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朱苗 Wiley中国市场部

2021年11月10日

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大纲

1. **Wiley**高品质资源介绍
2. **Wiley Online Library**电子资源使用技巧
3. **Wiley**期刊论文发表准备与流程
4. **Wiley**新常态，新服务

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Wiley高品质资源
介绍

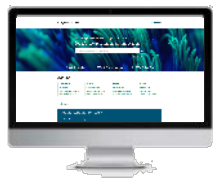


关于Wiley

- 创始于**1807**年，迄今已**210**年历史
- 服务于**1500**万研究人员和专业人士
- 与高校合作**222**个在线项目
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Wiley期刊影响力持续增长



近 **1,700** 种期刊



Impact factor: **508.702**
2020 JCR (Clarivate Analytics):
1/242 (Oncology)



1,281

种期刊被收录在2020JCR中



1,155

种期刊的影响因子均有所提高



在JCR的236种学科分类中,
Wiley期刊涵盖了其中的 **219** 种



219

种期刊在学科分类中排名前十



10,845,350

次引用Wiley的文章

613



学协会合作伙伴

*JCR is released annually and the 2020 report was published in June 2021



生命科学

- 350+ 期刊
- 50+ 开放获取期刊
- 130+ 学会协会合作伙伴
- 330+期刊被2020 JCR收录
- 3种期刊在2020 JCR所属学科分类中排名第一

Wiley在细胞和分子生物学领域的学科优势



35种期刊被
2020JCR收录



4种Wiley期刊在学科分类中排
名前十



40家学协会合作伙伴

- Wiley出版的细胞与分子生物学期刊，有30种期刊的影响因子在该学科类别中排名前五十，并且Wiley在相关的学科类别（例如细胞与组织工程，生物化学和蛋白质科学）中出版了超过100种期刊。
- Wiley在2020年发表了1900多篇文章，下载量达7000多万次。

主要的学协会及组织合作伙伴:

欧洲分子生物学组织 (EMBO)

欧洲生物化学学会联合会 (FEBS)

应用微生物学学会 (SfAM)

人类蛋白质组组织(Human Proteome Organization)

国际细胞计量学促进学会(International Society for Advancement of Cytometry)

纽约科学院(The New York Academy of Sciences)

蛋白质学会(The Protein Society)

生理学会(The Physiological Society)

国际细胞外囊泡学会(The International Society for Extracellular Vesicles).

特色期刊推荐

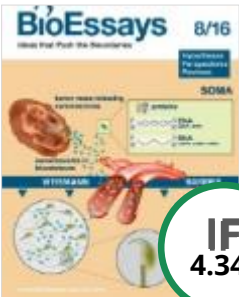
细胞分子生物学



Journal of Extracellular Vesicles
《细胞外囊泡期刊》

2020 JCR 排名:
7/195 细胞生物学

IF
25.841



BioEssays
《生物学论文集》

2020 JCR 排名:
22/93 生物化学与分子生物学

IF
4.345



Stem Cells
《干细胞》

2020 JCR 排名:
9/29 细胞与组织工程类

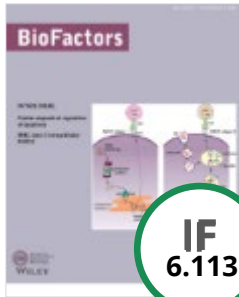
IF
6.277



FEBS Journal
《欧洲生化学会期刊》

2020 JCR 排名:
72/297 分子生物学类别

IF
5.542



BioFactors
《生物因子》

2020 JCR 排名:
64/297 生物化学与分子生物学

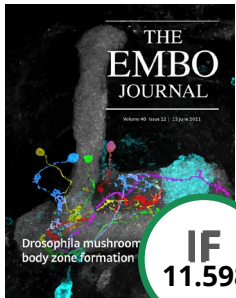
IF
6.113



Aging Cell
《老化细胞》

2020 JCR 排名:
4/53 细胞生物学

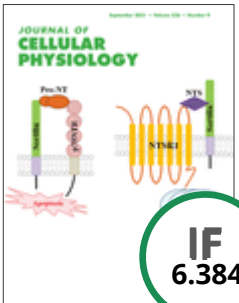
IF
9.304



The EMBO Journal
《欧洲分子生物学组织期刊》

2020 JCR 排名:
21/195 细胞生物学

IF
11.598



Journal of Cellular Physiology
《细胞生理学期刊》

2020 JCR 排名:
7/81 生物学

IF
6.384

Wiley在生态学、保护学与进化学领域的学科优势



40+种期刊被
2020JCR收录



11种Wiley期刊在学科分类中排
名前十



15家学协会合作伙伴

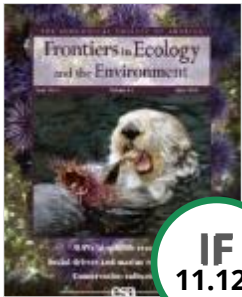
- 涵盖的领域包括：生物多样性保护、昆虫学、兽学和动物学。
- Wiley拥有在2020 JCR 的生物多样性保护的学科分类中前2名的期刊：Global Change Biology , Conservation Letters (金色OA期刊,与保护生物学协会合作出版)

主要的学协会合作伙伴包括:

美国生态学会(Ecological Society of America)
保护生物学协会(Society for Conservation Biology)
英国生态学会(British Ecological Society)
北欧生物学会(Nordic Society Oikos)
野生动物协会(The Wildlife Society)
国际植被科学协会(International Association for Vegetation Science)
日本草原科学学会(Japanese Society for Grassland Science)
日本生态学会(Ecological Society of Japan).

