.)	246
123	Transmission of the severe acute respiratory syndrome on aircraft (2003, Dowell, S. F.)	245
124	Orderly order in protein intrinsic disorder distribution: disorder in 3500 proteomes from viruses and the three domains of life (2012, Xue, B.)	244
125	Distinct patterns of IFITM-mediated restriction of filoviruses, SARS coronavirus, and influenza A virus (2011, Huang, I. C.)	244
126	Autophagy: Principles and significance in health and disease (2009, Todde, V.)	244
127	Detection of respiratory viruses by molecular methods (2008, Mahony, J. B.)	244
128	Transferrin receptor 1 is a cellular receptor for New World haemorrhagic fever arenaviruses (2007, Radoshitzky, S. R.)	244
129	Molecular basis of binding between novel human coronavirus MERS-CoV and its receptor CD26 (2013, Zhang, W.)	240
130	Induction of incomplete autophagic response by hepatitis C virus via the unfolded protein response (2008, Sir, D.)	240
131	Isolation of coronavirus envelope glycoproteins and interaction with the viral nucleocapsid (1980, Holmes, K. V.)	239
132	A pneumonia outbreak associated with a new coronavirus of probable bat origin (2020, Yang, X. L.)	236
133	A pneumonia outbreak associated with a new coronavirus of probable bat origin (2020, Yang, X. L.)	236
134	An efficient ribosomal frame-shifting signal in the polymerase-encoding region of the coronavirus IBV (1987, Brierley, I.)	236
135	Clinical features and viral diagnosis of two cases of infection with Middle East Respiratory Syndrome coronavirus: a report of nosocomial transmission (2013, Guery, B.)	235
136	Family cluster of Middle East respiratory syndrome coronavirus infections (2013, Zumla, A. I.)	234
137	Severe acute respiratory syndrome coronavirus spike protein expressed by attenuated vaccinia virus protectively immunizes mice (2004, Subbarao, K.)	233
138	Clinical features and complete genome characterization of a distinct human rhinovirus (HRV) genetic previously undetected HRV cluster, probably representing a species, HRV-C, associated with acute respiratory illness in children (2007, Chan, K. H.)	232
139	Ovarian tumor domain-containing viral proteases evade ubiquitin- and ISG15-dependent innate immune responses (2007, Snijder, E. J.)	231
140	Coronavirus replication complex formation utilizes components of cellular autophagy (2004, Prentice, E.)	230
141	Prior infection and passive transfer of neutralizing antibody prevent replication of severe acute respiratory syndrome coronavirus in the respiratory tract of mice (2004, Shieh, W. J.)	229
142	Retargeting of coronavirus by substitution of the spike glycoprotein ectodomain: Crossing the host cell species barrier (2000, Rottier, P. J. M.)	229
143	2014 MERS-CoV outbreak in Jeddah - A link to health care facilities (2015, Madani, T. A.)	228
144	Severe respiratory illness caused by a novel coronavirus, in a patient transferred to the United Kingdom from the Middle East, September 2012 (2012, Bermingham, A.)	228
145	Autophagosome supports coxsackievirus B3 replication in host cells (2008, Wong, J.)	228

