

Springer Nature Databases & Solutions

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INFORUM Prague

May 30th 2018

ADVANCING
DISCOVERY

The Springer Nature Protocols and Methods Portfolio



The **largest and highest quality** collection for protocols & methods on the market available through the **Springer Nature Experiments solution!**

Scope of Content Coverage

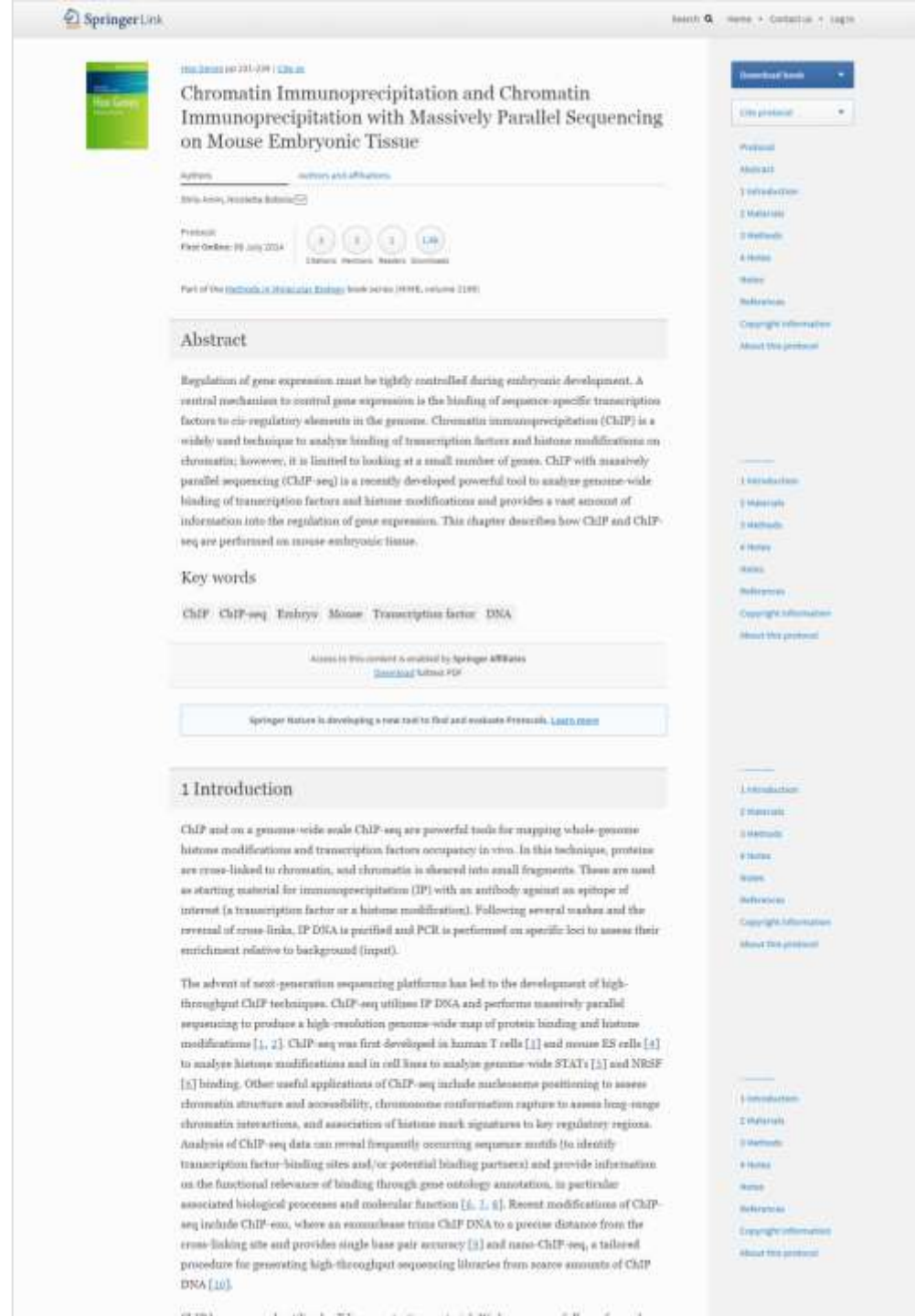
The Protocols & Methods Portfolio covers multiple areas across the life sciences such as:

- Biochemistry
- Bioinformatics
- Biotechnology
- Cancer Research
- Cell Biology
- Genetics/Genomics
- Imaging
- Immunology
- Infectious Diseases
- Microbiology
- Molecular Medicine
- Neuroscience
- Pharmacology and Toxicology
- Plant Science
- Protein Science



- Started in 1981, originally based on the classic book series “Methods in Molecular Biology”
- 180 book volumes & 3,000 protocols published per year¹
- More protocols per topic, covers several niche areas
- Content hosted on SpringerLink
- No protocols ever removed, updated/alternate versions added
- **47,000 protocols**

1) All publication metrics refers to data from end of 2017



The screenshot shows a detailed view of a protocol on the Springer Protocols platform. The title is "Chromatin Immunoprecipitation and Chromatin Immunoprecipitation with Massively Parallel Sequencing on Mouse Embryonic Tissue". The authors listed are "Serra-Aroca, Rosalinda Rodriguez". The protocol was first online on 19 July 2014. It is part of the "Methods in Molecular Biology" book series, volume 2189. The abstract states: "Regulation of gene expression must be tightly controlled during embryonic development. A central mechanism to control gene expression is the binding of sequence-specific transcription factors to cis-regulatory elements in the genome. Chromatin immunoprecipitation (ChIP) is a widely used technique to analyze binding of transcription factors and histone modifications on chromatin; however, it is limited to looking at a small number of genes. ChIP with massively parallel sequencing (ChIP-seq) is a recently developed powerful tool to analyze genome-wide binding of transcription factors and histone modifications and provides a vast amount of information into the regulation of gene expression. This chapter describes how ChIP and ChIP-seq are performed on mouse embryonic tissue." The key words are "ChIP, ChIP-seq, Embryo, Mouse, Transcription factor, DNA". The page also includes a table of contents with sections like Introduction, Materials, Methods, Notes, References, Copyright information, and About this protocol.

- Launched in 2004
- Thorough assessment of the methodological performance with comprehensive technical description
- Primarily research papers with an array of cutting-edge articles, opinions and news
- Publishes monthly with ~360 articles/year
- 2016 Impact Factor: 25.062, ranked *first* in “Biochemical Research Methods” (Journal Citation Reports)
- Content hosted on nature.com platform
- 4,700 articles

nature.com > nature methods > brief communications > article

nature methods

Access provided by Springer

Alfabeto: A Clusters: 1 More details

Brief Communication

Inducible and multiplex gene regulation using CRISPR-Cpf1-based transcription factors

Y Eshkol Tah, Benjamin P Kleinstern, James K Niles, Jonathan P Hsu, Jay E Hwang, Jingyi Gong, Jonathan S Blakeslee & J Keith Joung

Nature Methods **14**, 1102–1106 (2017)
doi:10.1038/nmeth.4482
Download Citation

Received: 14 June 2017
Accepted: 24 September 2017
Published online: 30 October 2017

Gene regulation Molecular engineering
Description

Abstract

Targeted and inducible regulation of mammalian gene expression is a broadly important capability. We engineered drug-inducible catalytically inactive Cpf1 nuclease fused to transcriptional activation domains to tune the expression of endogenous genes in human cells. Leveraging the multiplex capability of the Cpf1 platform, we demonstrate both synergistic and combinatorial gene expression in human cells. Our work should enable the development of multiplex gene perturbation library screens for understanding complex cellular phenotypes.

Main

Sequence-specific RNA-guided CRISPR-Cas nucleases are simple to program^{1,2}; the widely used *Streptococcus pyogenes* Cas9 (SpCas9) can be targeted to specific DNA sequences by an associated complementary guide RNA (gRNA), provided that a protospacer-adjacent motif (PAM) of the form NGG is also present. Catalytically inactive SpCas9 (dSpCas9) has been fused to transcriptional activation or repression domains to alter the expression of individual genes or to perform genome-wide library screens in mammalian cells³. Both small-molecule- and light-inducible dSpCas9-based fusions have been developed^{4,5,6}, which has enabled researchers to regulate the activity of this gene regulatory platform. Recently described CRISPR-Cpf1 nucleases offer additional capabilities beyond those of SpCas9—including shorter length CRISPR RNAs (crRNAs) for guiding Cpf1 to targets, the ability to target T-rich PAMs^{7,8}, and RNase processing of multiple crRNAs from a single transcript by RNase activity of Cpf1 (refs. 9,10). However, to our knowledge, ‘dead’ Cpf1 (dCpf1)-based gene regulators have thus far only been shown to repress gene expression in bacteria^{11,12} and plants (Arabidopsis)¹³.

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Associated Content

Collection
Genome Editing

Section	Figure	References
Abstract		
Main		
Methods		
References		
Acknowledgements		
Methods		
References		
Acknowledgements		

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- Launched in 2006
- Step-by-step format with critical steps, materials list and troubleshooting tips
- Publishes monthly with ~200 protocols/year
- Faster for publishing protocols for new techniques
- 2016 Impact Factor: 13.254, ranked *second* in “Biochemical Research Methods” (Journal Citation Reports)
- Content hosted on nature.com platform
- **2,400 protocols**

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nature.com > nature protocols > protocols > article

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Altmetric: 27 [More detail](#)

Protocol

Chromatin-state discovery and genome annotation with ChromHMM

Jesse Ernst & Michael Palis

Nature Protocols 12, 2475–2492 (2017)
doi:10.1038/nprot.2017.124
Download Citation

Published online: 08 November 2017

Chromatin | Chromatin analysis | Epigenetics | Gene regulation | Software

Abstract

Noncoding DNA regions have central roles in human biology, evolution, and disease. ChromHMM helps to annotate the noncoding genome using epigenomic information across one or multiple cell types. It combines multiple genome-wide epigenomic maps, and uses combinatorial and spatial mark patterns to infer a complete annotation for each cell type. ChromHMM learns chromatin-state signatures using a multivariate hidden Markov model (HMM) that explicitly models the combinatorial presence or absence of each mark. ChromHMM uses these signatures to generate a genome-wide annotation for each cell type by calculating the most probable state for each genomic segment. ChromHMM provides an automated enrichment analysis of the resulting annotations to facilitate the functional interpretations of each chromatin state. ChromHMM is distinguished by its modeling emphasis on combinations of marks, its tight integration with downstream functional enrichment analyses, its speed, and its ease of use. Chromatin states are learned, annotations are produced, and enrichments are computed within 1 d.