特色期刊推荐

生态学、保护学与进化生物学



Frontiers in Ecology and the Environment
《生态学与环境新领域》

2020 JCR排名:
4/166 生态学

IF
11.123



Methods in Ecology and Evolution
《生态学与进化方法》

2020 JCR排名:
7/178 生态学

IF
7.78



Global Change Biology
《全球变化生物学》

2020 JCR排名:
1/60 生物多样性保护类别

IF
10.863



Ecological Monographs
《生态学论丛》

2020 JCR排名:
6/166 生态学

IF
10.315



Journal of Applied Ecology
《应用生态学期刊》

2020 JCR排名:
4/60 生态学

IF
6.528



Ecology Letters
《生态学通讯》

2020 JCR排名:
8/166 生态学

IF
9.492



Conservation Letters
《自然保护通信》

2020 JCR排名:
2/60 生物多样性保护

IF
8.105



Molecular Ecology
《分子生态学》

2020 JCR排名:
7/50 进化生物学

IF
6.185



自然科学

- 超过32种期刊在JCR学科领域内排名前十
- 超过150家学协会合作伙伴
- 233种期刊被JCR收录
- 6种期刊在其所属JCR学科领域内排名第一

Wiley在化学领域的学科优势



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名前十



110家学协会合作伙伴

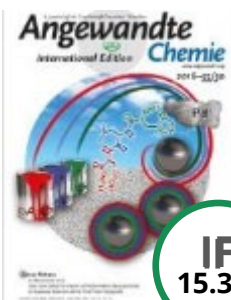
- Wiley与全球领先的化学学协会合作以发表最高质量的研究成果，在85个化学的细分领域中发表超26000篇文章。
- 23种学协会出版期刊

主要的学协会合作伙伴: SCI (化学工业协会), Société Chimique de France (法国化学会), ChemPubSoc Europe (欧洲化学会), Gesellschaft Deutscher Chemiker (德国化学会) .

亚太地区主要学协会合作伙伴: The Chemical Society of Japan (日本化学会), Chinese Chemical Society (中国化学会), Asian Chemical Editorial Society (亚洲化学编辑学会)

特色期刊推荐

化学



Angewandte Chemie International Edition 《应用化学国际版》

2020 JCR 排名:
2/178 多学科化学

IF
15.336



Wiley Interdisciplinary Reviews - Computational Molecular Science 《Wiley 跨学科评论:分子信息科学》

2020 JCR 排名:
6/178 多学科化学
1/58 数学与计算生物学

IF
25.113



Mass Spectrometry Reviews 《质谱学评论》

2020 JCR 排名:
1/43 光谱

IF
10.946



Medicinal Research Reviews 《医药研究评论》

2020 JCR 排名:
2/63 药物化学
7/275 药学与药理学

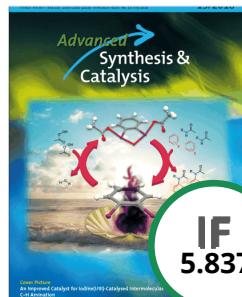
IF
12.944



ChemSusChem 《可持续发展化学》

2020 JCR 排名:
27/178 多学科化学
4/44 绿色和可持续科技

IF
8.929



Advanced Synthesis & Catalysis 《高级合成与催化》

2020 JCR 排名:
11/74 应用化学
7/57 有机化学

IF
5.837



Chemistry - A European Journal 《化学: 欧洲期刊》

2020 JCR 排名:
52/178 多学科化学

IF
5.236



ChemCatChem 《催化化学》

2020 JCR 排名:
50/162 物理化学

IF
5.686

Wiley在物理和材料领域的学科优势



38种期刊被
2020JCR收录



11种Wiley期刊在学科分类中排
名前十



5家学协会合作伙伴

- Wiley的物理和材料科学领域的内容涵盖能源、可持续性、工程、纳米科学、机器人科学、生物系统以及材料物理和聚合物等领域。
- Wiley有11本材料学期刊在2020 JCR材料学细分领域内排名前10。

重要学协会合作伙伴：美国陶瓷学会(American Ceramic Society).