146	Receptor and viral determinants of SARS-coronavirus adaptation to human ACE2 (2005, Guan, Y.)	227
147	Development of three multiplex RT-PCR assays for the detection of 12 respiratory RNA viruses (2005, Bellau-Pujol, S.)	225
148	Coronavirus genome - prediction of putative functional domains in the non-structural polyprotein by comparative amino-acid sequence-analysis (1989, Gorbalenya, A. E.)	223
149	Coronavirus transcription - subgenomic mouse hepatitis-virus replicative intermediates function in rna-synthesis (1990, Sawicki, S. G.)	222
150	Severe acute respiratory syndrome coronavirus open reading frame (ORF) 3b, ORF 6, and nucleocapsid proteins function as interferon antagonists (2007, Kopecky-Bromberg, S. A.)	221
151	Lambda interferon renders epithelial cells of the respiratory and gastrointestinal tracts resistant to viral infections (2010, Drosten, C.)	220
152	Characterization of severe acute respiratory syndrome-associated coronavirus (SARS-CoV) spike glycoprotein-mediated viral entry (2004, Simmons, G.)	220
153	Feline infectious peritonitis viruses arise by mutation from endemic feline enteric coronaviruses (1998, Vennema, H.)	220
154	Heptad repeat sequences are located adjacent to hydrophobic regions in several types of virus fusion glycoproteins (1990, Chambers, P.)	220
155	Wildlife trade and global disease emergence (2005, Karesh, W. B.)	218
156	CD209L (L-SIGN) is a receptor for severe acute respiratory syndrome coronavirus (2004, Jeffers, S. A.)	217
157	Simultaneous detection of fourteen respiratory viruses in clinical specimens by two multiplex reverse transcription nested-PCR assays (2004, Coiras, M. T.)	217
158	Proteolytic cleavage of the e2-glycoprotein of murine coronavirus - activation of cell-fusing activity of virions by trypsin and separation of 2 different 90k-cleavage fragments (1985, Holmes, K. V.)	217
159	Panmicrobial oligonucleotide array for diagnosis of infectious diseases (2007, Briese, T.)	216
160	Engineering the largest RNA virus genome as an infectious bacterial artificial chromosome (2000, Enjuanes, L.)	215
161	A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: a study of a family cluster (2020, Chan, K. H.)	214
162	Delayed antiviral plus immunomodulator treatment still reduces mortality in mice infected by high inoculum of influenza A/H5N1 virus (2008, Chan, K. H.)	214
163	Real-time reverse transcription PCR (qRT-PCR) and its potential use in clinical diagnosis (2005, Bustin, S. A.)	214
164	Autophagic machinery activated by dengue virus enhances virus replication (2008, Lee, Y. R.)	213
165	pH-dependent entry of Severe acute respiratory syndrome coronavirus is mediated by the spike glycoprotein and enhanced by dendritic cell transfer through DC-SIGN (2004, Huang, Y.)	213
166	Feline coronavirus type II strains 79-1683 and 79-1146 originate from a double recombination between feline coronavirus type I and canine coronavirus (1998, Rottier, P. J. M.)	213
167	Antivirals and antiviral strategies (2004, De Clercq, E.)	212
168	Early transmission dynamics in Wuhan, China, of novel coronavirus-infected pneumonia (2020, Yang, B.)	211
169	Development and evaluation of a novel loop-mediated isothermal amplification method for rapid detection of severe acute respiratory syndrome coronavirus (2004, Thai, H. T. C.)	210
170	Interaction between heptad repeat 1 and 2 regions in spike protein of SARS-associated coronavirus: implications for virus fusogenic mechanism and identification of fusion inhibitors (2004, Liu, S. W.)	210
171	Structure of coronavirus main proteinase reveals combination of a chymotrypsin fold with an extra alpha-helical domain (2002, Ziebuhr, J.)	210
172	Mannose-binding lectin in innate immunity: past, present and future (2006, Dommett, R. M.)	209
173	Plasma inflammatory cytokines and chemokines in severe acute respiratory syndrome (2004, Wong, C. K.)	209
174	Frequency and natural history of rhinovirus infections in adults during autumn (1997, Arruda, E.)	209
175	Reverse genetics with a full-length infectious cDNA of severe acute respiratory syndrome coronavirus (2003, Prentice, E.)	208
176	Establishment of B-cell lymphoma cell lines persistently infected with hepatitis C virus in vivo and in vitro: the apototic effects of virus infection (2003, Lai, M. M. C.)	204
177	Clinical features and virological analysis of a case of Middle East respiratory syndrome coronavirus infection (2013, Muth, D.)	203
178	Pegylated interferon-alpha protects type 1 pneumocytes against SARS coronavirus infection in macaques (2004, Fouchier, R. A. M.)	200
179	Human bocavirus: Passenger or pathogen in acute respiratory tract infections? (2008, Mackay, I. M.)	199
180	Viral upper respiratory tract infection and otitis media complication in young children (2008, Chonmaitree, T.)	199
181	Persistence of rhinovirus and enterovirus RNA after acute respiratory illness in children (2004, Ruuskanen, O.)	199
182	Cytoplasmic viral replication complexes (2010, den Boon, J. A.)	198
183	Adoptive transfer of eae-like lesions from rats with coronavirus-induced demyelinating encephalomyelitis (1983, Termeulen, V.)	197
184	The papain-like protease of severe acute respiratory syndrome coronavirus has deubiquitinating activity (2005, Baker, S. C.)	196

185	Coronaviruses in poultry and other birds (2005, Cavanagh, D.)	196
186	Systematic assembly of a full-length infectious cDNA of mouse hepatitis virus strain A59 (2002, Weiss, S. R.)	196
187	The genome organization of the nidovirales: Similarities and differences between arteri-, toro-, and coronaviruses (1997, Rottier, P. J. M.)	196
188	Impaired heart contractility in apelin gene-deficient mice associated with aging and pressure overload (2007, Kuba, K.)	195
189	Nidovirus transcription: how to make sense...? (2006, Snijder, E. J.)	195
190	Identification of a novel coronavirus in bats (2005, Peiris, J. S. M.)	195
191	An enteric coronavirus infection of cats and its relationship to feline infectious peritonitis (1981, Pedersen, N. C.)	195
192	Pan-viral screening of respiratory tract infections in adults with and without asthma reveals unexpected human coronavirus and human rhinovirus diversity (2007, Wang, D.)	193

