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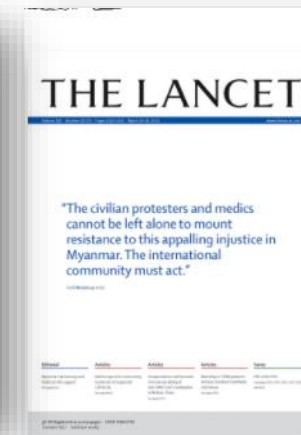
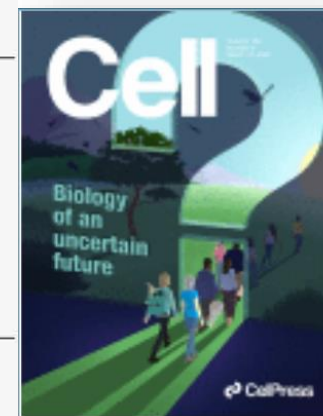
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# Main aim

- I don't know where to find literature
- I don't know what worth to read, too many articles
- I don't know how to read them effectively and summarize what I've read
- How to extract ideas for my study





Database use tips – make searching more efficiently by locking in the core content and big data tool for choosing research topic


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Measurement: Journal of the International Measurement Confederation

Volume 168, 15 January 2021, Article number 108335

## SARS-CoV, MERS-CoV and SARS-CoV-2: A Diagnostic Challenge (Article)

Ezhilan, M.<sup>a</sup>, Suresh, I.<sup>a</sup>, Nesakumar, N.<sup>b</sup>  

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Tamil Nadu 613401, India

### Abstract

The highly pathogenic MERS-CoV, SARS-CoV and SARS-CoV-2 cause acute respiratory syndrome and are often fatal. These new vi problems to global health in general and primarily to infection control and public health services. Accurate and selective assessme SARS-CoV and SARS-CoV-2 would assist in the effective diagnosis of infected individual, offer clinical guidance and aid in assessin outcomes. In this mini-review, we review the literature on various aspects, including the history and diversity of SARS-CoV-2, SAR: CoV, their detection methods in effective clinical diagnosis, clinical assessment of COVID-19, safety guidelines recommended by V Organization and legal regulations. This review article also deals with existing challenges and difficulties in the clinical diagnosis Developing alternative diagnostic platforms by spotting the shortcomings of the existing point-of-care diagnostic devices would preventing future outbreaks. © 2020 Elsevier Ltd

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### Comparison of NMR structural and dynamics features of the urea and guanidine-denatured states of GED

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#### ABSTRACT

Denatured states of proteins, the starting points as well as the intermediates of folding *in vivo*, play important roles in biological function. In this context, we describe here urea unfolding and characterization of the denatured state of GTPase effector domain (GED) of dynamin created by 8.7 M urea. These are compared with similar data for guanidine induced denaturation reported earlier. The unfolding characteristics in the two cases, as measured by the optical probes, are significantly different, urea unfolding proceeding via an intermediate. The structural and motional characteristics, determined by NMR, of the two denatured states are also strikingly different. The urea-denatured state shows a combination of  $\alpha$ - and  $\beta$ -preferences in contrast to the exclusively  $\beta$ -preferences in the guanidine-denatured state. Higher <sup>15</sup>N transverse relaxation rates suggest higher folding propensities in the urea-denatured state. The implications of these to GED folding are discussed. © 2020 Elsevier Inc. All rights reserved.

Denatured states of proteins are beginning to be recognized as important entities in the biological world—a denatured state of a protein is defined as the lowest energy ‘non-native’ state under a given set of conditions [1]. Inside a living cell, the environmental conditions like local intracellular ion concentrations, interaction with various ligands etc. can vary significantly from organelle to organelle [2], and even within the same organelle there can be variations due to signaling processes and interactions with different molecules. All these processes tightly regulate the translational and post-translational processes which decide the fate of the newly synthesized polypeptide chain. Thus a particular protein may see different environments which lead to different denatured states during the course of its function. Some of the denatured states may lead to soluble aggregates, which occasionally lead to diseases [3].

When a polypeptide chain begins to fold starting from a denatured ensemble, each molecule in the ensemble can, in-principle, fold along a different path. In this scenario, the starting state in terms of the conformational preferences across the polypeptide chain will have a significant influence on the path the molecule adopts; different denaturing environments inside a cell can create different initial states for the protein to fold from. If the chain already has some structure, that may form the nucleus for additional structure to build upon, and this will reduce the search options for the polypeptide chain in the multi-dimensional conformational space it may have to

be removed for a new structure to get formed for the protein to move towards the native state. Thus the number of folding paths for a given protein would be dictated by the number and nature of structural preferences across the length of the chain.