特色期刊推荐

材料科学



Advanced Materials 《先进材料》

2020 JCR 排名:
5/178 材料科学, 多学科
3/106 纳米科学与纳米技术

IF
30.849



Advanced Energy Materials 《先进能源材料》

2020 JCR 排名:
10/333 材料科学, 多学科
5/114 能源与燃料

IF
29.368



Advanced Functional Materials 《先进功能材料》

2020 JCR 排名:
15/333 材料科学, 多学科
6/106 纳米科学与纳米技术

IF
18.808



Small 《Small期刊》

2020 JCR 排名:
24/333 材料科学, 多学科
12/106 纳米科学与纳米技术

IF
14.188



Advanced Healthcare Materials 《高级医用材料》

2020 JCR 排名:
4/40 材料科学, 生物材料

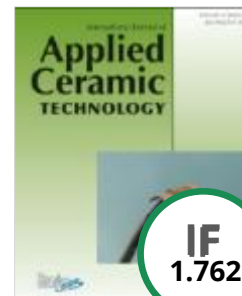
IF
9.933



Journal of the American Ceramic Society 《美国陶瓷学会会刊》

2020 JCR 排名:
4/29 材料科学, 陶瓷学

IF
3.784



International Journal of Applied Ceramic Technology 《国际应用陶瓷技术期刊》

2020 JCR 排名:
11/29 材料科学, 陶瓷学

IF
1.762



International Journal of Applied Glass Science 《国际应用玻璃科学期刊》

2020 JCR 排名:
10/29 材料科学, 陶瓷学

IF
1.917

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按照不同学科浏览相关内容（最全的多学科在线资源平台之一，包含17个学科大类，126个子学科）

Subjects	
Agriculture, Aquaculture & Food Science	▼
Architecture & Planning	▼
Art & Applied	▼
Business, Economics, Finance & Accounting	▼
Chemistry	▼
Computer Science & Information Technology	▼
Earth, Space & Environmental Sciences	▼
Humanities	▼
Law & Criminology	▼
Life Sciences	▼
Mathematics & Statistics	▼
Medicine	▼
Nursing, Dentistry & Healthcare	▼
Physical Sciences & Engineering	▼
Psychology	▼
Social & Behavioral Sciences	▼
Veterinary Medicine	▼

Physical Sciences & Engineering		^
Astronomy	Materials Science	
Biomedical Engineering	Mechanical Engineering	
Civil Engineering & Construction	Nanotechnology	
Electrical & Electronics Engineering	Physics	
Energy	Polymer Science & Technology	
Industrial Engineering	Security Management	

按照学科了解高影响力及最新研究进展情况

Wiley Online Library

Search

SUBJECT

Materials Science

查看该学科下相关主题

Topics

Analysis/Characterization of Nanosystems

Batteries & Fuel Cells

Biomaterials

Biopolymers

Carbon Materials

Ceramics

Composites

Condensed Matter

Construction Materials

Construction Materials

Corrosion

Crystallography

Dental Technology & Materials Science

Electronic Materials

Electronic Materials

Failure Fracture

General & Introductory Materials Science

Inorganic Electronics

Joining, Welding and Adhesion

Magnetic Materials

Magnetism

Materials for Energy Systems

Materials Characterization

Materials Processing

Materials Science Special Topics

Metals & Alloys

Optical & Non-Linear Optical Materials

Optics & Photonics

Organic Electronics

Photonics & Lasers

Polymer processing

Polymer Characterization

Polymer Physics

Polymer Science & Technology General

Polymer Synthesis

Polymers Special Topics

Porous Materials

Properties of Materials

Semiconductor Physics

Sensor Materials

Soft Matter

Solid State Physics

Theory, Modeling & Simulation

Thin Films, Surfaces & Interfaces

Articles

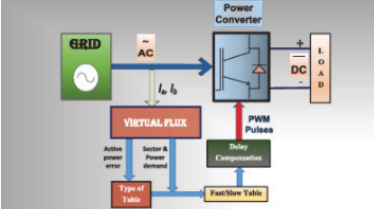
高被引文下章 (Most Cited)

最新发表的文章 (Most Recent)

An advanced virtual flux integrated multifold table-based direct power control with delay compensation for active front-end rectifiers

Abinash Rath, Gopalakrishna Srungavarapu, Monalisa Pattnaik

International Transactions on Electrical Energy Systems | First Published: 7 November 2021



Here, an advanced virtual flux technology is used to avoid the time differential operations. Different lookup tables are used as per the demand, which are designed based upon the normalized values of active and reactive power slopes. This work provides restitution for the unavoidable inaccuracy caused by this control delay in conventional DPC techniques.