7. References

Bonilla-Aldana, D. Katterine; **Quintero-Rada, Keidenis**; **Montoya-Posada, Juan Pablo**; **Ramírez-Ocampo, Sebastián**; **Paniz-Mondolfi, Alberto**; **Rabaan, Ali A.**; **Sah, Ranjit**; **Rodríguez-Morales, Alfonso J.** (2020). "SARS-CoV, MERS-CoV and now the 2019-novel CoV: Have we investigated enough about coronaviruses?–A bibliometric analysis". *Travel medicine and infectious disease*, v. 33, 101566.
https://doi.org/10.1016/j.tmaid.2020.101566

Callon, Michael; **Courtial, Jean-Pierre**; **Turner, William A.**; **Bauin, Serge** (1983). "From translations to problematic networks: An introduction to co-word analysis". *Information (International Social Science Council)*, v. 22, n. 2, pp. 191-235.
https://doi.org/10.1177/053901883022002003

Callon, Michael; **Courtial, Jean Pierre**; **Laville, Francoise** (1991). "Co-word analysis as a tool for describing the network of interactions between basic and technological research: The case of polymer chemsitry". *Scientometrics*, v. 22, n. 1, pp. 155-205.
https://doi.org/10.1007/BF02019280

Casero-Ripollés, Andreu (2020). "Impact of Covid-19 on the media system. Communicative and democratic consequences of news consumption during the outbreak". *El profesional de la información*, v. 29, n. 2, e290223.
https://doi.org/10.3145/epi.2020.mar.23

Cobo, Manuel-Jesús; **López-Herrera, Antonio-Gabriel**; **Herrera-Viedma, Enrique**; **Herrera, Francisco** (2011). "An approach for detecting, quantifying, and visualizing the evolution of a research field: A practical application to the Fuzzy Sets Theory field". *Journal of informetrics*, v. 5, n. 1, pp. 146-166.
https://doi.org/10.1016/j.joi.2010.10.002

Cobo, Manuel-Jesús; **López-Herrera, Antonio-Gabriel**; **Herrera-Viedma, Enrique**; **Herrera, Francisco** (2012). "SciMAT: A new science mapping analysis software tool". *Journal of the American Society for Information Science and Technology*, v. 63, n. 8, pp. 1609-1630.
https://doi.org/10.1002/asi.22688

Coulter, Neal; **Monarch, Ira**; **Konda, Suresh** (1998). "Software engineering as seen through its research literature: A study in co-word analysis". *Journal of the American Society for Information Science*, v. 49, n. 13, pp. 1206-1223.
https://doi.org/10.1002/(SICI)1097-4571(1998)49:13%3C1206::AID-ASI7%3E3.0.CO;2-F

Garfield, Eugene (1986). "Towards Scientography". *Current comments*, n. 43, pp. 324-335.
http://www.garfield.library.upenn.edu/essays/v9p324y1986.pdf

Garfield, Eugene; **Merton, Robert K.** (1979). "Citation indexing: Its theory and application in science, technology, and humanities". New York: Wiley. ISBN: 978 0 471025597

He, Qin (1999). "Knowledge discovery through co-word analysis". *Library trends*, v. 48, n. 1, pp. 133-159.
https://www.ideals.illinois.edu/bitstream/handle/2142/8267/librarytrendsv48i1i_opt.pdf

Hirsch, Jorge E. (2005). "An index to quantify an individual's scientific research output". *Proceedings of the National academy of Sciences*, v. 102, n. 46, pp. 16569-16572.
https://doi.org/10.1073/pnas.0507655102

Hossain, Md-Mahbub (2020). "Current status of global research on novel coronavirus disease (Covid-19): A bibliometric analysis and knowledge mapping". *F1000 Research.*
https://doi.org/10.2139/ssrn.3547824

Lázaro-Rodríguez, Pedro; **Herrera-Viedma, Enrique** (2020). "Noticias sobre Covid-19 y 2019-nCoV en medios de comunicación de España: el papel de los medios digitales en tiempos de confinamiento". *El profesional de la información*, v. 29, n. 3, e290302.
https://doi.org/10.3145/epi.2020.may.02

López-Robles, José-Ricardo; **Guallar, Javier**; **Otegi-Olaso, José-Ramón**; **Gamboa-Rosales, Nadia-Karina** (2019a). "El profesional de la información (EPI): bibliometric and thematic analysis (2006-2017)". *El profesional de la información*, v. 28, n. 4, e280417.
https://doi.org/10.3145/epi.2019.jul.17

López-Robles, José-Ricardo; **Otegi-Olaso, Jose-Ramón**; **Porto-Gómez, Igone**; **Cobo, Manuel-Jesús** (2019b). "30 years of intelligence models in management and business: A bibliometric review". *International journal of information management*, v. 48, pp. 22-38.
https://doi.org/10.1016/j.ijinfomgt.2019.01.013