In view of all these, it is important to understand the characteristics of the various denatured states, with regard to their topologies, heterogeneities and motional characteristics, their modulations due to changes in environmental conditions, etc. at atomic level detail. *In vitro*, different denatured states can be created by use of different denaturants, such as, Gdn-HCl, urea, SDS, extreme pH conditions, etc. Although these may not exactly represent the denatured states, *in vivo*, they help sample the ensemble quite widely and thus allow investigation of the folding processes, in general.

In this background, we present here a comparative study of the structural and dynamics characteristics of urea-denatured and Gdn-HCl-denatured states of the GTPase effector domain (GED) of dynamin, a crucial protein in clathrin mediated endocytosis. GED plays important roles both in dynamin assembly around the neck of the clathrin coated vesicles, and assists the N-terminal GTPase domain in GTP hydrolysis required for dynamin function [4,5]. The recombinant form of GED has been shown to self-assemble and form large megadalton-sized oligomers *in vitro* [6,7] even at micro-molar concentrations. We first describe the global characteristics of urea-mediated unfolding of GED, as studied by optical

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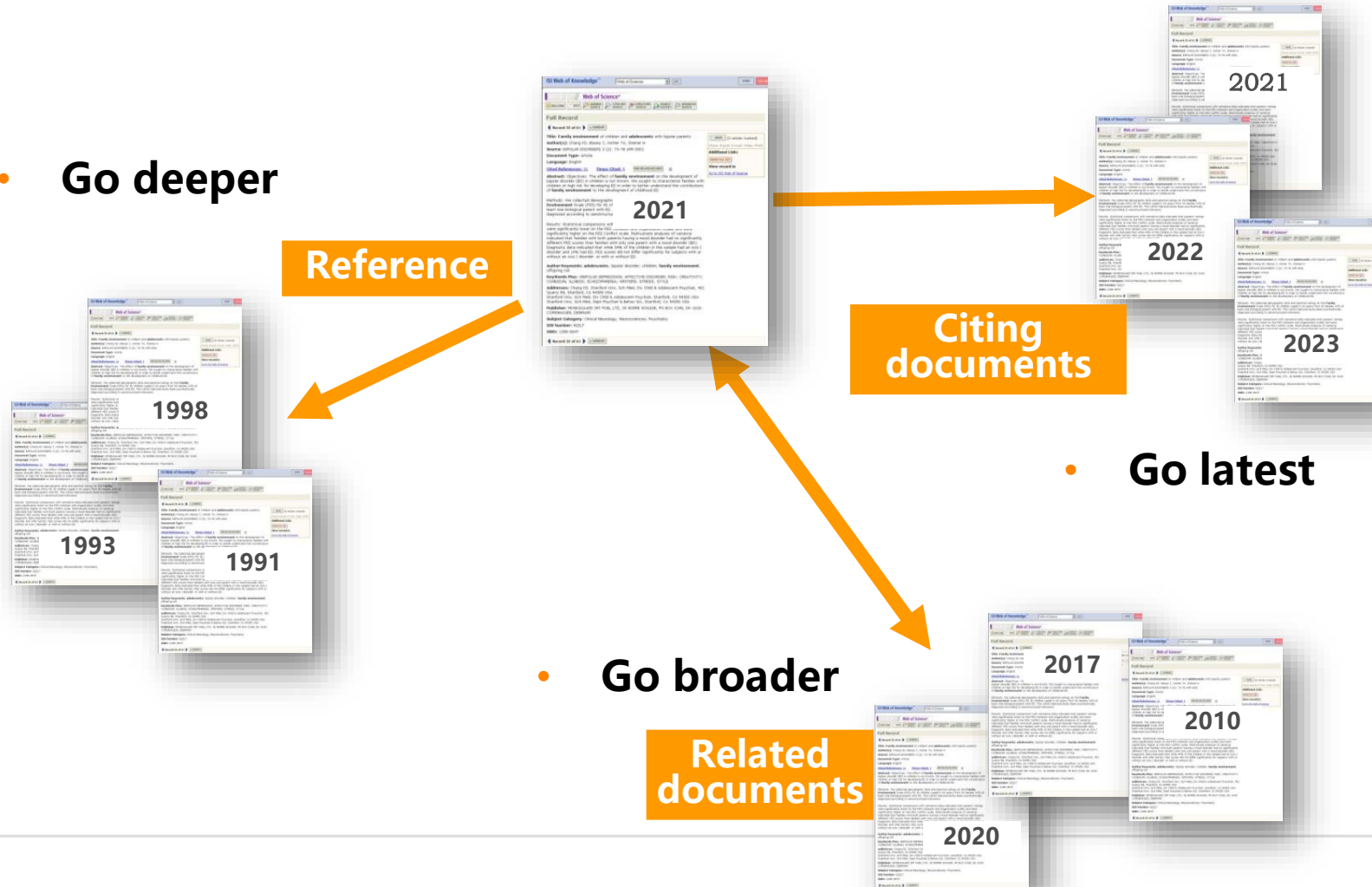