Abstract | Full text | PDF | References | Request permissions

Reliability analysis of an active distribution network integrated with solar, wind and tidal energy sources

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Joining, Welding and Adhesion

Magnetic Materials

Magnetism

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Materials Characterization

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Polymer Characterization

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Polymer Science & Technology General

Polymer Synthesis

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Sensor Materials

Soft Matter

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Theory, Modeling & Simulation

Thin Films, Surfaces & Interfaces

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Journals X

Filters

Subjects ^

BIOMEDICAL ENGINEERING 7

CHEMISTRY 3

LIFE SCIENCES 3

MATERIALS SCIENCE 5

MEDICAL SCIENCE 2

MORE (1) ^

Published in ^

Advanced Biology 2

Advanced Healthcare Materials 1

Advanced NanoBiomed Research 1

ChemNanoMat 1

Peptide Science 1

Small Methods 1

LESS ^

Author v

7 results for "Biomaterials" anywhere

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Publications (7)

Refine Search v

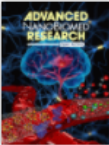
Sorted by: Relevance v



Journal

ChemNanoMat

Volume 1, 2015 - Volume 7, 2021



Journal  Open Access

Advanced NanoBiomed Research

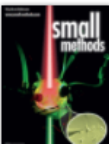
Volume 1, 2021 - Volume 1, 2021



Journal

Advanced Healthcare Materials

Volume 1, 2012 - Volume 10, 2021



Journal

Small Methods

Volume 1, 2017 - Volume 5, 2021

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一般检索—按条件筛选检索结果

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MOFS

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34,665 results for "MOFS" anywhere

检索数量

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Articles & Chapters (34,665)

Collections (233)

Filters

对检索结果筛选

Publication Type ^

Journals32,407

Books1,949

Reference works309

Publication Date ^

Last Week157

Last Month591

Last 3 Months1,711

Last 6 Months3,284

Last 2 Years12,134

MORE (2) v

Refine Search v

Sorted by: Relevance v

可以按照相关性，出版日期排列

Export Citation(s)Download PDF(s)

Review

MOFs-Derived Carbon-Based Metal Catalysts for Energy-Related Electrocatalysis

Tongzhou Wang, Xuejie Cao, Lifang Jiao

Small | Volume 17, Issue 22

First published: 18 January 2021

Collections: Emerging Crystalline Porous Materials

Abstract v

Forschungsartikel

一般检索—按条件筛选检索结果

Filters

Publication Type ^

出版类型

Journals32,407

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+ ACCOUNTING120

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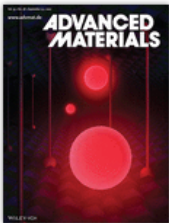
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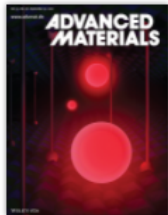
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Flexible electronics have gained considerable attention for application in wearable devices. Organic transistors are potential candidates to develop flexible integrated circuits (ICs). A primary technique for maximizing their reliability, gain, and operation speed is the modulation of charge-carrier behavior in the respective transistors fabricated on the same substrate. In this work, heterogeneous functional dielectric patterns (HFDP) of ultrathin polymer gate dielectrics of poly($\pm$)endo,exo-bicyclo[2.2.1]hept-ene-2,3-dicarboxylic acid, diphenylester (PNDPE) are introduced. The HFDP that are obtained via the photo-Fries rearrangement by ultraviolet radiation in the homogeneous PNDPE provide a functional area for charge-carrier modulation. This leads to programmable threshold voltage control over a wide range (-1.5 to $+0.2$ V) in the transistors with a high patterning resolution, at 2 V operational voltage. The transistors also exhibit high operational stability over 140 days and under the bias-stress duration of 1800 s. With the HFDP, the performance metrics of ICs, for example, the noise margin and gain of the zero- V_{GS} load inverters and the oscillation frequency of ring oscillators are improved to 80%, 1200, and 2.5 kHz, respectively, which are the highest among the previously reported zero- V_{GS} -based organic circuits. The HFDP can be applied to much complex and ultraflexible ICs



