



GETTING STARTED WITH SPRINGER NATURE EXPERIMENTS

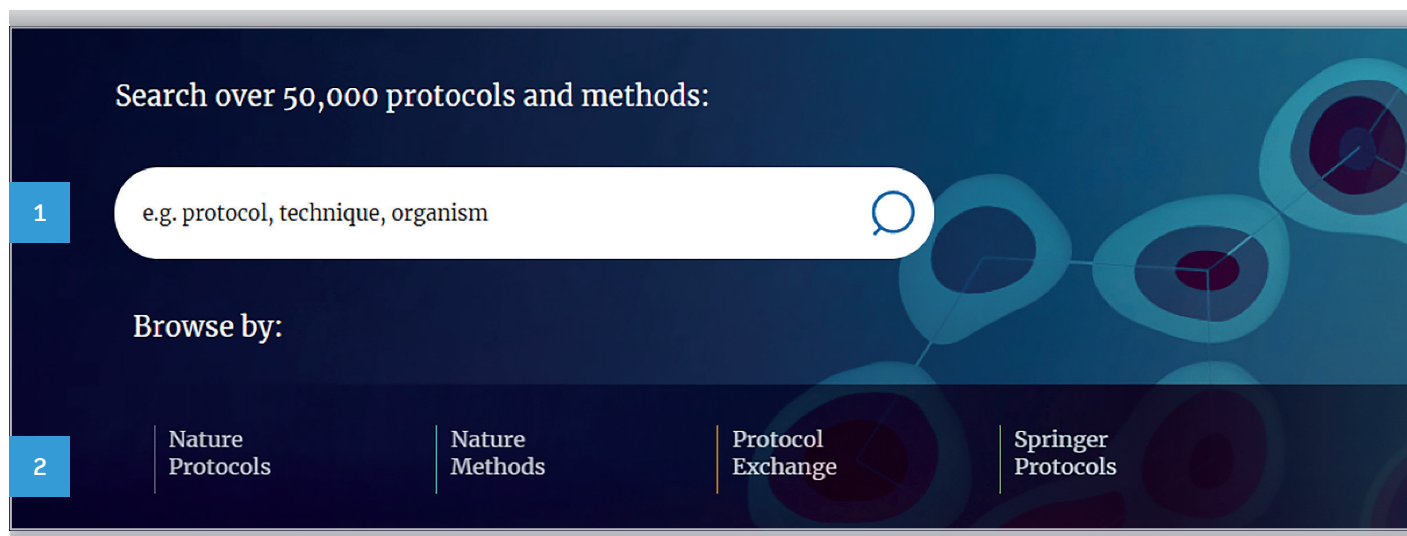
ADVANCING
DISCOVERY

This guide explains how to perform a basic search, refine your search results, use the Article Evaluation Pages, and access full-text content using Springer Nature Experiments: the research solution for protocols and methods.

To access the platform, visit **experiments.springernature.com**.
It is free to use and you do not need to log in.