Introduction

Mapping of epigenomic marks, such as histone modifications, histone variants, regions of open chromatin, and related marks, has emerged as a powerful means to annotate genomes, to identify putative regulatory elements, and to study their changing activity across different cell types and in human disease^{1,2,3,4}. Individual marks can be studied in isolation, either through aggregation of their genome-wide signal tracks relative to a set of predetermined annotations⁵, such as transcription start sites or exon boundaries, or by discovery of narrow peaks or broader domains in which the mark is present in greater frequency than that of the surrounding regions⁶. However, additional information can be gained by studying combinations of multiple marks in their spatial

Associated Content

Nature Biotechnology | Analysis
Discovery and characterization of chromatin states for systematic annotation of the human genome
Jesse Ernst & Michael Palis

Nature | Article
Mapping and analysis of chromatin state dynamics in nine human cell types
Jesse Ernst, Pragna Khavariwala, ... | Bradley E. Bernstein

Nature Methods | Correspondence
ChromHMM: automating chromatin-state discovery and characterization
Jesse Ernst & Michael Palis

Sections | Figure | References

Abstract
Introduction
Materials

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protocol exchange

- Launched in 2006
- Open source, open access repository where users can share and browse protocols
- Content often complements Nature Methods content
- Content hosted on nature.com platform
- 900+ protocols

The screenshot displays the 'protocol exchange' website interface. At the top, there's a navigation bar with links: Home, Browse, Share protocol, Lab groups, About, and Contact. Below this, the main heading reads 'A protocol for *in vivo* detection of reactive oxygen species' by Edward Owusu-Ansah, Amir Yavari & Utpal Banerjee. The authors' affiliation is listed as Banerjee Lab (University of California). The protocol was published in Protocol Exchange (2008) on 10/10/2008 and published online on 27 February 2008.

The 'Introduction' section describes the use of 2',7'-dichlorofluorescein (H2DCF) and Dihydroethidium (DHE) for detecting reactive oxygen species (ROS) production in live tissues, specifically in *Drosophila*. It highlights the advantages of these dyes for real-time detection and the ability to compare mutant and wild-type phenotypes. The protocol involves imaging ROS production using either H2DCF or DHE, comparing mutant and wild-type cells, and capturing images using confocal microscopy.

On the right side of the page, there are several promotional banners:

- A 'BROWSE BY SUBJECT' section with a dropdown menu showing 'All protocols (3349)' and a 'Go' button.
- A green banner for 'pipedrive' with the text 'Organize your sales on the go with mobile CRM' and a 'Track my deals' button.
- A 'nature' banner with the text 'High impact research from Nature. Faster coverage of new research.'
- A 'Science jobs from naturejobs' section listing various positions such as 'Team Leader in Drug Discovery Biology', 'Post Doc Fellow - Structural Biology and Drug Discovery', 'Lead Biologist & Project Manager - Drug Discovery (Neuroscience)', 'Medicinal Chemistry, Organic Chemistry and Chemical Biology', and 'Principal Institute Research Scientist - Drug Discovery, Biology & Translation'.
- A 'Science events from natureevents' section listing conferences like 'RCCT 2018 - 54th International Conference on Medicinal Chemistry - "Interfacing Chemical Biology and Drug Discovery"', 'Evolutionary Biology and Ecology of Cancer', and 'Next Gen Immunology'.

At the bottom of the page, there's a 'Figures at a glance' section.

- Launched Oct. 2017
- Advanced searching platform spanning the **entire** Springer Nature Protocols & Methods Portfolio
- Searching/browsing content is free; licenses are required for full-text access

Search over 50,000 protocols and methods:

e.g. protocol, technique, organism



Browse by:

Nature
Protocols

Nature
Methods

Protocol
Exchange

Springer
Protocols

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Finding the Appropriate Scientific Protocol is Very Inefficient



What do Researchers Struggle with When Looking for Protocols & Methods and How Can Experiments Help?

Finding protocols and methods



- Aggregated search of SN Protocols and Methods content - **over 56 000 articles!**
- Dedicated filters, optimized search and intelligent article indexing

Evaluating if they are relevant



- Extract relevant information for at-a-glance evaluation of the search results - **Search Page**
- Overview of the article's key information - **Landing Page**

SPRINGER NATURE | Experiments
Advanced Search

- Sophisticated **search filters** to narrow down results (publication year, video, technique, article type, article source)
- **Sort results** by relevance, publication time, citations, downloads
- More search concepts being developed (e.g., for cell lines, organisms, equipment & reagents)

Search over 50,000 protocols and methods:

crispr

Publication Year: 2018

Video: Videos available: 15

Technique: Show all

Article Category: Show all

Source: Nature Research, Nature Methods, Nature Protocols, Protocol Exchange, Springer, Methods in Molecular Biology, Nature Methods, Springer Protocols Handbook, Methods in Pharmacology and Toxicology

636 results for "CRISPR"

Sort by: Relevance

Springer Protocols (2014) Series: Methods in Molecular Biology Book: CRISPR

Clustered Regularly Interspaced Short Palindromic Repeats (CRISPRs) Analysis of Members of the *Mycobacterium tuberculosis* Complex

Techniques: CRISPR, PCR, Genotyping, Agarose Gel Electrophoresis, Electrophoresis

Citations: 1 Downloads: 3,117

Springer Protocols (2018) Series: Methods in Molecular Biology Book: CRISPR

Annotation and Classification of CRISPR-Cas Systems

Techniques: CRISPR, Genomics, Protein Structure Comparison, Sequence Comparison

Citations: 38 Downloads: 4,394

Springer Protocols (2018) Series: Methods in Molecular Biology Book: CRISPR

Using the CRISPR-Cas System to Productively Select Mutations in Genes Essential for Its Function

Techniques: CRISPR, PCR, Mutagenesis, Electroporation, Electrophoresis

Model: *Escherichia coli*, *Saccharomyces cerevisiae*

Downloads: 5,471

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Article Evaluation Page

Gives key information for evaluation and comparison of protocols and methods

- **Abstract and references**
- **Keywords** (supplied by the author & extracted by us)
- **Citation history and last 3 citations:** gives the user confidence that the protocol is being successfully used in other research projects
- **Article history:** are there updates, older versions, corrections?
- **Figures and Videos**

Take our survey and help shape this product. For help contact us at experiments@springer.com

SPRINGER NATURE | Experiments | e.g. protocol, technique, organism

Cell Sensitivity Assays: The MTT Assay

Series: Methods in Molecular Biology > Book: [Cancer Cell Culture](#)

Protocol: 34 March 2011 | DOI: 10.1007/978-1-61779-080-5_20

Authors: John Meertse, Gerjan J. Kasper, Jacqueline Cloos [†] [show](#)

[Full text](#)

Citation history

Author contact info

Keywords

Cytotoxicity (MTT) Assay, Optical Density Measurement, Cytotoxicity Assay, Cell Sensitivity Assay, MTT, 3-(4,5-Dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide, Viability assay, IC50, LC50, Drug sensitivity assay

Citations

295

History

2011 (This version)
2004 June A, Plumf

Article history

Keyword overview

Abstract

The MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide) assay is based on the conversion of MTT into formazan crystals by living cells, which determines mitochondrial activity. Since for most cell populations the total mitochondrial activity is related to the number of viable cells, this assay is broadly used to measure the in vitro cytotoxic effects of drugs on cell lines or primary patient cells. In this chapter the protocol of the assay is described including important considerations relevant for each step of the assay as well as its limitations and possible applications. [less](#)

Full abstract

Latest Citations (295)

- Kaqin Wang et al., 2018, [Journal of Functional Foods](#)
- R. H. E. Fijen et al., 2018, [Journal of Breath Research](#)
- Ahmed Abd-Rabou et al., 2018, [International Journal of Pharmacology](#)

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Figures & videos

Fig. 1

Figures and videos

Last three citations

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Key Benefits of SN Protocols and Methods Portfolio



Access the **largest** and most comprehensive collection of protocols & methods



Oldest and **most prestigious** books and journals in the protocols and methods field