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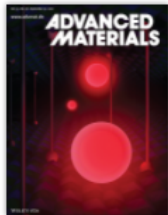
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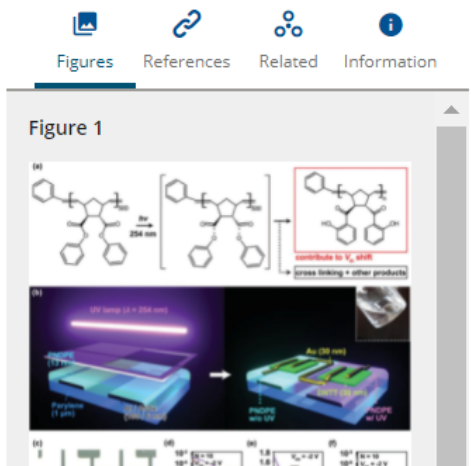
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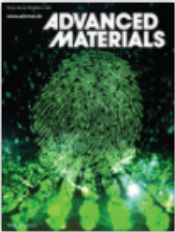
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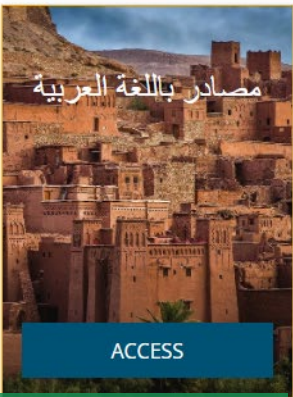
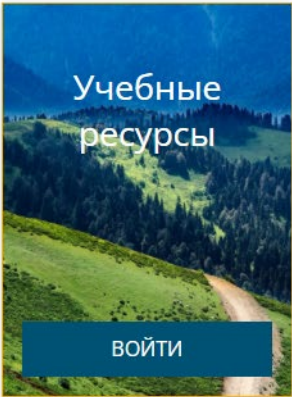
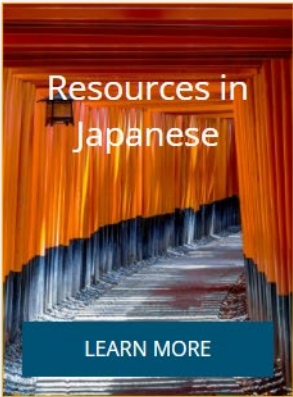
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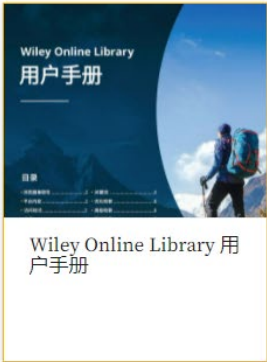
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RESEARCH ARTICLE

The 2019-new coronavirus epidemic: Evidence for virus evolution

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Silvia Angeletti⁴ | Massimo Ciccozzi²

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Abstract

There is a worldwide concern about the new coronavirus 2019-nCoV as a global public health threat. In this article, we provide a preliminary evolutionary and molecular epidemiological analysis of this new virus. A phylogenetic tree has been built using the 15 available whole genome sequences of 2019-nCoV, 12 whole genome sequences of 2019-nCoV, and 12 highly similar whole genome sequences available in gene bank (five from the severe acute respiratory syndrome, two from Middle East respiratory syndrome, and five from bat SARS-like coronavirus). Fast unconstrained Bayesian approximation analysis shows that the nucleocapsid and the spike glycoprotein have some sites under positive pressure, whereas homology modeling revealed some molecular and structural differences between the viruses. The phylogenetic tree showed that 2019-nCoV significantly clustered with bat SARS-like coronavirus sequence isolated in 2015, whereas structural analysis revealed mutation in Spike Glycoprotein and nucleocapsid protein. From these results, the new 2019-nCoV is distinct from SARS virus, probably transmitted from bats after mutation conferring ability to infect humans.

KEYWORDS

coronavirus, epidemiology, macromolecular design, SARS coronavirus

1 | INTRODUCTION

The family Coronaviridae comprises a group of large, single, plus-stranded RNA viruses isolated from several species, and it is previously known to cause the common cold and diarrheal illnesses in humans.^{1,2} In 2003, a new coronavirus (severe acute respiratory syndrome coronavirus [SARS-CoV]) was associated with the SARS outbreak.^{1,2} Recently, a new coronavirus (2019-nCoV) has emerged in the region of Wuhan (China) as a cause of severe respiratory infection in humans. Since December 2019, different cases of pneumonia of unknown origin associated with permanence at the Wuhan market in China have been reported.^{3,4} A new coronavirus, named 2019-nCoV, belonging to the Orthocoronavirinae subfamily, distinct

from MERS-CoV and SARS-CoV, was described.⁵ To date, a total of 1975 pneumonia cases have been confirmed in China (the State Council Information Office in Beijing, capital of China, 26 January 2020).^{5,7} Animal to human transmission is considered the origin of epidemics, as many patients declared to have visited a local fish and wild animal market in Wuhan in November. Quite recently, evidence has been gathered for the animal to the human and interhuman transmission of the virus.^{7,8}

Although prompt diagnosis and patient isolation are the hallmarks for initial control of this new epidemic, molecular epidemiology, evolutionary models, and phylogenetic analysis can help estimate genetic variability and the evolutionary rate, which in turn have important implications for disease progression as

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well as for drug and vaccine development. In this short report, we provide a phylogenetic tree of the 2019-nCoV and identify sites of positive or negative selection pressure in distinct regions of the virus.