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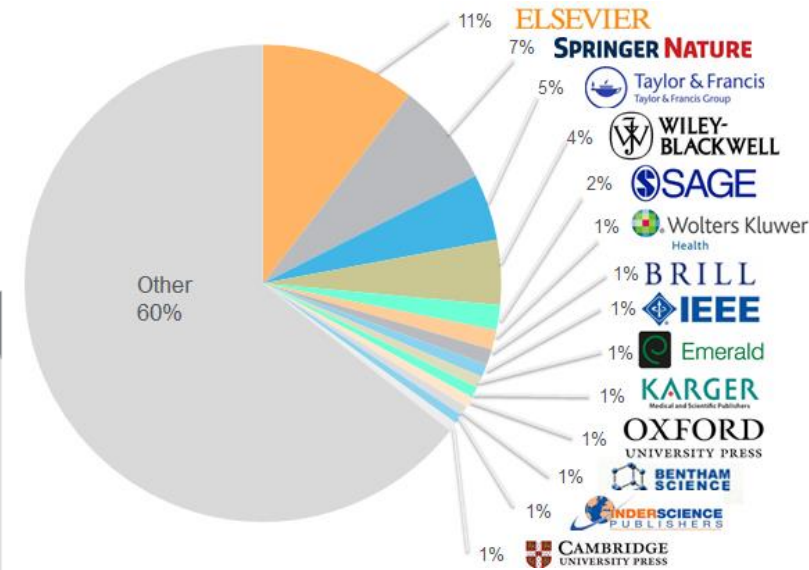
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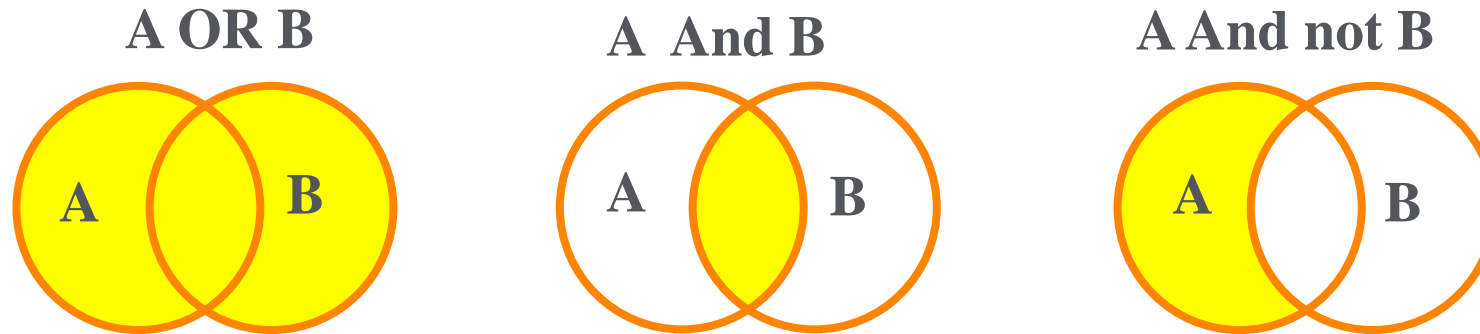
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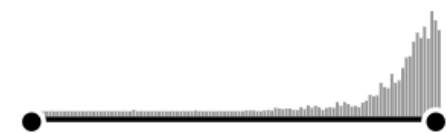
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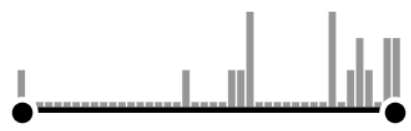
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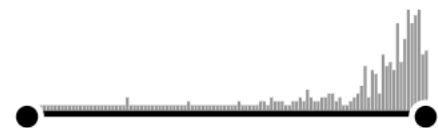