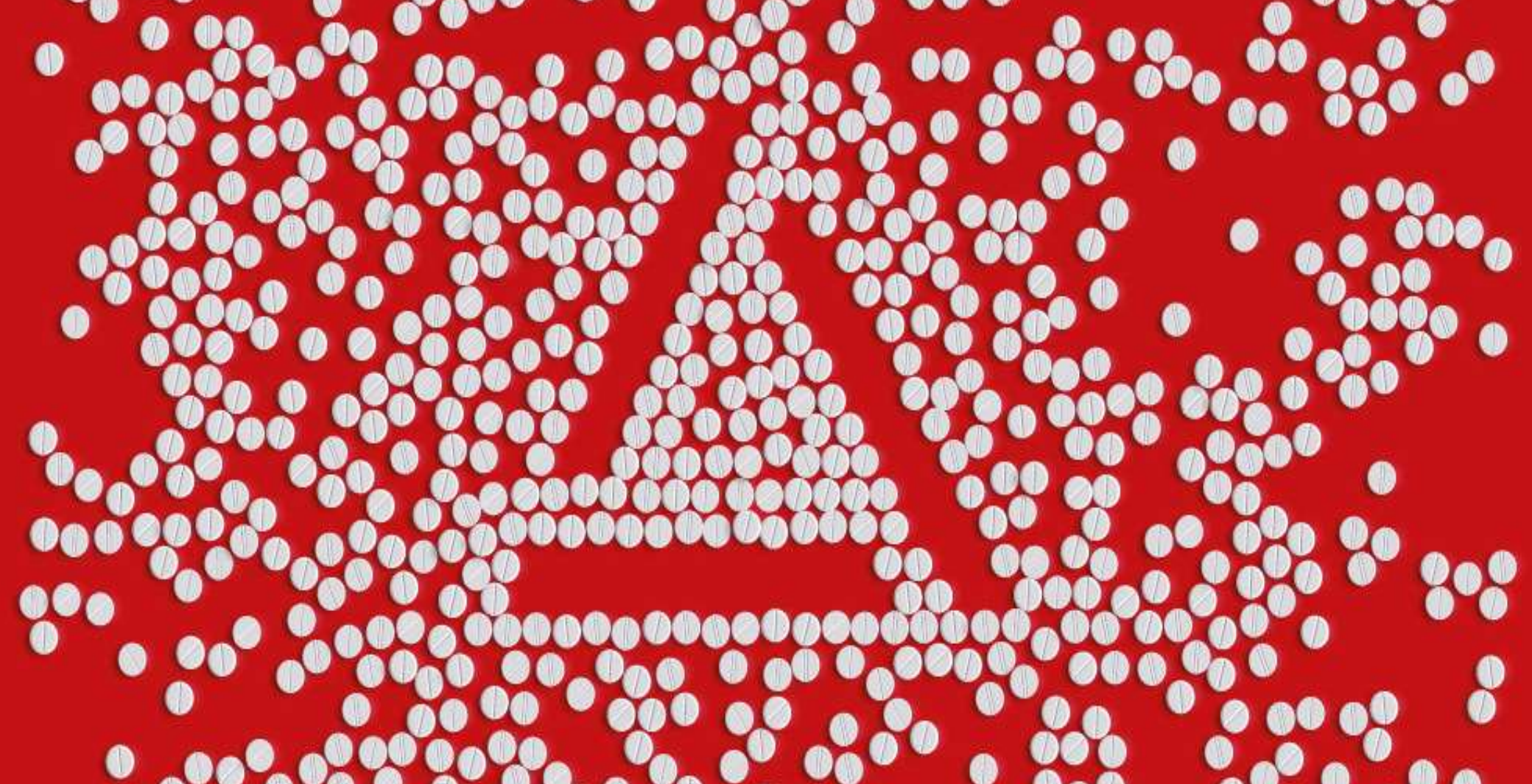


Easily search and browse through the entire portfolio with *Experiments*



Save valuable time with *Experiments* advanced filtering and search options

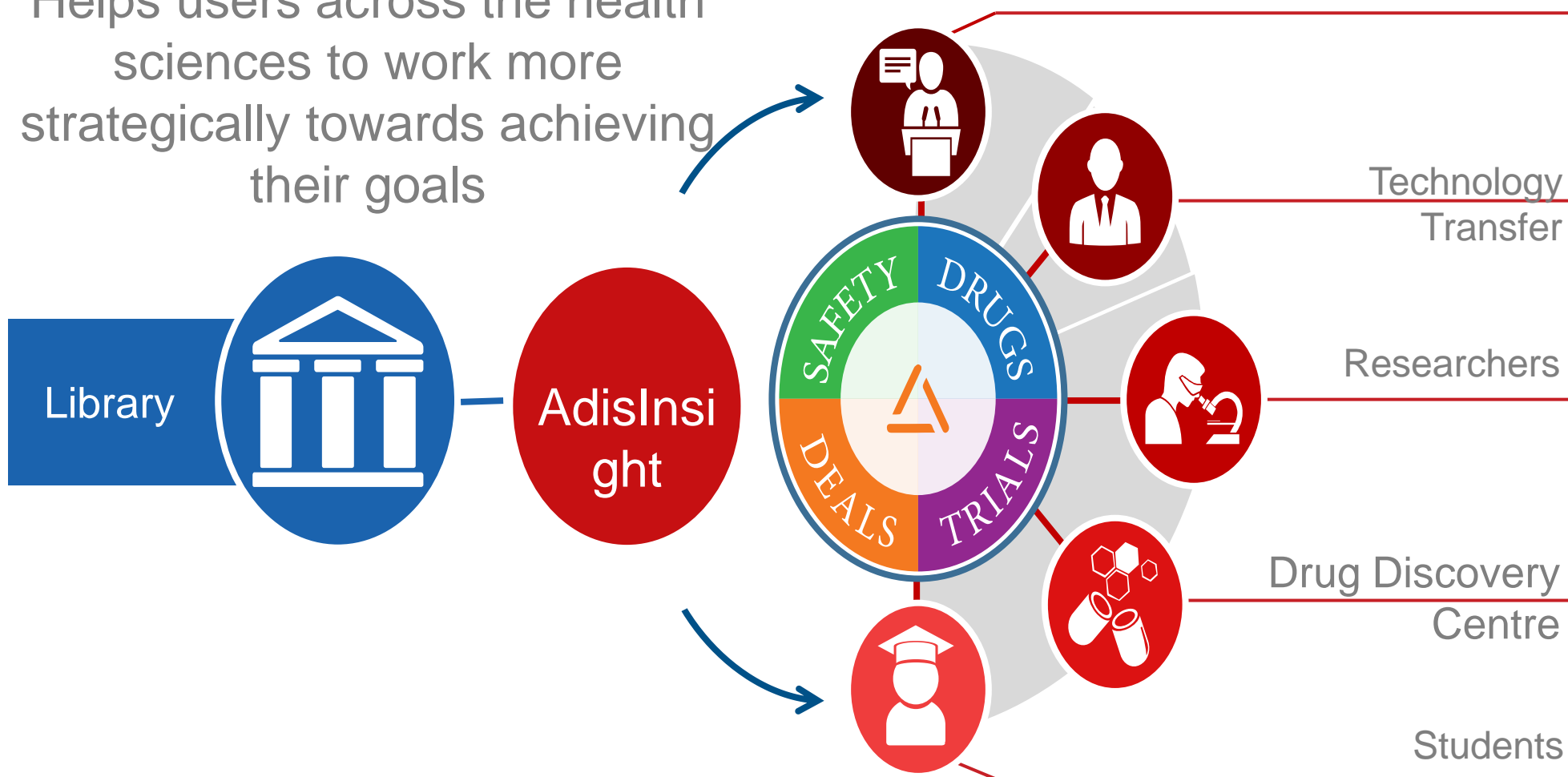
Questions?



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Life Sciences




Significant working
experience and
knowledge



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and accreditation
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Certification



Methodical process for
creating content





DRUGS

Drug treatments being developed
worldwide

How well they work

Who is working on them

How soon they will be available



TRIALS

Clinical trials being performed

Study centre and investigator
details

Trial design

Outcomes and results

Purchases and acquisitions

Joint ventures

Agreements for licensing, R&D
and more

Benchmarking of deal values and
terms

DEALS

Adverse drug reaction case
reports

Drug safety studies

Regulatory news

SAFETY

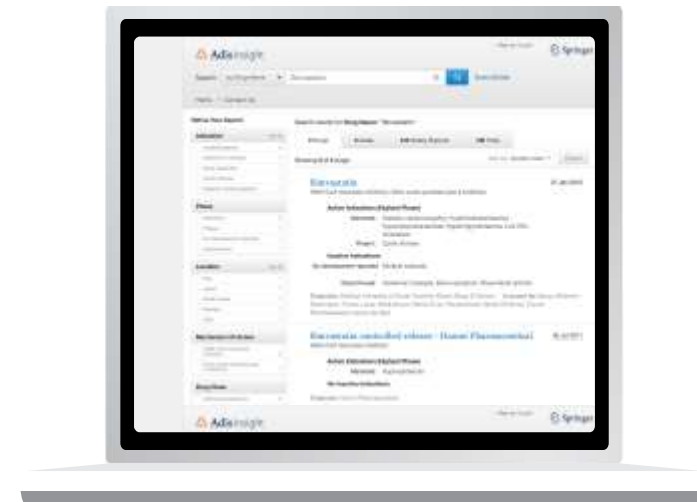
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Single search platform



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Continuous monitoring of global sources to check for new data



Assessing

New data is reviewed and assessed to extract relevant information, based on its significance and scientific merit

Categorizing

Detailed indexing is applied to support highly-focused searching



Validating Assessing

Verified across multiple sources
New data is reviewed and assessed to extract relevant information, to resolve discrepancies and remove bias, based on its significance and



Categorizing

Detailed indexing is applied to support highly-focused searching

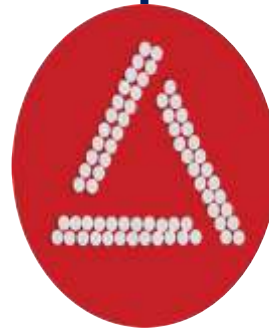
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Concise narratives tell the story using the most compelling evidence



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SpringerMaterials: The Materials Science Database

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What is SpringerMaterials?