2 | MATERIAL AND METHODS

The complete genomes of 15 2019-nCoV sequences have been downloaded from GISAID (<https://www.gisaid.org/>) and GenBank (<http://www.ncbi.nlm.nih.gov/genbank/>). A dataset has been built using five highly similar sequences for SARS, two sequences for the Middle East respiratory syndrome (MERS), and five highly similar sequences for bat SARS-like coronavirus. The percentage of similarity has been identified using a basic local alignment search tool (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>); eventually duplicated sequences have been excluded from the datasets. The dataset including 27 sequences has been aligned using multiple sequence alignment online tool⁹ and manually edited using BioEdit program v7.0.5.¹⁰

Maximum likelihood (ML) methods were employed for the analyses because they allow for testing different phylogenetic hypotheses by calculating the probability of a given model of evolution generating the observed data and by comparing the probabilities of nested models by the likelihood ratio test. The best-fitting nucleotide substitution model was chosen by jModeltest software.¹¹ ML tree was reconstructed using generalized time-reversible plus gamma distribution and invariant sites (+G+I) as an evolutionary model using MEGA-X.¹²

The adaptive evolution server (<http://www.datamonkey.org/>) was used to find eventual sites of positive or negative selection. For this purpose, the following test has been used: fast unconstrained Bayesian approximation (FUBAR).¹³ This test allowed us to infer the site-specific pervasive selection, the episodic diversifying selection across the region of interest, and to identify episodic selection at individual sites.¹⁴ The statistically significant positive or negative selection was based on P value less than .05.¹⁴

Homology models have been built relying on the website SwissModel.¹⁵ Structural templates have been searched and validated using the software available within the SwissModel environment and HHPred.¹⁶ Homology models have been validated using the QMEAN tool.¹⁷ Three-dimensional structures have been analyzed and displayed using PyMOL.¹⁸ To map the structural variability of the N, E, S, and M regions of the virus and their sites under selection pressure, homology modeling has been applied to the sequence of 2019-nCoV.

3 | RESULTS

The ML phylogenetic tree, performed on whole genome sequences, is represented in Figure 1. In the tree, MERS virus sequences formed a distinct clade (clade I) from Bat SARS-like coronavirus, SARS virus, and the 2019-nCoV clustering together in clade II. This clade includes

4 | DISCUSSION

The data reported above show that the new 2019-nCoV significantly clustered with a sequence from the bat SARS-like coronavirus isolated in 2015. Moreover, in the phylogenetic tree, these two sequences are separated from the other bat SARS-like coronavirus sequences, suggesting that this bat SARS-like coronavirus is homologous and genetically more similar to the 2019-nCoV than to the other sequences of Bat SARS-like coronavirus. This supports the hypothesis that the transmission chain began from the bat and reached the human. All other genomic sequences represented in the phylogenetic tree, also including SARS and MERS coronavirus, clustered separately, thus excluding the fact that the virus involved in the actual epidemic could belong to these subgenus. The structural analysis of two important viral proteins, the nucleocapsid and the spike-like nucleoprotein (protein S), confirmed the significant similarity of the new coronavirus with the bat-like SARS coronavirus and its difference from SARS coronavirus.

From the selective pressure and structural analysis, mutations of surface proteins, as the spike protein S, and of nucleocapsid N protein conferring stability to the viral particle have been shown. The viral spike protein is responsible for virus entry into the cell after binding to a cell receptor and membrane fusion, two key steps in viral infection and pathogenesis. The N protein is a structural protein involved in virion assembly, playing a pivotal role in virus transcription and assembly efficiency. Mutation of these proteins could determine two important characteristics of the coronavirus isolated during the 2019-nCoV epidemic: a higher ability to infect and enhanced pathogenicity than the bat-like SARS coronavirus but lower pathogenicity than SARS coronavirus. These features can explain the 2019-nCoV zoonotic transmission and its initial lower severity than SARS epidemic. These results do not exclude the fact that further mutation due to positive selective pressure could lead to a more severe disease. The region could be highly conserved.

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Silvia Angeletti and Massimo Ciccozzi contributed equally to this study.

