

UNSILO

Reviewer Finder FAQ

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Is UNSILO Reviewer Finder a UI product or an API?

UNSILO Reviewer Finder is an API that integrates with Manuscript Tracking Systems (MTS). To demonstrate the capabilities of this API, UNSILO has developed a showcase UI for its features that editors and other trial users can trial. The normal customer adoption procedure is to trial the showcase, and if they are interested in adopting the product, then requesting an integration with an MTS or making use of an already existing integration with an MTS. Integrations are either built or being developed for several MTS suites. Read more in [What systems offer integration with the API?](#)

What are the key benefits?

- Auto-match manuscripts to reviewers independently of generic/ manual keyword tags.
- Find reviewers based on analyses that include their most recently published papers.
- Related H-indexes that are calculated relative to the context of each individual manuscript.
- Auto-match reviewers to manuscripts across synonymous terms and abbreviations.
- Email addresses can automatically filter to show the most recently published address.
- Automatically detect and filter out 3-year co-author and current co-affiliation COIs.
- Avoid sending invites to reviewers that are not in scope with their published expertise.
- Easily integrate the Reviewer Finder API to surface results in your existing review system.
- Reviewer Finder does not replace humans: the editor decides which reviewers to contact.

What subjects does it find reviewers in?

UNSILO and the Reviewer Finder use a technology that is based around a background corpus. Currently, PubMed serves as the backdrop for Reviewer Finder. Suitable manuscripts only include those that match PubMed's scope of biomedical, health, and life sciences research. The technology is domain agnostic, and we are working on expansion into other subjects.

What systems offer integration with the API?

We are keen to provide integration with any MTS software that you use. We are currently working on Q1 2020 integrations with Editorial Manager and Manuscript Manager. Trials are underway with eJP and BenchPress customers that could prompt integrations, and other proprietary systems are also most welcome to integrate the API, as done by [PeerJ](#). ScholarOne currently are not planning to integrate the service, so we recommend that interested customers trial the UNSILO web showcase first, and pending their trial conclusions, contact ScholarOne to make their interests known. Contact us to discuss integration with these or any other systems: info@unsilo.ai.

What does it cost?

We offer Reviewer Finder at very competitive tier pricing based on the amount of annual submissions across all participating journals per customer, and we offer discount incentives for onboarding, multi-year license agreements, and purchase of multiple products. Estimate base pricing for Reviewer Finder in the table below and contact us for a conversation about possible discounts and a quote: info@unsilo.ai.

Service	Number of annual manuscript submissions to the Reviewer Finder API							
	1	2	3	4	5	6	7	8
	< 500	500 – 1,000	1,001 – 2,500	2,501 – 5,000	5,001 – 10,000	10,001 – 15,000	15,001 – 20,000	> 20,000
Reviewer Finder price (EUR)	€500	€1,000	€2,500	€5,000	€10,000	€15,000	€20,000	To be negotiated

How do I get trial access?

We offer journals and publishers 1-month non-binding trials via a secure UNSILO web showcase. Contact us to enquire about trial access: info@unsilo.ai. If you are a systems owner who wants to consider trial API integration with your system, please review [Where can I find API documentation?](#)

What file formats are accepted?

The solution accepts .doc, .docx, txt, and .pdf. The solution does not yet support LaTeX files.

How does UNSILO Related H-index work?

Reviewer Finder provides a range of decision support proxies that help editors assess suitability of reviewers. One such proxy is the unique UNSILO Related H-index.

- Traditional H-indexes do not necessarily say much about a reviewer’s matching with a manuscript. Some of a reviewer’s publications and citations may not relate much to the topic of a given manuscript.
- UNSILO Related H-indexes count reviewer publications that are similar, or as we say ‘related’, to a manuscript. A reviewer’s expertise may vary on different topics, and as a result, the reviewer may score different H-indexes for different manuscripts .
- The H-index figures are for reference only, and can be ignored if you prefer to use other metrics.