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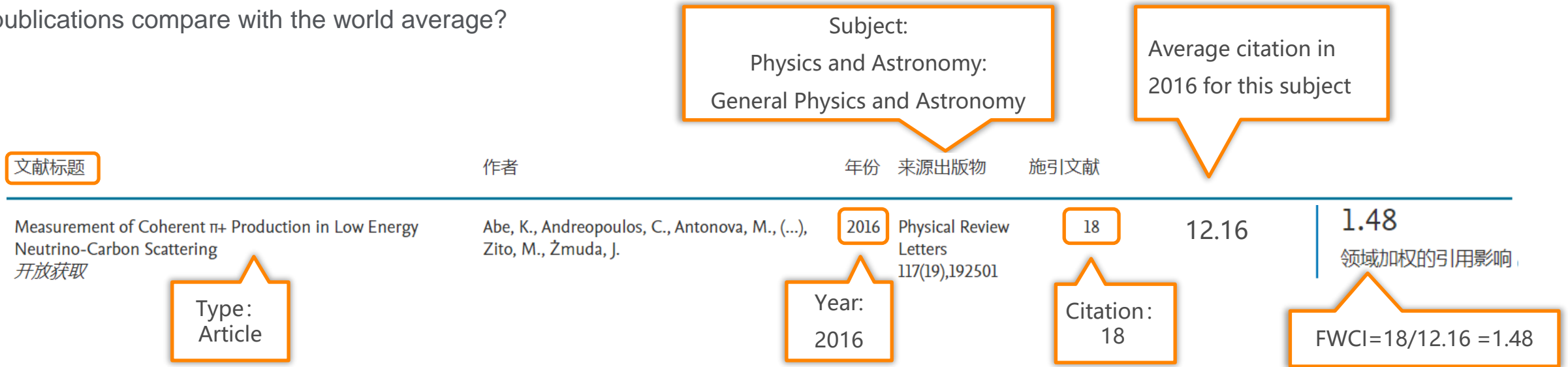
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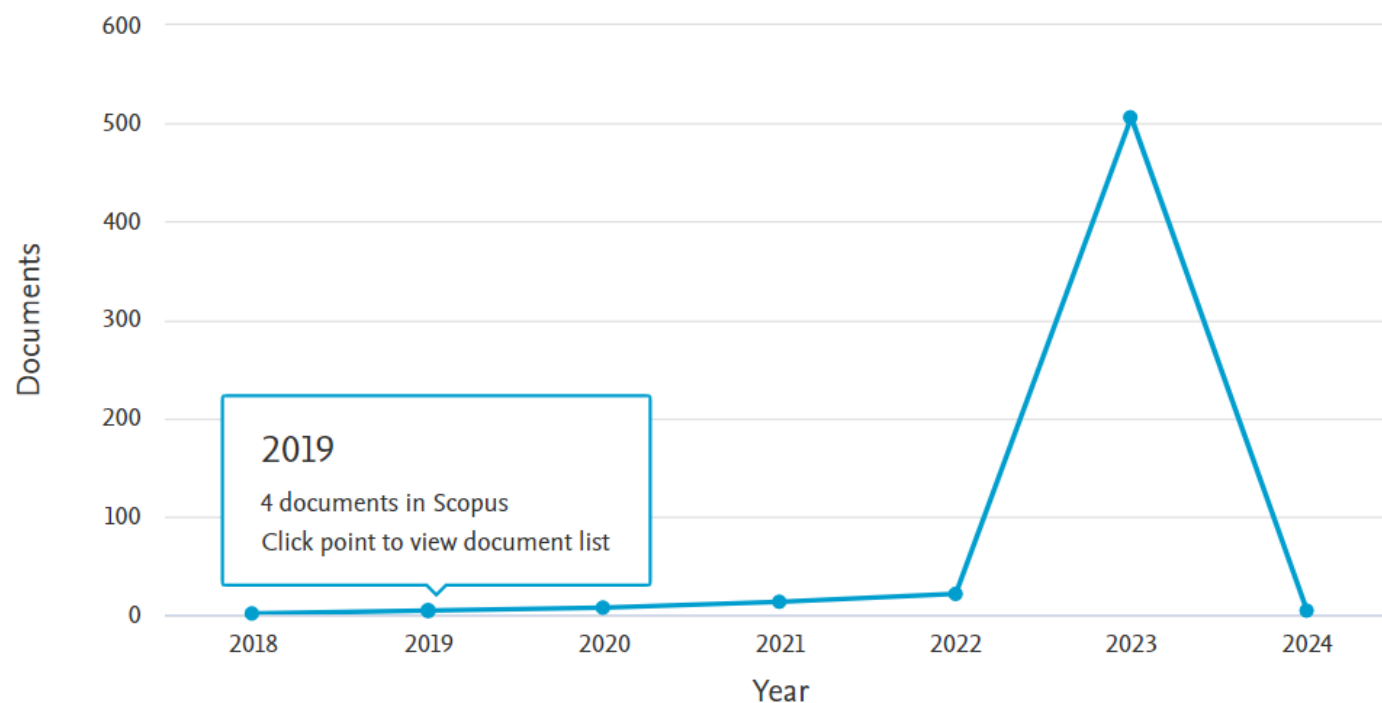
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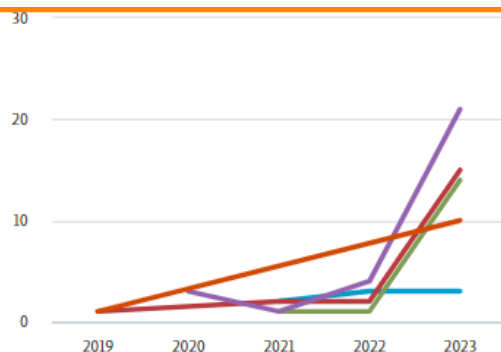
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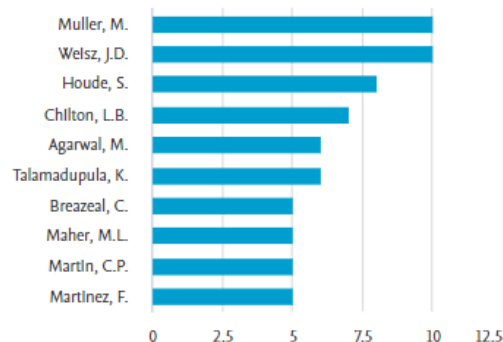
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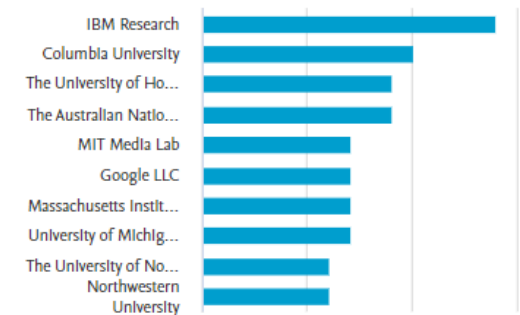