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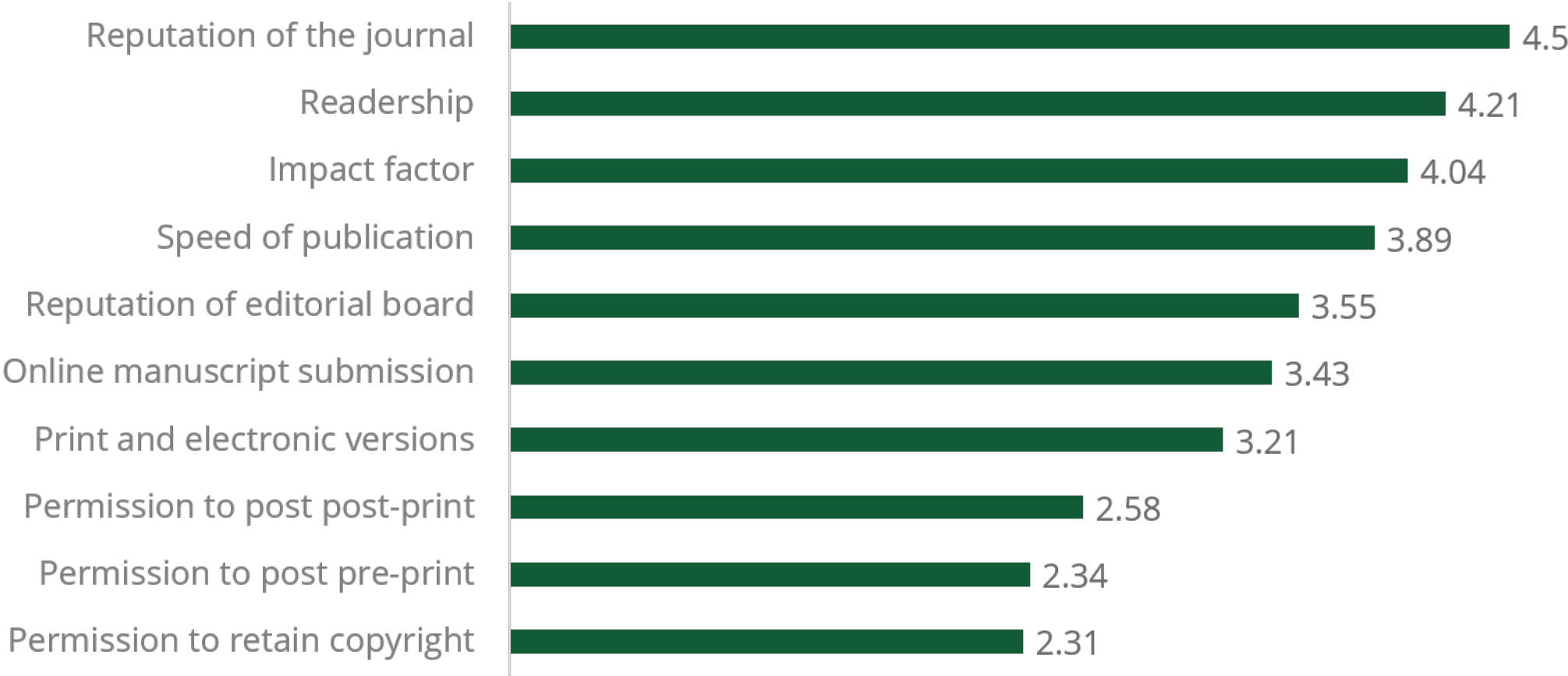
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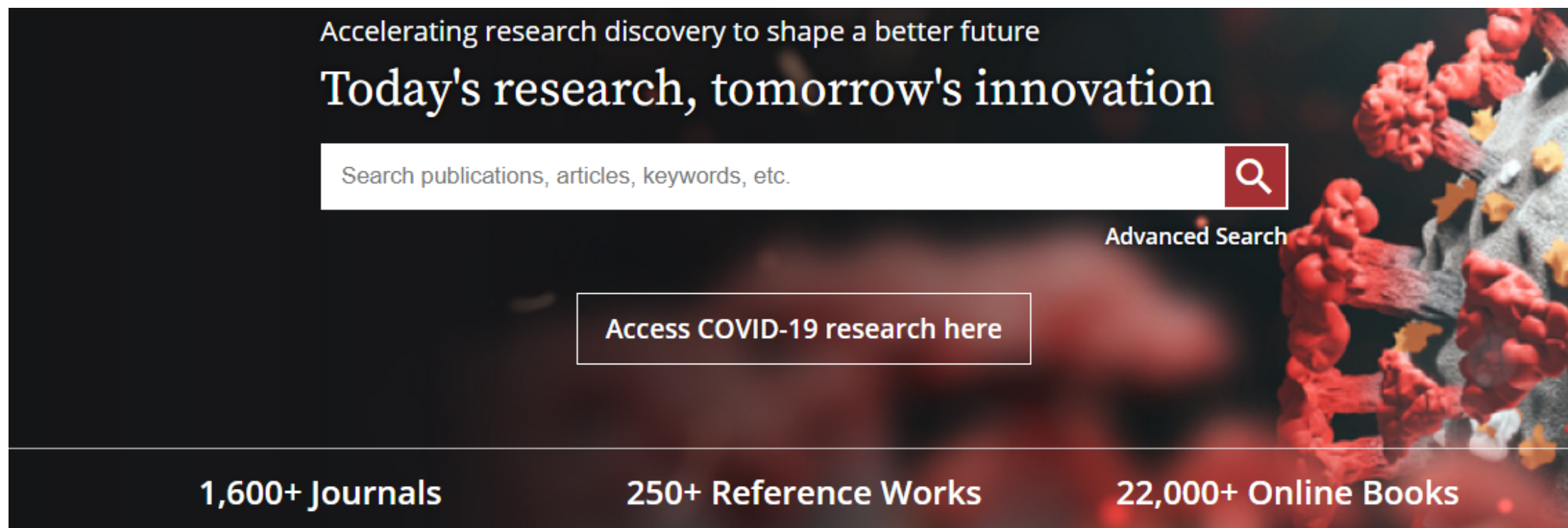
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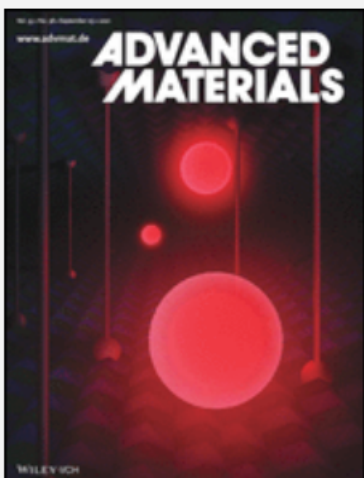