SpringerMaterials: A Curated Database of **Material** Properties

Major Material Types & Property Classes include

Metals
& Alloys

Ceramics
& Glasses

Polymers

Organic
Substances

Composites

Atoms
& Nuclei



Physical



Chemical



Thermodynamic



Electromagnetic



Structural



Mechanical



Spectroscopic



Nuclear

SpringerMaterials Users: A (Small) Selection



Chemistry



Polymer Chemist

Polyolefin heat capacities



Surface Scientist

Gas adsorption isotherms



Crystallographer

Crystal structures & atomic positions



Analytical Chemist

NMR spectral data



Engineering



Mechanical Engineer

Alloy tensile strengths



Chemical Engineer

Thermodynamic data



Metallurgist

Alloy corrosion data



Nuclear Engineer

Radiation shielding data



Physics



Spectroscopist

Raman spectra



Nuclear Physicist

Neutron resonance parameters



Condensed Matter Researcher

Doped metal band gaps

SpringerMaterials: *Building a Modern Database*



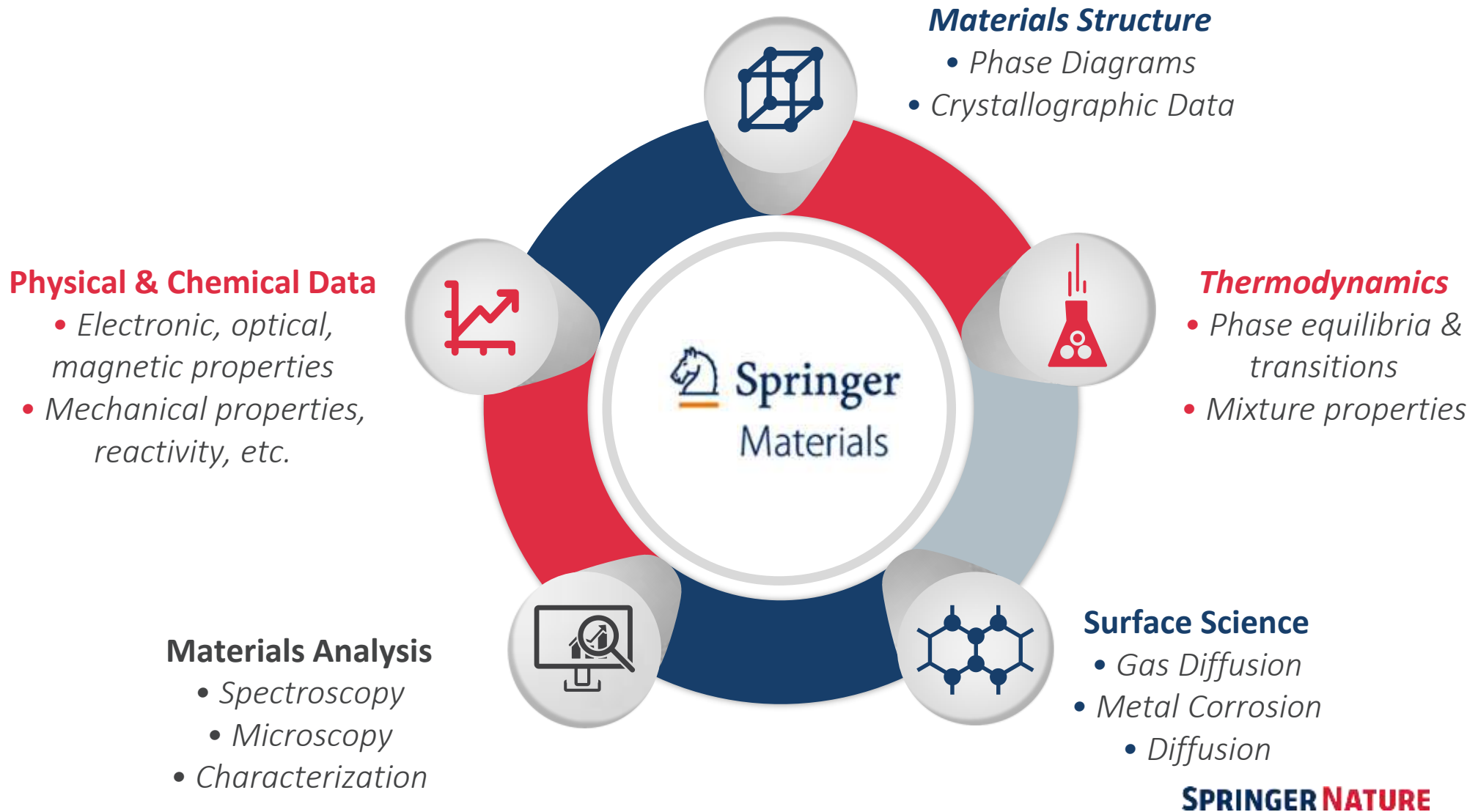
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Digitization, Enrichment, and Consolidation of Data

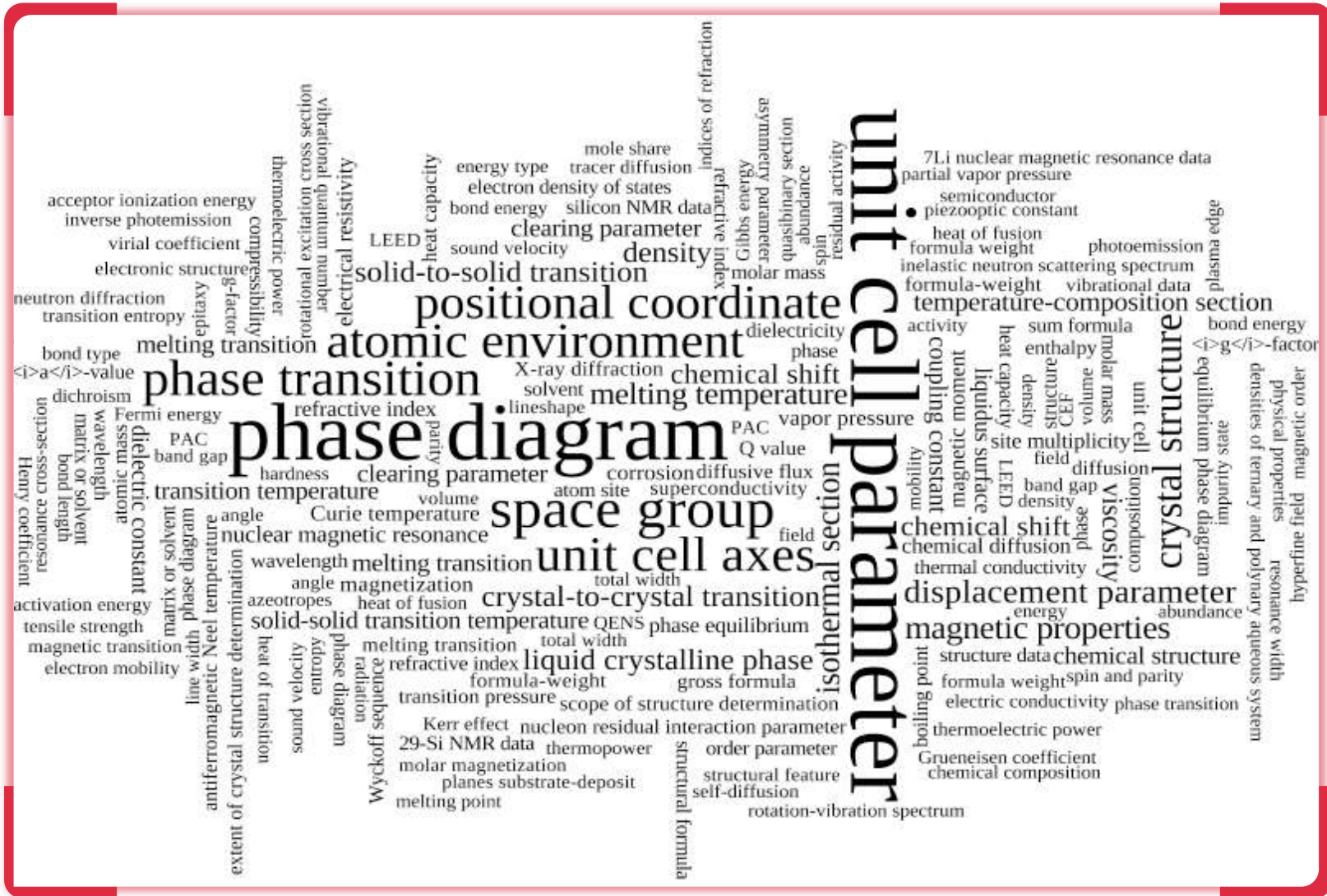
Functionalities Specialized for Materials Science

Data sources: *Classic Landolt-Börnstein series, MSI Eureka, Linus Pauling Files – Inorganic Solid Phases, Polymer Thermodynamics Database (ATHAS), Dortmund Databank of Separation Technology, Springer Handbooks (e.g., VDI Heat Atlas), Adsorption Database, NIST Corrosion Database, SpringerMaterials Fundamentals Handbooks*