A generic H-index of 20 means that the researcher has 20 papers, each of which has been cited 20+ times. An UNSILO Related H-index of 20 means that the researcher has 20 papers that are related to the manuscript you need reviewers for, and each of which has been cited 20+ times.

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Ian H Gilbert
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Wellcome Centre for Anti-infectives Research, Drug Discovery Unit, Division of Biological Chemistry and Drug Discovery, University of Dundee, DD1 5EH Dundee, United Kingdom

17+ years of related experience
 82 related papers published
 Related H-Index: **23**
 Latest publication: 2019
 Latest journal: ChemMedChem
 Favorite journal: Journal of medicinal chemistry (16)

Concept groups
 Author's coverage of concept groups from your manuscript.

- Protein N-myristoyltransferase...
- Protozoan
- Malaria

All covered concepts
 Author's coverage of concepts from your manuscript.

N-myristoyltransferase N-myristoyltransferase inhibitors
 DDD85646 SHOW MORE >

Related papers published by Ian H Gilbert

Selective Inhibitors of Protozoan Protein N-myristoyltransferases as Starting Points for Tropical Disease Medicinal Chemistry

Example of the Related H-Index. This score by nature of its calculation does not intend to match generic H-Indexes found elsewhere.

Brannigan, 3, Edward W.

Department, Kent, United Kingdom, 3 Department of Chemistry, University of York, York, United Kingdom, 4 Opportunities for Partnership in Medicine, Pfizer Worldwide Research and Development, Kent, United Kingdom, 5 Institute of Chemical Biology, Department of Chemistry, Imperial College, London, United Kingdom, 6 Division of Parasitology, Medical Research Council National Institute for Medical Research, London, United Kingdom, 7 Department of Biology, University of York, York, United Kingdom, Northeastern University, United States of America
 Corresponding author: * E-mail: ku.ca.lairepmi@11leeb.a Current address: Institute of Chemical Biology, Department of Chemistry, Imperial College, London, United Kingdom
 Conceived and designed the experiments: ASB DFS RJL GPW EWT AJW AAH. Performed the experiments: GPW JEM. Analyzed the data: ASB GPW JEM. Contributed reagents/materials/analysis tools: JAB JEM. Wrote the paper: ASB GPW TP JAB DFS.

Abstract.
 Inhibition of N-myristoyltransferase has been validated pre-clinically as a target for the treatment of fungal and trypanosome infections, using species-specific inhibitors.

Ian Gilbert
 Head of Biological Chemistry and Drug Discovery, University of Dundee
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	All	Since 2014
Citations	7221	3909
h-index	50	31
i10-index	130	97

YEAR

Example of the same researcher's generic H-index calculated by Google Scholar. It naturally does not match the UNSILO Related H-index, because they are based on different corpuses and also calculate differently.

TITLE

Automated design of...
 J Besnard, GF Ruda, V Nature 492 (7428), 215

N-myristoyltransferase...
 JA Frearson, S Brand, S Nature 464 (7289), 728

A novel multiple-sta...
 B Baragaña, I Hallyburton, Nature 522 (7556), 315

Design and synthesis of a series of melamine-based nitroheterocycles with activity against trypanosomatid parasites 186 2005
 A Ballani, GJ Bueno, ML Stewart, V Yardley, R Brun, MP Barrett, IH Gilbert
 Journal of medicinal chemistry 48 (17), 5570-5579

Lessons learnt from assembling screening libraries for drug discovery for neglected diseases 185 2008
 R Brenk, A Schipani, D James, A Krasowski, IH Gilbert, J Frearson, ...
 ChemMedChem: Chemistry Enabling Drug Discovery 3 (3), 435-444

Anti-trypanosomatid drug discovery: an ongoing challenge and a continuing need 151 2017
 MC Field, D Horn, AH Fairlamb, MAJ Ferguson, DW Gray, KD Read, ...
 Nature Reviews Microbiology 15 (4), 217-231

Target assessment for antiparasitic drug discovery 136 2007
 JA Frearson, PG Wyatt, IH Gilbert, AH Fairlamb
 Trends in parasitology 23 (12), 589-595

Synthesis and biological evaluation of s-triazine substituted polyamines as potential new anti-trypanosomal drugs 132 2001
 B Klenke, M Stewart, MP Barrett, R Brun, IH Gilbert
 Journal of medicinal chemistry 44 (21), 3440-3452

How does concept grouping work?

