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Web of Science - discovery and citation analysis tool.

Introduction to platform

Marcin Kapczyński Solutions Specialists and Customer Education 20.04.2020

Web of Science Data Difference - Selectivity, Structure and Certainty

Platform Breadth & Depth: 155M Records | 34K Journals | 1.6B Cited References | Backfiles 1864 | 80M Patents | 7.3M Data Sets Highly Curated Core Collection: 21K Journals | 1.3B Cited References | Backfiles 1900 | 12.5M Funding data | 254 Subject Categories



Group

Save Time, Build Reputation

Less data wrangling by using Web of Science's clean, structured data for research and analysis. Build reputation, prepare citation reports and complete historical bibliographies for grant proposals and tenure reviews. Find global collaborators, publishers, and funders.

Empower Researchers, Increase Access

Access a range of indicators to assess collection needs. Better understand important trends and breakthroughs to support institutional research demands and lead OA awareness and discovery.

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Review a range of indicators of comparative journal guality, set in the context of their field and region to find expansion opportunities. Find peer reviewers and potential authors and editors to drive publishing aims.

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At the heart of the *Web of Science* platform





WoS Core Collection Dataset

Objective, Complete and Optimal Coverage



- 21,000+ journals indexed cover-to-cover
- Multidisciplinary
 - International
- Influential



Careful and objective journal selection performed by a dedicated editorial team that is independent from any commercial or publishing activities

N	/eb of Science
Web	of Science Core Collection: Citation Indexes
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100% with cited references (1.48 Billion) provide industry leading metadata to power your discovery and analytics

II:

Editorial Quality Curate the content

Metrics begin with selected, trusted, valuable content.

Curation means successfully maintaining a collection of high-quality content.

Adding new journals and removing problem journals are the result of applying the same criteria.

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1. Initial Triage	2. Editorial Triage		3. Editorial Evaluation
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Buchman, A.; Akbari, O. S. Site-specific transgenesis of the Drosophila melanogaster Y-chromosome using CRISPR/Cas9. INSECT MOLECULAR BIOLOGY (2019)

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RESEARCH ARTICLE

A Programmable Dual-RNA–Guided **DNA Endonuclease in Adaptive Bacterial Immunity**

Martin Jinek,^{3,2}* Krzysztof Chylinski,^{3,4}* Ines Fonfara,⁴ Michael Hauer,²† Jennifer A. Doudna,^{1,2,5,4}‡ Emmanuelle Charpentier⁴‡

Clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated (Cas) systems protein deri provide bacteria and archaea with adaptive immunity against viruses and plasmids by using CRISPR RNAs (crRNAs) to guide the silencing of invading nucleic acids. We show here that in a subset of these systems, the mature crRNA that is base-paired to trans-activating crRNA (tracrRNA) mid DNA o forms a two-RNA structure that directs the CRISPR-associated protein Cas9 to introduce a protospac double-stranded (ds) breaks in target DNA. At sites complementary to the crRNA-guide sequence, ture crRNA. the Cas9 HNH nuclease domain cleaves the complementary strand, whereas the Cas9 RuvC-like domain cleaves the noncomplementary strand. The dual-tracrRNA:crRNA, when engineered as a Car9-catalyz single RNA chimera, also directs sequence-specific Cas9 dsDNA cleavage. Our study reveals a family of endonucleases that use dual-RNAs for site-specific DNA cleavage and highlights the potential to exploit the system for RNA-programmable genome editing.

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MECHANICAL SYSTEMS AND SIGNAL PROCESSING Volume: 120 Pages: 180-202 DOI: 10.1016/j.ymssp.2018.10.021 Published: APR 1 2019 Document Type: Article View Journal Impact

Abstract

In recent years, the development of long-term structural health monitoring systems for preventive conservation of historic monumental buildings is receiving a growing trend of scientific interest. Nevertheless, the damage detection effectiveness of these systems is still debated, especially in respect to complex masonry palaces where both local and global failure mechanisms can be activated, whereby the majority of the documented successful applications are limited to masonry towers. In particular, one major issue that needs to be solved in order to derive damage sensitive features is associated to the removal of the effects of changes in environmental conditions and, primarily, of ambient temperature, from static and dynamic signatures. This paper aims to contribute to improving knowledge in this field, by investigating temperature effects on static and dynamic response of an iconic Italian monumental palace: the Consoli Palace in Gubbio. With the purpose of early detecting earthquake-induced damages, as well as damages caused by material degradation associated to awkward environmental conditions, a simple low-cost mixed static and dynamic long-term structural health monitoring system has been installed on the Palace by the authors in July 2017. After discussing surveys, ambient vibration tests, diagnostic investigations, numerical modeling and model calibration of the Palace, the analysis of the first year of monitoring data is presented. This analysis shows that, differently from what observed in other literature works on historic masonry towers, the natural frequencies of the Palace show a marked and sometimes non-linear decreasing trend with increasing ambient temperature, that can be effectively removed through linear statistical filtering provided that dynamic regression models, using past values of predictors, are used. On the other side, the evolution of the amplitudes of two major cracks monitored within the building also shows a marked



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Funding Agency	Grant Number			
European Union	LSHB-CT2007-037740			
Deutsche Forschungsgemeinschaft	1175			
Bundesministerium fur Bildung und Forschung BioChance Plus	0313827			

Close funding text

We thank F. Julicher, G. Feigenson, J. Howard, P. Schwille, C. Brangwynne, H.-T. He, G. van Meer, and members of the Simons lab for critical reading of this paper. A special thank you goes to M. Surma, M. Gerl, and I. Levental for their construction of and contribution to the figures. This work was supported by European Union FP6 Lipid PRISM grant no. LSHB-CT2007-037740, Deutsche Forschungsgemeinschaft Schwerpunktprogramm 1175, and Bundesministerium fur Bildung und Forschung BioChance Plus grant no. 0313827.

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- Web of Science captures authors acknowledgments and funding acknowledgement data from all titles in the Core Collection from August 2008 forwards.
- Research administrators can use this data to develop a reliable understanding of funding trends and opportunities.

Funding

Funding Agency	Grant Number
European Union	LSHB-CT2007-037740
Deutsche Forschungsgemeinschaft	1175
Bundesministerium fur Bildung und Forschung BioChance Plus	0313827

Close funding text

We thank F. Julicher, G. Feigenson, J. Howard, P. Schwille, C. Brangwynne, H.-T. He, G. van Meer, and members of the Simons lab for critical reading of this paper. A special thank you goes to M. Surma, M. Gerl, and I. Levental for their construction of and contribution to the figures. This work was supported by European Union FP6 Lipid PRISM grant no. LSHB-CT2007-037740, Deutsche Forschungsgemeinschaft Schwerpunktprogramm 1175, and Bundesministerium fur Bildung und Forschung BioChance Plus grant no. 0313827.

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- The algorithm that assigns the preferred funding name was developed based on the existing InCites funding agency unification
- The data is searchable (<u>http://images.webofknowledge.com/WOKRS533JR18/help/WOS/hs_funding_agency.html</u>)
- Currently, we have approximately 1,100 preferred funder names that appear in 1,9M WOS Core Collection records.
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- We also welcome feedback to help refine and prioritize further enhancements You can submit it through the Data Corrections form using the "Funding/Grant Info" category (<u>https://support.clarivate.com/ScientificandAcademicResearch/s/datachanges?language=en_US</u>)

More information

Clarivate Libguides http://clarivate.libguides.com/home

Web of Science You Tube Channel https://www.youtube.com/user/WoSTraining





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Thank you!

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