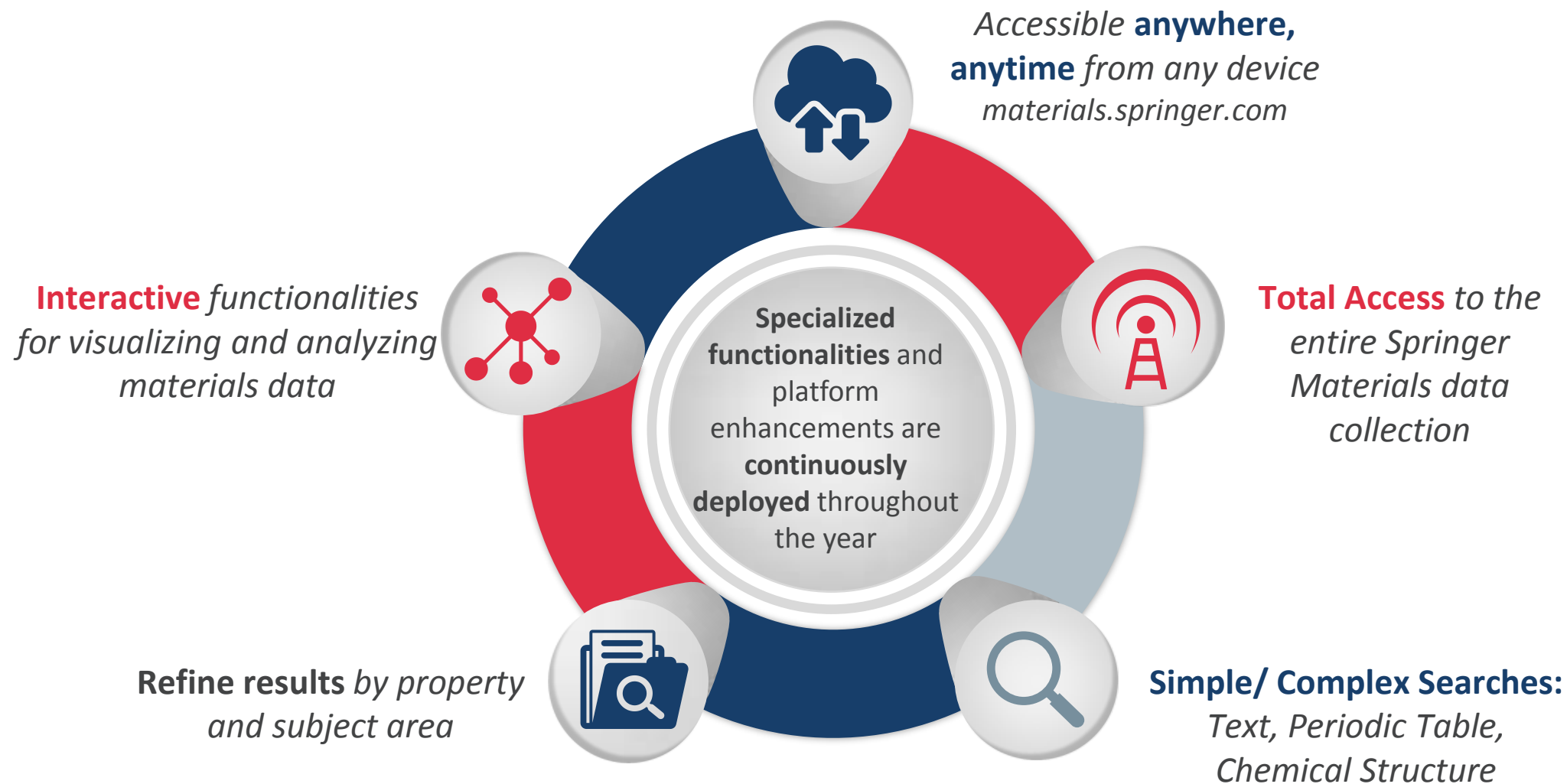
Coverage of Key Materials Science Topics

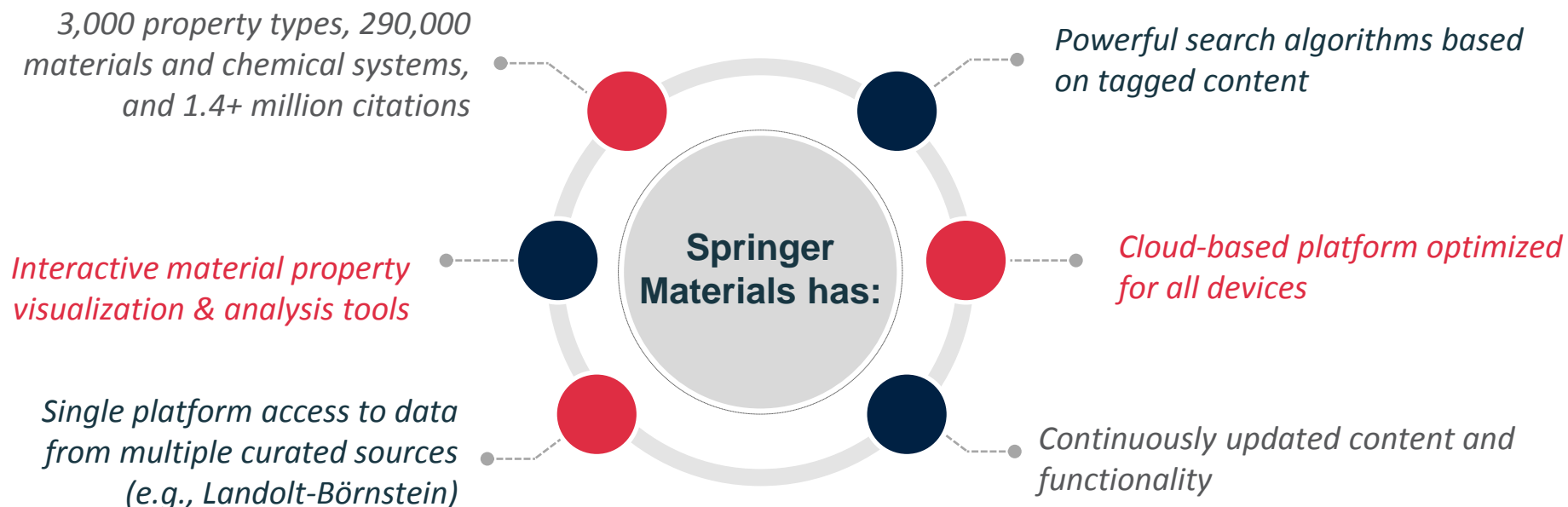


Typical SpringerMaterials Content at a Glance



SpringerMaterials Functionality Overview





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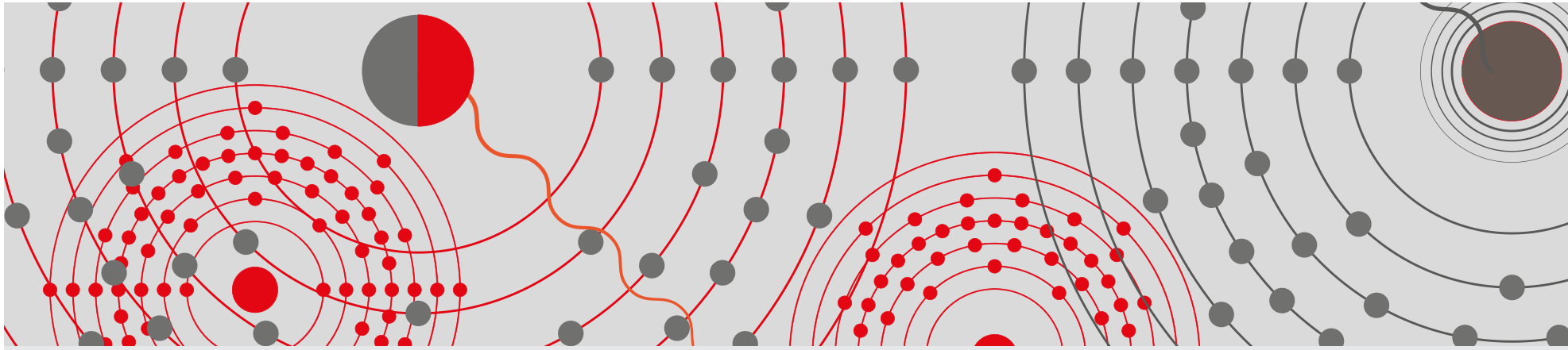


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Intuitive search functions - text, elemental component, chemical structure; easily sort & refine results

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Nano

a Nature Research Solution

natureresearch

Agenda

01

About Nanotechnology

02

What is Nano and how does it support researchers?

03

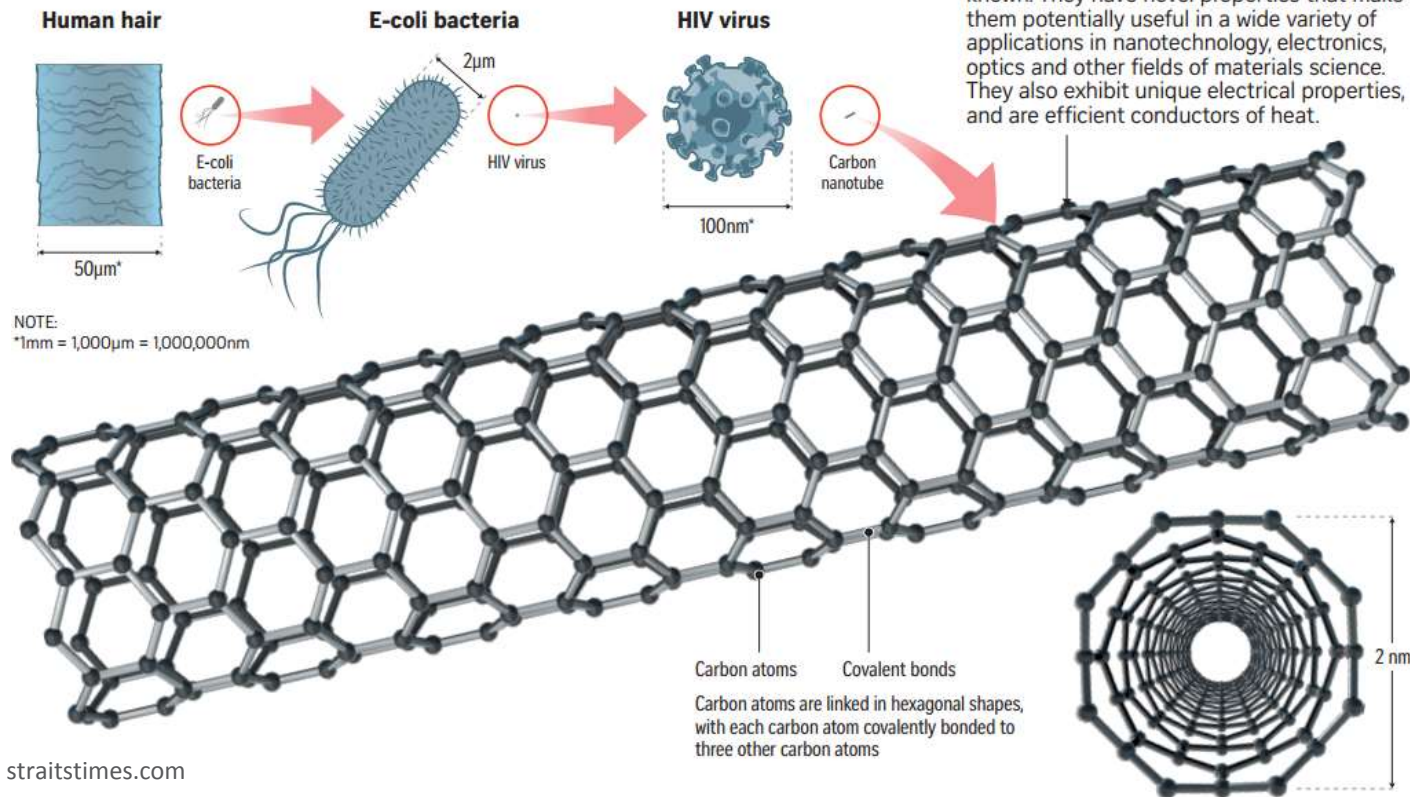
What makes Nano unique?