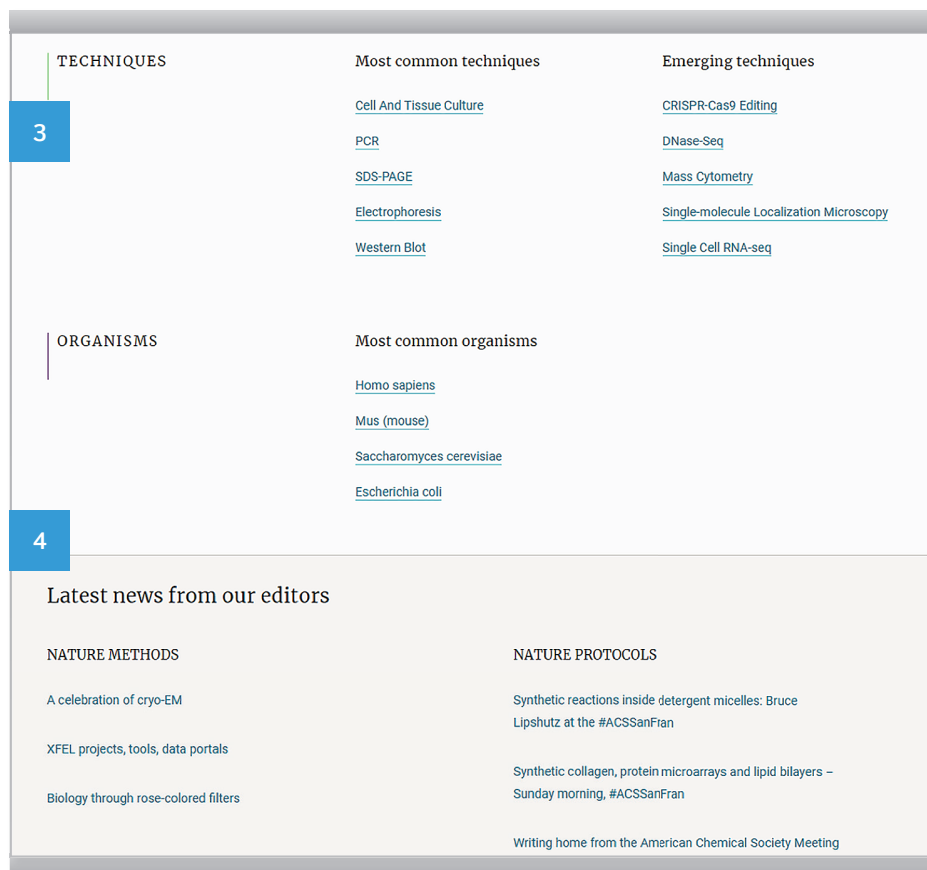
Homepage

1. You can start your search straight away using the search bar on the homepage:



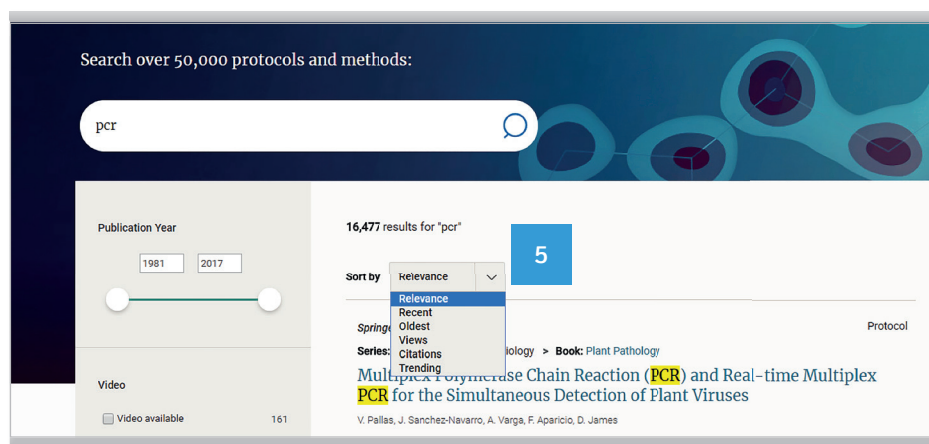
You can also follow the links on this page to:

2. Browse content by source publication.
3. Run searches for the most common techniques and organisms, or emerging techniques.
4. Check out recent blog posts from our editorial teams.



Performing a search

The search works across all Springer Nature protocols and methods content and has been optimised specifically for this purpose with recognition of common scientific synonyms and abbreviations. After entering your search term and clicking the search icon, you will reach the results page.



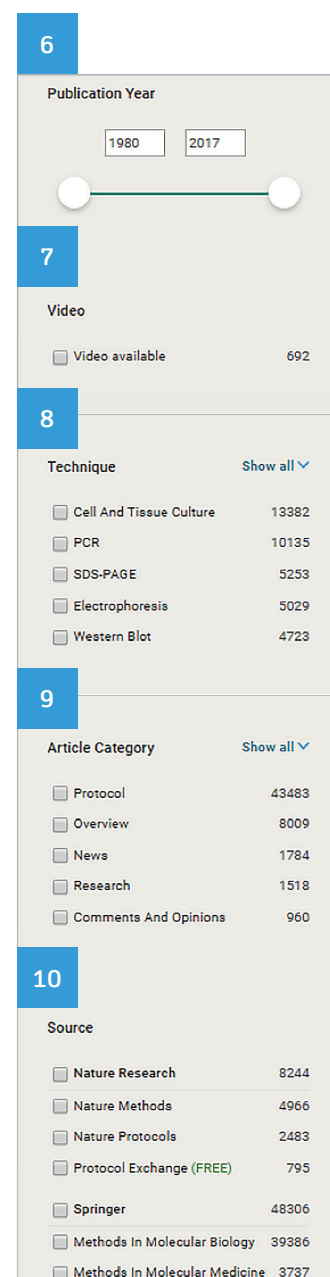
The search results page

- By default, search results are sorted by relevance but you also have the option to sort them by date of publication, views, citations and trending content (based on the number of downloads within the last month).

Refining your search results

In the left-hand column of the search results screen, you will find the search filters. These enable you to easily narrow down your search by:

- Publication year** – enter a start year and end year into the boxes or use the sliders to refine results to only those published within this date range. Content is available from 1980 to present.
- Video available** - filters to show just the articles with video content.
- Technique** – the techniques with the most matches will be shown in this collapsed menu, but you can click “Show all” to view the full list. This filter is powered by our in-house ontologies and AI/text-mining tools which enable us to identify and normalise techniques within full-text and deliver the most relevant results to you.
- Article category** – choose from different types of content, including protocols, overviews (introduction articles), reviews and research (articles and brief communications). Click “Show all” to expand the filter.
- Source** – refine results to a specific journal title or book series from the Springer Nature portfolio.