The solution matches reviewers with manuscripts based on overarching subjects that emerge when the software vectors and clusters concepts extracted from manuscripts and reviewer publication histories. This improves matching of more reviewers with niche/ edge content, and matching of manuscripts with reviewers who have smaller concept fingerprints. For more on concepts, please read [What are concepts?](#)

Imagine that the software extracts 100 concepts from a manuscript and 100 concepts from a reviewer profile, but only finds direct overlaps between concepts on 40%. Initially one may assume the reviewer is not appropriate. However, if the software clusters and groups the concepts into overarching topics, one may discover that the reviewer does indeed match the manuscript through the mix of overarching topics and concepts. Contact us to test how well it works: info@unsilo.ai.

The screenshot displays the 'Reviewer Finder' interface. On the left, a sidebar shows 'Concept groups found in manuscript' with a tree structure: 'Hepatitis C Virus Polymerase', 'Virus', and 'Genotype 3a Hepatitis'. Under 'Genotype 3a Hepatitis', several concept tags are listed: 'Hepatitis C Virus Genotype 3a', 'Genotype 2a isolate', 'Genotype 3a Hepatitis', 'Genotype 3a Virus', 'Genotype 3a', 'Virus Genotype', and '3a Hepatitis'. Below this, a reviewer profile for 'Jens Bukh' is shown, including his email and a list of his associated concepts with progress bars: 'Hepatitis C Virus Polymerase', 'Virus', and 'Genotype 3a Hepatitis'. On the right, a snippet of a manuscript abstract is visible, titled 'Amino Acid Substitutions in Genotype 3a Hepatitis C Virus Polymerase Protein Affect Responses to Sofosbuvir.' A red box highlights the title and author list, with an arrow pointing to the concept tags in the sidebar, labeled 'Example of concept grouping'.

Amino Acid Substitutions in Genotype 3a Hepatitis C Virus Polymerase Protein Affect Responses to Sofosbuvir.

Peter A. C. Wing¹, Meleri Jones¹, Michelle Cheung¹, Sampath DaSilva¹, Connor Bamford², Wing-Yiu Jason Lee¹, Elihu Aranday-Cortes², Ana Da Silva Filipe², John McLauchlan², David Smith^{3, 4}, William Irving^{5, 6}, Morven Cunningham¹, Azim Ansari^{3, 4}, Eleanor Barnes^{3, 4}, Graham R. Foster¹.

Example of concept grouping

Abstract.

Sofosbuvir is a frequently used pan-genotype inhibitor of hepatitis C virus (HCV) polymerase. This drug eliminates most chronic HCV infections, and resistance-associated substitutions in the polymerase are rare. However, HCV genotype 3 responds slightly less well to sofosbuvir-based therapies than other genotypes. We collected data from England's National Health Service Early Access Program to search for virus factors associated with sofosbuvir treatment failure. We collected patient serum samples and used the capture-fusion assay to assess viral sensitivity to sofosbuvir in 14 HCV genotype 3 samples. We identified polymorphisms associated

[SEE ALL REVIEWERS](#)

Stefan Zeuzem
zeuzem@em.uni-frankfurt.de
 Goethe-Universität, Frankfurt am Main, Germany
 17+ years of related experience
 200+ related papers published
 Related H-index: 67
 Latest publication: 2019
 Latest journal: *European journal of gastroenterology & hepatology*
 Favorite journal: *Journal of hepatology* (74)

Concept groups
 Author's coverage of concept groups from your manuscript.

- > Hepatitis C Virus Polymerase
- > Virus
- < Genotype 3a Hepatitis

Hepatitis C Virus Genotype 3a Genotype 2a Isolate
 Genotype 3a Hepatitis Genotype 3a Virus Genotype 3a
 Virus Genotype 3a Hepatitis

All covered concepts
 Author's coverage of concepts from your manuscript.