Nanoscience & technology – quick intro

- Nanoscience & technology is the **understanding and control of matter at the nanometer scale** where unique phenomena enable novel applications.

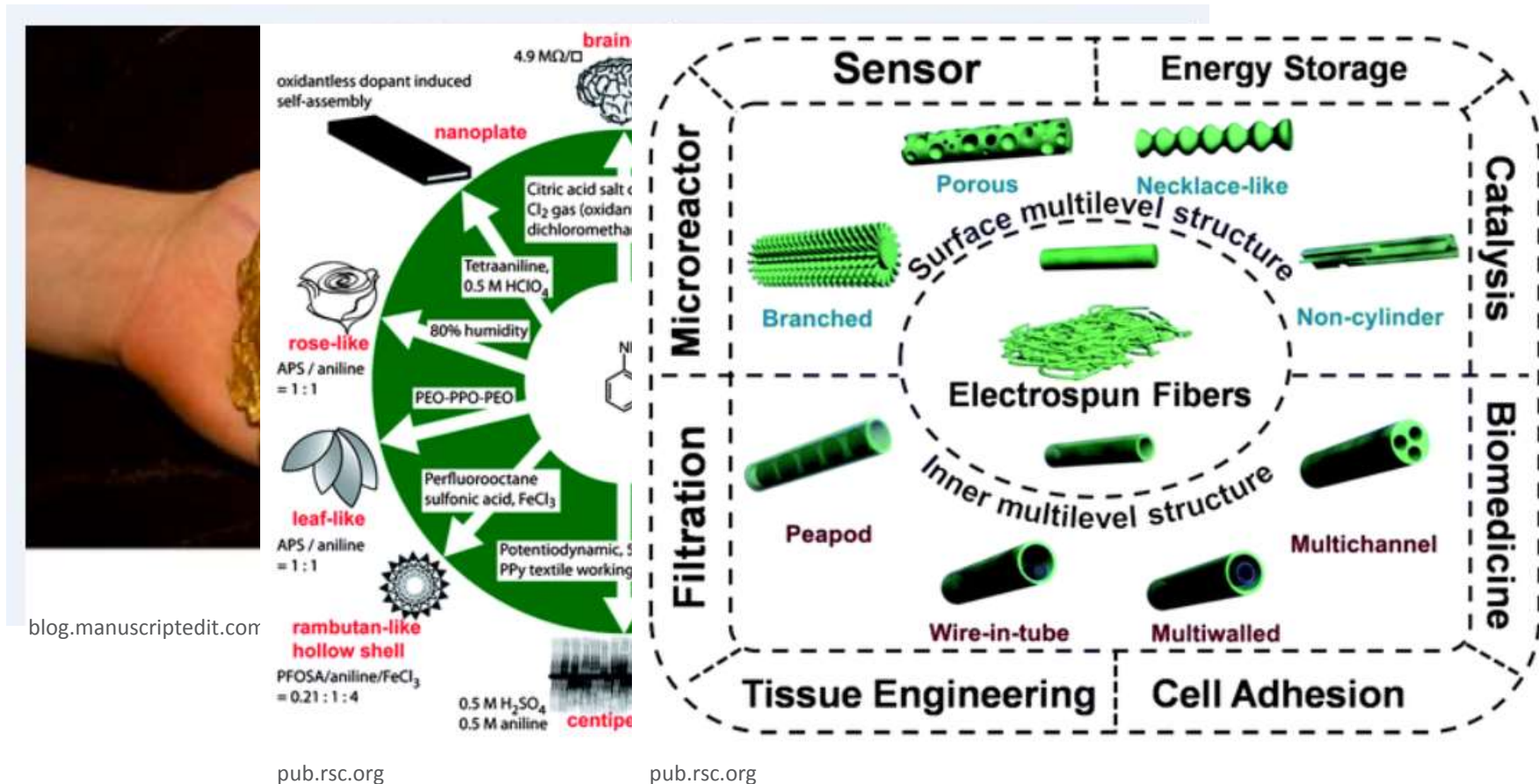
WHAT IS NANOTECHNOLOGY?

It is science, engineering and technology at scales going down to as small as a billionth of a metre.



Nanoscience & technology – quick intro

- Nanoscience & technology is the **understanding and control of matter at the nanometer scale** where unique phenomena enable novel applications.



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Nanoscience & technology – quick intro

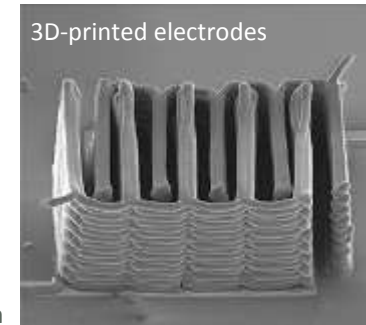
- It **impacts a vast range of fields**, including chemistry, physics, biology, medicine, energy, IT, transportation and environmental science among many others.



Multitech.com



endlhausen-pharma.de



3D-printed electrodes

roqgy.com

seas.harvard.edu



Metal oxide nanoparticles

BASF.com

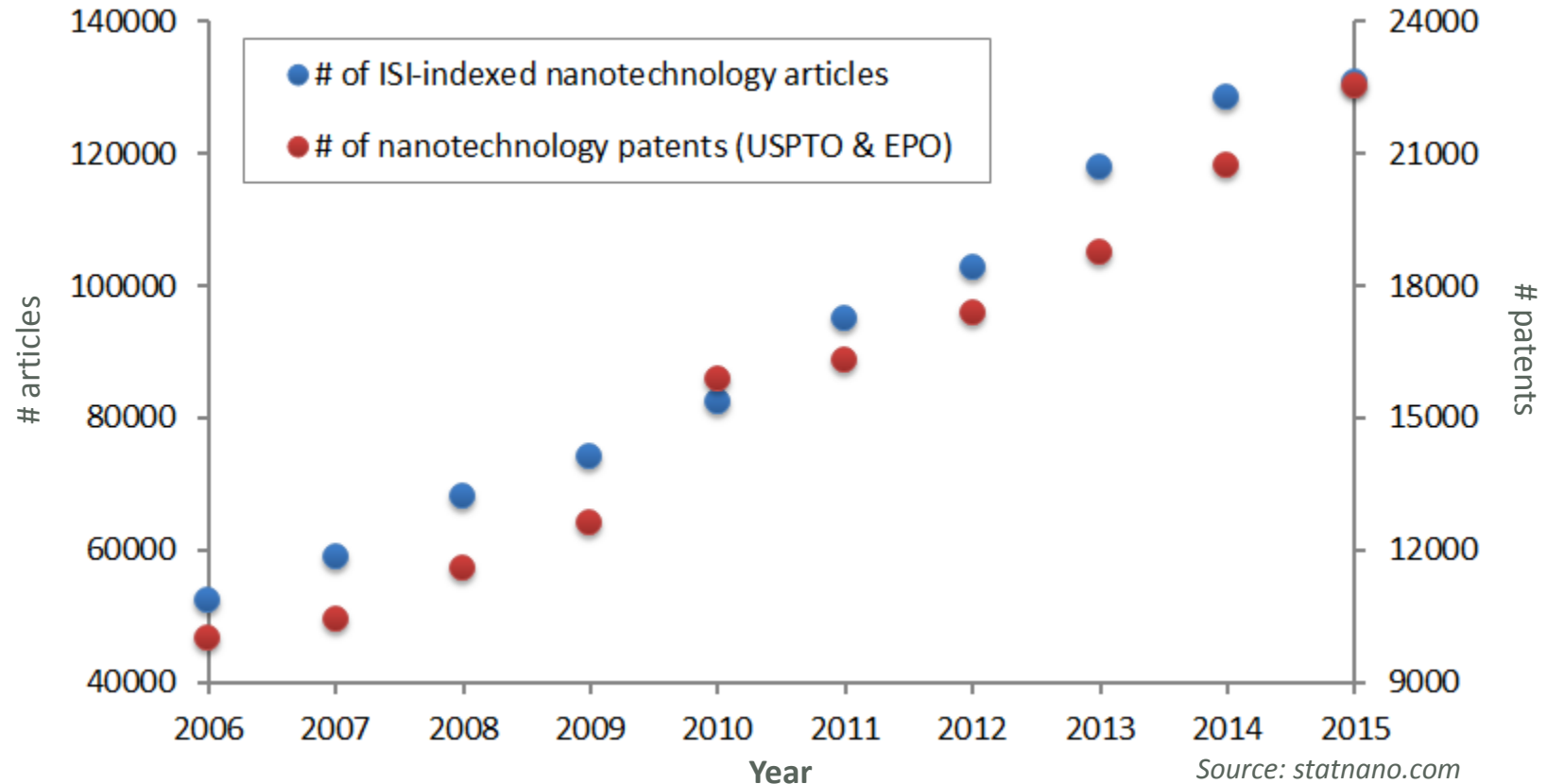


- Its economic impacts have already been realized** and is expected to expand and grow through a wide breadth of channels.

Different estimates of nanotechnology's economic contribution

Estimate	Geographic scope	Definition of nanotechnology	Source
Revenues of USD 731 billion in 2012	Worldwide	Nano-enabled products	Lux Research
Market size of USD 26 billion in 2014	Worldwide	Narrow definition of nanotechnology applications	BCC Research
Market size of USD 100 billion in 2011	Worldwide	Nanomedicines	BCC Research
Market value of final products of USD 300 billion in 2010	Worldwide	(unclear)	Roco (2001)

Nanoscience & technology – a booming field



- Vast amount of **information and data scattered** throughout journals and patents require classification, indexing and curation for proper management and effective communication.
- Currently **no standardized nomenclature** for nanomaterials.