López-Robles, José-Ricardo; **Otegi-Olaso, José-Ramón**; **Porto-Gómez, Igone**; **Gamboa-Rosales, Hamurabi**; **Gamboa-Rosales, Nadia-Karina** (2020). "Understanding the intellectual structure and evolution of competitive intelligence: A bibliometric analysis from 1984 to 2017". *Technology analysis & strategic management*, v. 32, n. 5, pp. 604-619.
https://doi.org/10.1080/09537325.2019.1686136

Martínez, Miguel-Ángel; **Cobo, Manuel-Jesús**; **Herrera, Manuel**; **Herrera-Viedma, Enrique** (2015). "Analyzing the scientific evolution of social work using science mapping". *Research on social work practice*, v. 25, n. 2, pp. 257-277.
https://doi.org/10.1177/1049731514522101

Martínez, Miguel-Ángel; **Herrera, Manuel**; **López-Gijón, Javier**; **Herrera-Viedma, Enrique** (2014). "H-Classics: Characterizing the concept of citation classics through H-index". *Scientometrics*, v. 98, n. 3, pp. 1971-1983.
https://doi.org/10.1007/s11192-013-1155-9

Moed, Henk F. (2009). "New developments in the use of citation analysis in research evaluation". *Archivum immunologiae et therapiae experimentalis*, v. 57, 13.
https://doi.org/10.1007/s00005-009-0001-5

Moed, Henk F.; **De-Bruin, R. E.**; **Van-Leeuwen, Thed** (1995). "New bibliometric tools for the assessment of national research performance: Database description, overview of indicators and first applications". *Scientometrics*, v. 33, n. 3, pp. 381-422.
https://doi.org/10.1007/BF02017338

Moral-Muñoz, José A; **Herrera-Viedma, Enrique**; **Santisteban-Espejo, Antonio**; **Cobo, Manuel-Jesús** (2020). "Software tools for conducting bibliometric analysis in science: An up-to-date review". *El profesional de la información* v. 29, n. 1, e290103.
https://doi.org/10.3145/epi.2020.ene.03

Pérez-Dasilva, Jesús-Ángel; **Meso-Ayerdi, Koldobika**; **Mendiguren-Galdospín, Terese** (2020). "Fake news y coronavirus: detección de los principales actores y tendencias a través del análisis de las conversaciones en *Twitter*". *El profesional de la información*, v. 29, n. 3, e290308.
https://doi.org/10.3145/epi.2020.may.08

Rodríguez-Morales, Alfonso J.; **Cardona-Ospina, Jaime A.**; **Gutiérrez-Ocampo, Estefanía**; **Villamizar-Peña, Rhuvi**; **Holguin-Rivera, Yeimer**; **Escalera-Antezana, Juan-Pablo**; **Alvarado-Arnez, Lucia-Elena**; **Bonilla-Aldana, D. Katterine**; **Franco-Paredes, Carlos**; **Henao-Martínez, Andrés F.** (2020). "Clinical, laboratory and imaging features of Covid-19: A systematic review and meta-analysis". *Travel medicine and infectious disease*, v. 34, 101623.
https://doi.org/10.1016/j.tmaid.2020.101623

Sahin, Ahmet-Riza; **Erdogan, Aysegul**; **Agaoglu, Pelin-Mutlu**; **Dineri, Yeliz**; **Cakirci, Ahmet-Yusuf**; **Senel, Mahmut-Egemen**; **Okyay, Ramazan-Azim**; **Tasdogan, Ali-Muhittin** (2020). "2019 novel coronavirus (Covid-19) outbreak: a review of the current literature". *EJMO*, v. 4, n. 1, pp. 1-7.
https://dx.doi.org/10.14744/ejmo.2020.12220

Thelwall, Mike; **Thelwall, Saheeda** (2020). "Covid-19 tweeting in English: Gender differences". *El profesional de la información,* v. 29, n. 3, e290301.
https://doi.org/10.3145/epi.2020.may.01

Torres-Salinas, Daniel (2020). "Ritmo de crecimiento diario de la producción científica sobre Covid-19. Análisis en bases de datos y repositorios en acceso abierto". *El profesional de la información*, v. 29, n. 2, e290215.
https://doi.org/10.3145/epi.2020.mar.15

Wang, Jian (2013). "Citation time window choice for research impact evaluation". *Scientometrics*, v. 94, n. 3, pp. 851-872.
https://doi.org/10.1007/s11192-012-0775-9

WHO (2020). "Coronavirus disease 2019 (Covid-19)". *WHO Situation report*. *World Health Organization*, n. 72.
https://apps.who.int/iris/bitstream/handle/10665/331685/nCoVsitrep01Apr2020-eng.pdf