Evaluating your results

Within each search result, you will find a number of details that will help you to carry out an at-a-glance evaluation:

11. Article type.
12. Source and date of publication.
13. Title and authors.
14. Abstract snippet.
15. Techniques and organisms used, automatically extracted by our indexing tools.
16. Number of citations and downloads, based on data from Altmetrics or Bookmetrix.
17. You will also be able to see when a video is available within the protocol or method.

Once you have refined your results, you can click on a search result title to view the article evaluation page.

Search
results

12	Nature Methods (2013)	11	Brief Communication
13	Heritable genome editing in <i>C. elegans</i> via a CRISPR-Cas9 system		
	Ari E Friedland, Yonatan B Tzur, Kevin M Esvelt, Monica P Colaiácovo ... John A Calarco ✉		
14	We report the use of clustered, regularly interspaced, short palindromic repeats (CRISPR)-associated endonuclease Cas9 to target genomic sequences in the <i>Caenorhabditis elegans</i> germ line using single-guide RNAs that are expressed from a <i>U6</i> small ...		
15	Techniques: CRISPR-Cas9 Editing Organisms: <i>Caenorhabditis elegans</i>		
16	Citations: 262 Downloads: 27,782		Video available 17

18. **Keywords associated with this article:** in blue you can see the keywords automatically extracted by our extraction tools. Clicking any of these will perform a new search for the selected keyword. The keywords in black are those supplied by the author. We have removed duplicates from the keywords supplied by authors.
19. **Citation graph:** this shows the total number of citations as well as the citation trend of this particular article over the last 5 years.
20. **History:** This is an easy way to see whether an older and/or newer version of this protocol is available. For example, if the Editors have published an update following a significant development. Retractions, Erratums, Corrigendums or Addendums associated with the article will also be listed here. Clicking the links will take you to the related article's profile page.
21. **Abstract:** as published with the original article.
22. **Figures and videos:** here you can see all of the figures and videos associated with this article.
23. **Latest Citations:** A list of the last 3 articles that cited this particular protocol or method.

SPRINGER NATURE | Experiments

e.g. protocol, technique, organism

Q

Predicting the effects of coding non-synonymous variants on protein function using the SIFT algorithm

nature protocols

Vol. 4 (2009) > Issue: 7 (July)

Protocol | 25 June 2009 | DOI: 10.1038/nprot.2009.86

Authors: Prateek Kumar¹, Steven Henikoff^{1,3}, Pauline C Ng^{2,3}

Affiliations: [show](#)

Full text

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KEYWORDS

[Amino Acid Substitution](#), GI number, RefSeq identifier, UniProt, NCBI, Probability matrix

24

CITATIONS

2,157

Year	Citations
2014	~300
2015	~450
2016	~500
2017	~450
2018	~400

19

20

HISTORY

[2015 Robert Vaser...Pauline C Ng](#)
2009 (This version)

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Abstract

The effect of genetic mutation on phenotype is of significant interest in genetics. The type of genetic mutation that causes a single amino acid substitution (AAS) in a protein sequence is called a non-synonymous single nucleotide polymorphism (nsSNP). An nsSNP could potentially affect the function of the protein, subsequently altering the carrier's phenotype. This protocol describes the use of the 'Sorting Tolerant From Intolerant' (SIFT) algorithm in predicting whether an AAS affects protein function. To assess the effect of a substitution, SIFT assumes that important positions in a protein sequence have been conserved throughout evolution and therefore substitutions at these positions may affect protein function. Thus, by using sequence homology, SIFT predicts the effects of all possible substitutions at each position in the protein sequence. The protocol typically takes 5–20 min, depending on the input. SIFT is available as an online tool (<http://sift-dna.org>). [less](#)

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Latest Citations (2,157)

1. Isel Grau et al., 2018, Lecture Notes in Networks and Systems
2. Jay P. Ross et al., 2017, Neurobiology of Aging
3. Elvin Yildiz et al., 2017, Current Eye Research

FIGURES & VIDEOS

Figure 1 : 'Sorting Tolerant From Intolerant' (SIFT) algorithm flowchart for scoring individual amino acid substitutions (AASs).

Accessing the full-text content

Clicking on the Full text button (24) within the article profile page will take you through to the content on its source platform – nature.com for content from *Nature Protocols* and *Nature Methods* or SpringerLink for content from SpringerProtocols.

Please note that you will need to have a current subscription to access the full-text content from *Nature Protocols*, *Nature Methods* and SpringerProtocols (with the exception of some book titles). All of the content from Protocol Exchange is free to access. Please check with your librarian, or ask them to contact us if you cannot access the full-text content.

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