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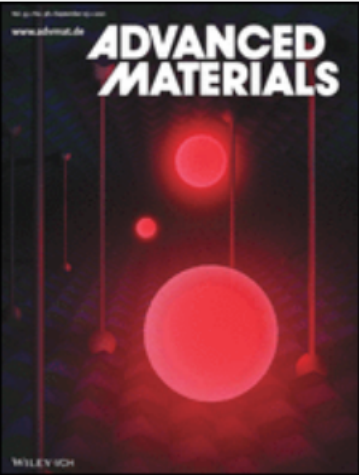
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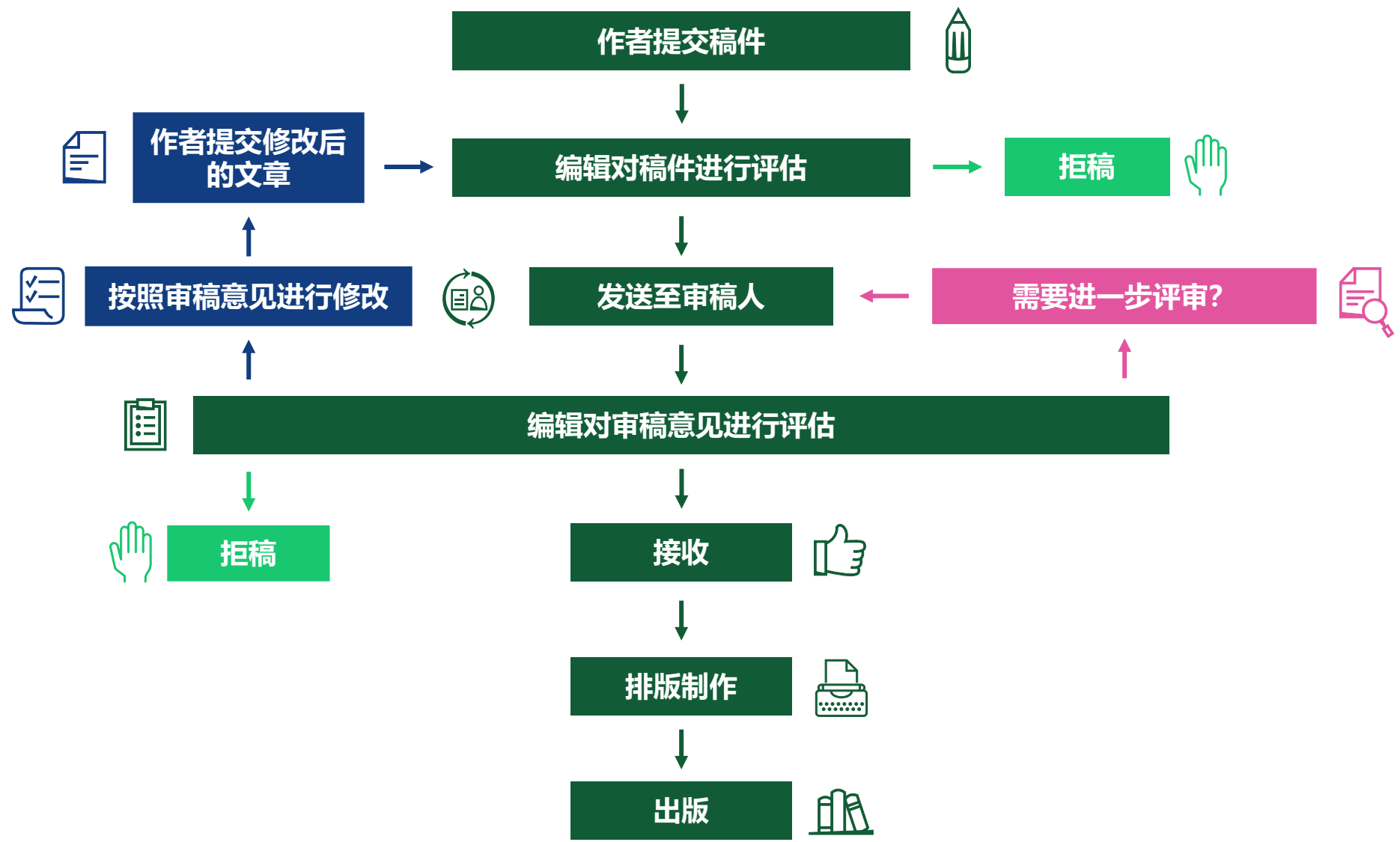
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