Major pain points with existing resources

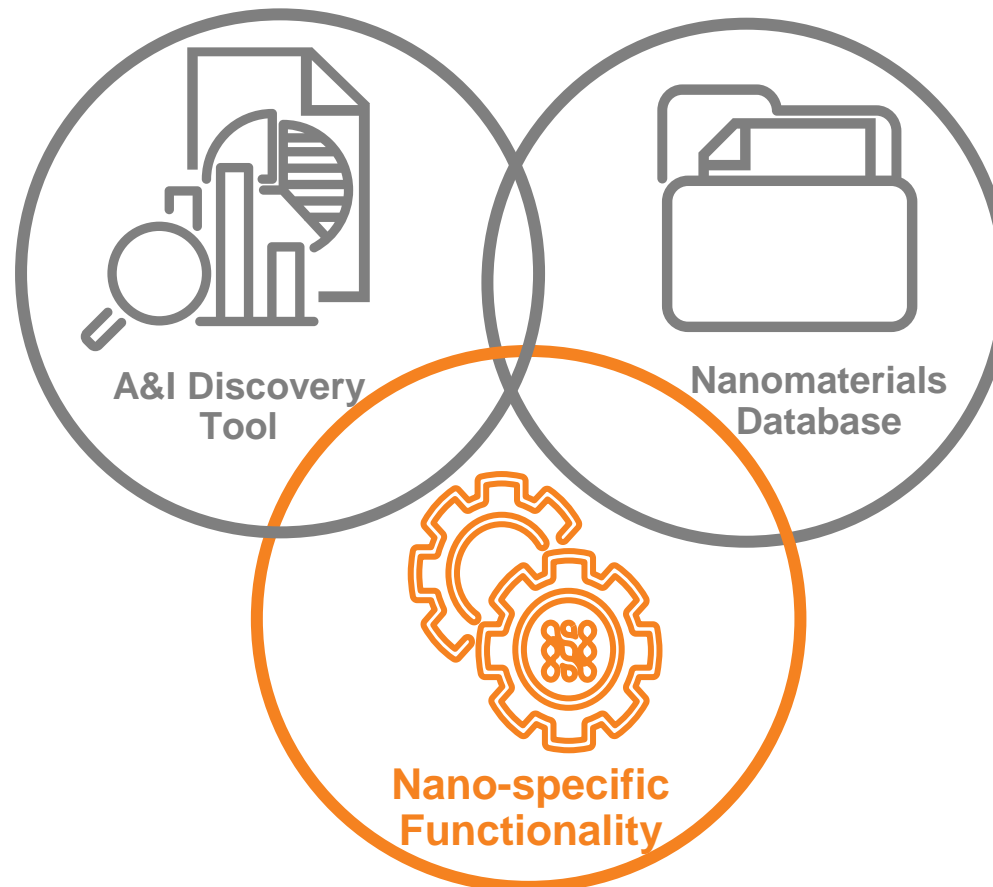
1. Large number of irrelevant search results
2. Validating relevancy requires access to the original source
3. Scattered information for similar nanomaterials/devices
4. No single list available for nanomaterials/devices with certain properties or for specific applications
5. Tedious to reconstruct preparation methods and steps for nanomaterials/devices from text



Nano – made by Nanotechnology experts

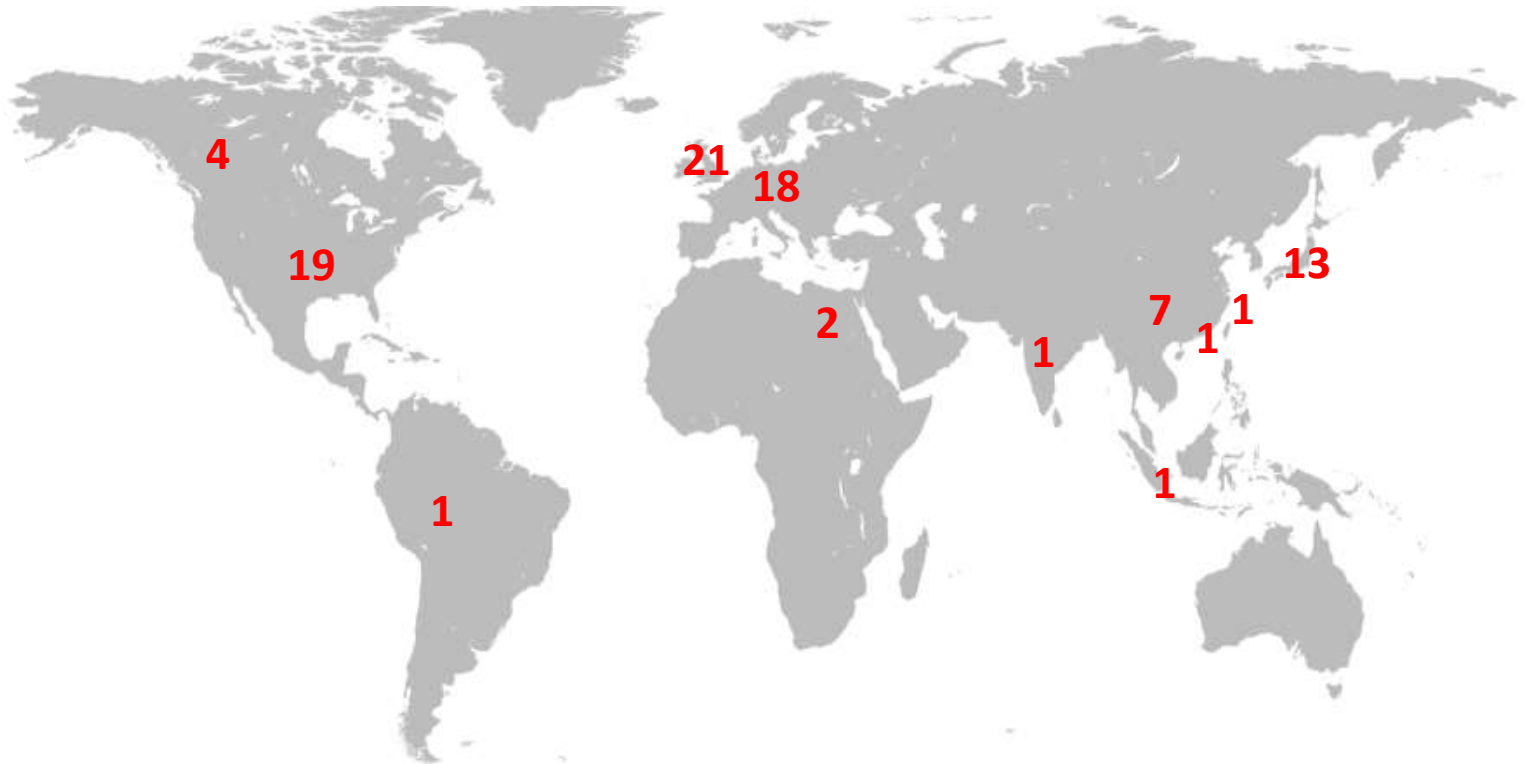
Nano at nano.nature.com provides highly indexed and structured information related to nanotechnology derived from high-impact journals and patents.

Nano combines the key features of



Nano is a user proven solution

- Early market research based on 218 online survey respondents and 28 in-depth phone interviews gave us the confidence to start this ambitious project. One general feedback is “Building a nanoscience-dedicated discovery tool is a great idea!”
- We have been conducting multiple rounds of user testing to ensure platform functionalities and features serve practical purposes and add values to the users.



89 nano researchers across the globe have participated in user testing to date natureresearch

How Nano helps researchers?

Find nanotechnology information precisely without looking into the full text

Information on similar nanomaterials is compiled into summaries from multiple sources

Preparation steps for nanomaterials can be easily found and visualized

Nanomaterials with specific properties and application can be quickly enlisted



What makes Nano unique?