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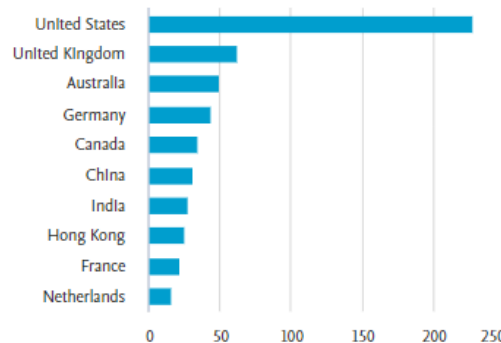
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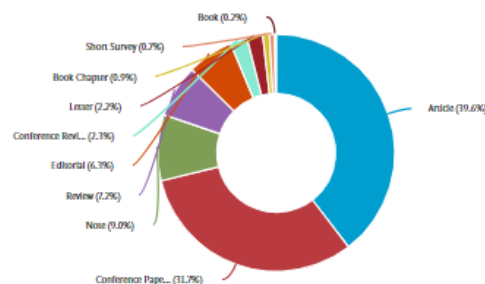
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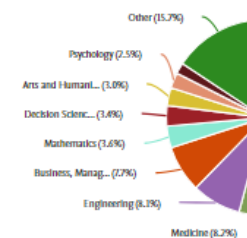
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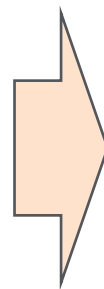
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