Sofosbuvir Hepatitis C Virus Genotype NS5b

Amino Acid Substitutions in Genotype 3a Hepatitis C Virus Polymerase Protein Affect Responses to Sofosbuvir.

Peter A. C. Wing 1, Meleri Jones 1, Michelle Cheung 1, Sampath DaSilva 1, Connor Bamford 2, Wing-Yiu Jason Lee 1, Elihu Aranday-Cortes 2, Ana Da Silva Filipe 2, John McLauchlan 2, David Smith 3, 4, William Irving 5, 6, Morven Cunningham 1, Azim Ansari 3, 4, Eleanor Barnes 3, 4, Graham R. Foster 1.

1 Barts Liver Centre, Blizard Institute, Queen Mary University of London, London, UK; 2 Medical Research Council, University of Glasgow Centre for Virus Research, Glasgow, UK; 3 Nuffield Department of Medicine, University of Oxford, Oxford, UK; 4 National Institute for Health Research, Oxford Biomedical Research Centre, Oxford University National Health Service Trust, Oxford, UK; 5 National Institute for Health Research, Oxford National Health Service Trust, Oxford, UK; 6 National Institute for Health Research, Oxford National Health Service Trust, Oxford, UK

ABSTRACT.
 Sofosbuvir is a frequently used pan-genotype inhibitor of hepatitis C virus (HCV) polymerase. This drug eliminates most chronic HCV infections, and resistance-associated substitutions in the polymerase are rare. However, HCV genotype 3 responds slightly less well to sofosbuvir-based therapies than other genotypes. We collected data from England's National Health Service Early Access Program to search for virus factors associated with sofosbuvir treatment failure. We collected patient serum samples and used the capture-fusion assay to assess viral sensitivity to sofosbuvir in 14 HCV genotype 3 samples. We identified polymorphisms associated

Example of concept group matching between reviewer and manuscript

What are concepts?

Concepts are words and phrases in a text that UNSILO software detects as significant compared to all the other texts in the corpus. They can be imagined as the 'fingerprint' of texts. UNSILO software identifies concepts without the use of any pre-existing taxonomy or ontology, but by analyzing text.

Concepts are the pieces of text that define what any given sentence is about, without any of the filler words. Take for instance the sentence:

“However, HCV genotype 3 responds slightly less well to sofosbuvir-based therapies than other genotypes”.

The high level concepts here are:

- HCV genotype 3
- Sofosbuvir-based therapies
- genotypes

Now scale this analysis across all the sentences in a text for a full fingerprint. UNSILO software recognizes the concepts and automatically scores them for importance in the entire text. Concepts form the basis of many UNSILO services, including Reviewer Finder's ability to match manuscripts with the publication data of potential reviewers.

What are the software license agreement terms?

Contact us for our software license agreement: info@unsilo.ai.

What happens to uploaded content after reviewer suggestions are generated?

UNSILO guards the confidentiality of uploaded content and never shares it with third parties or reproduces the original text of uploaded content. UNSILO may train machine learning models and build algorithms to recognize and extract structural and qualitative aspects of the content, and any mathematical models, algorithms, and digital representations of knowledge trained on the content belongs to UNSILO, but the original content remains the copyright of the author or publisher.

To facilitate seamless user access, service debugging, and technical support, content is stored for a caching period of up to 30 days after the last user interaction with the content, after which period all content is securely deleted. In order to provide analytics and trend analysis to our partners and users, UNSILO may store limited metrics and statistical information deduced from content beyond the Caching Period, including i) Concept Fingerprints, ii) Metadata such as Author Information, and iii) Aggregated Concept Scores. UNSILO guarantees that the original full text of content cannot in any way be reconstructed from information persisted beyond the caching period.

Where can I find API documentation?

Read here for the latest [Reviewer Finder API documentation](#)

How often is the software updated?

The backdrop that is analyzed in order to find reviewers is updated daily with new publications. The software itself is updated as often as weekly, and improvements are communicated to customers in release updates.