**Faster
Insight**

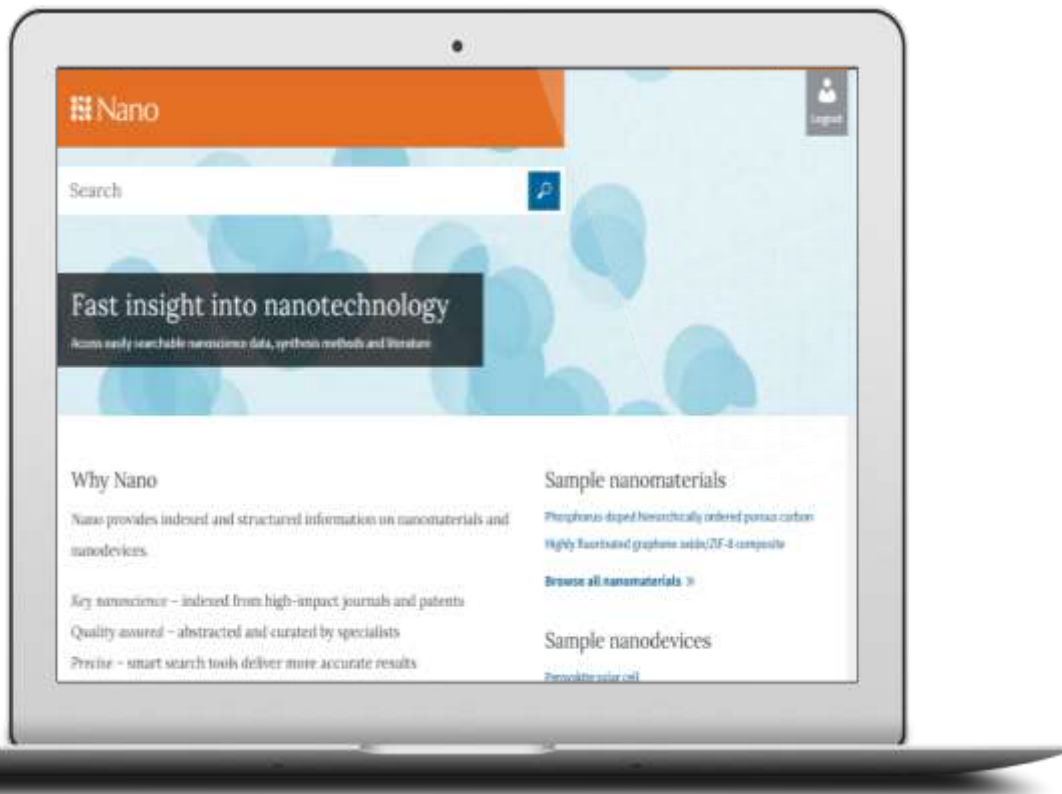


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Specific**

**Competitive
Edge**

Nano Specific

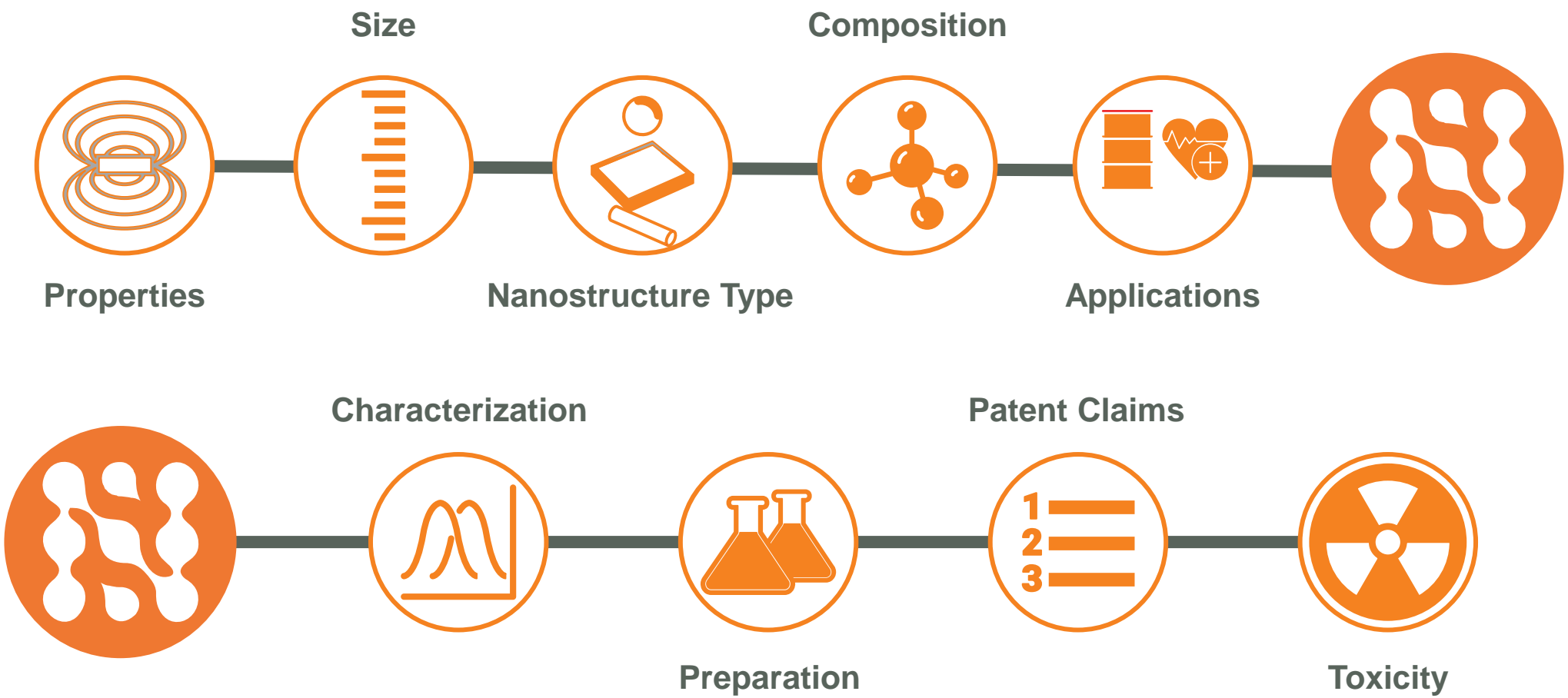
The **only research solution covering nanomaterials**.
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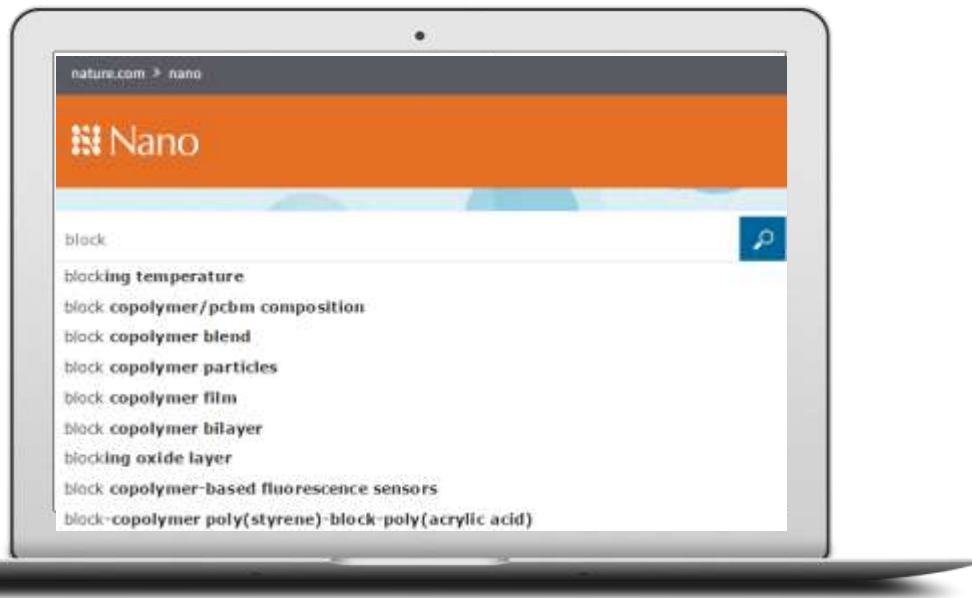
- Curated nanomaterial summaries
- Indexed data from a broad range of multidisciplinary relevant journals
- Search as precise as possible

A Profile Includes



Faster Insight

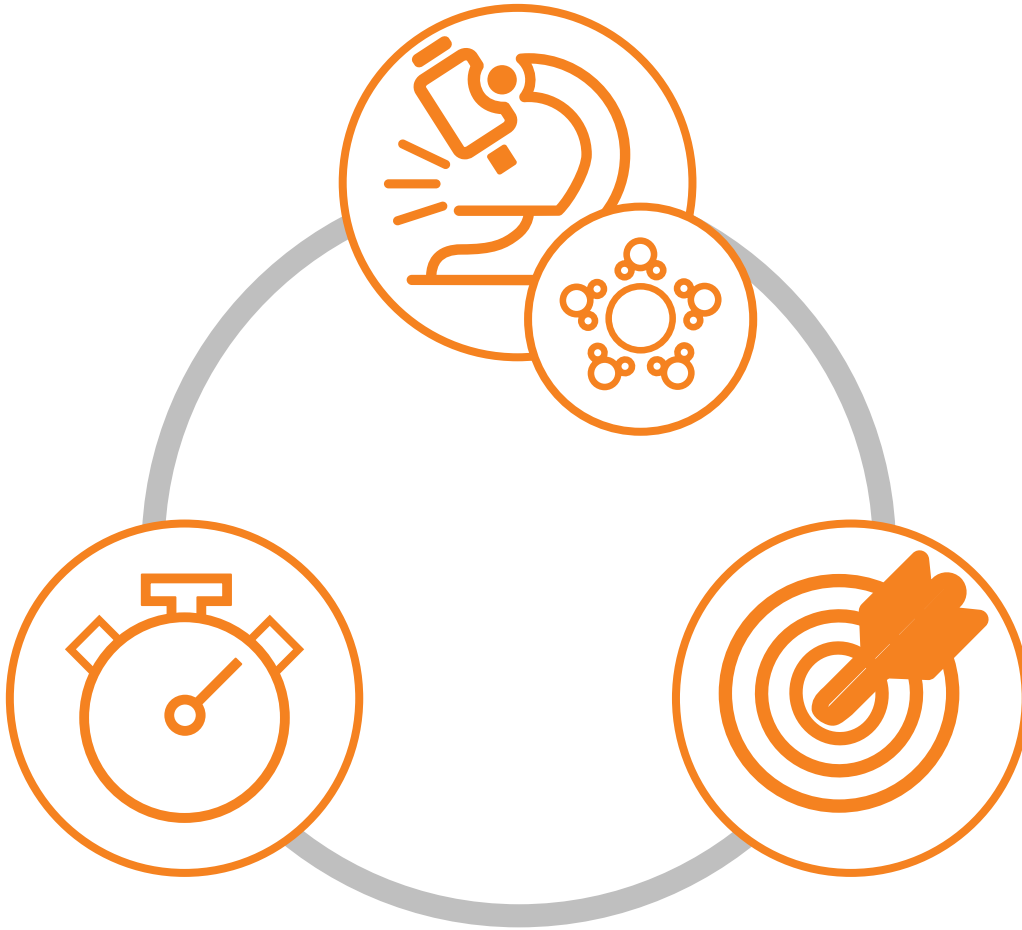
Centralized nanotech-related articles in one space



Curated summaries from **top journals** worldwide...

- Indexed data from a broad range of relevant journals
- Search as precise as possible
- Curated nanomaterial summaries

Your Competitive Edge



Keep up-to-date with
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Insight**



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