A tool supported by R430D024432, R44MH119094

SCISCORE FOR RIGOR AND REPRODUCIBILITY

Anita Bandrowski
Martijn Roelandse

REPRODUCIBILITY CRISIS

the effect size of a poorly controlled study is about 50% bigger than the effect size of a well controlled study.

Is it possible that poorly controlled animal studies are repeated using proper controls in clinical trials and fail because the effects were never significant to begin with?

SciScore

AMERICAN SOCIETY FOR MICROBIOLOGY | mBio® AN OPEN ACCESS JOURNAL PUBLISHED BY THE AMERICAN SOCIETY FOR MICROBIOLOGY

mBio. 2019 Jul-Aug; 10(4): e01942-19.
Published online 2019 Aug 27. doi: 10.1128/mBio.01942-19

PMCID: PMC6712400
PMID: 31455655

Interaction of the Ankyrin H Core Effector of *Legionella* with the Host LARP7 Component of the 7SK snRNP Complex

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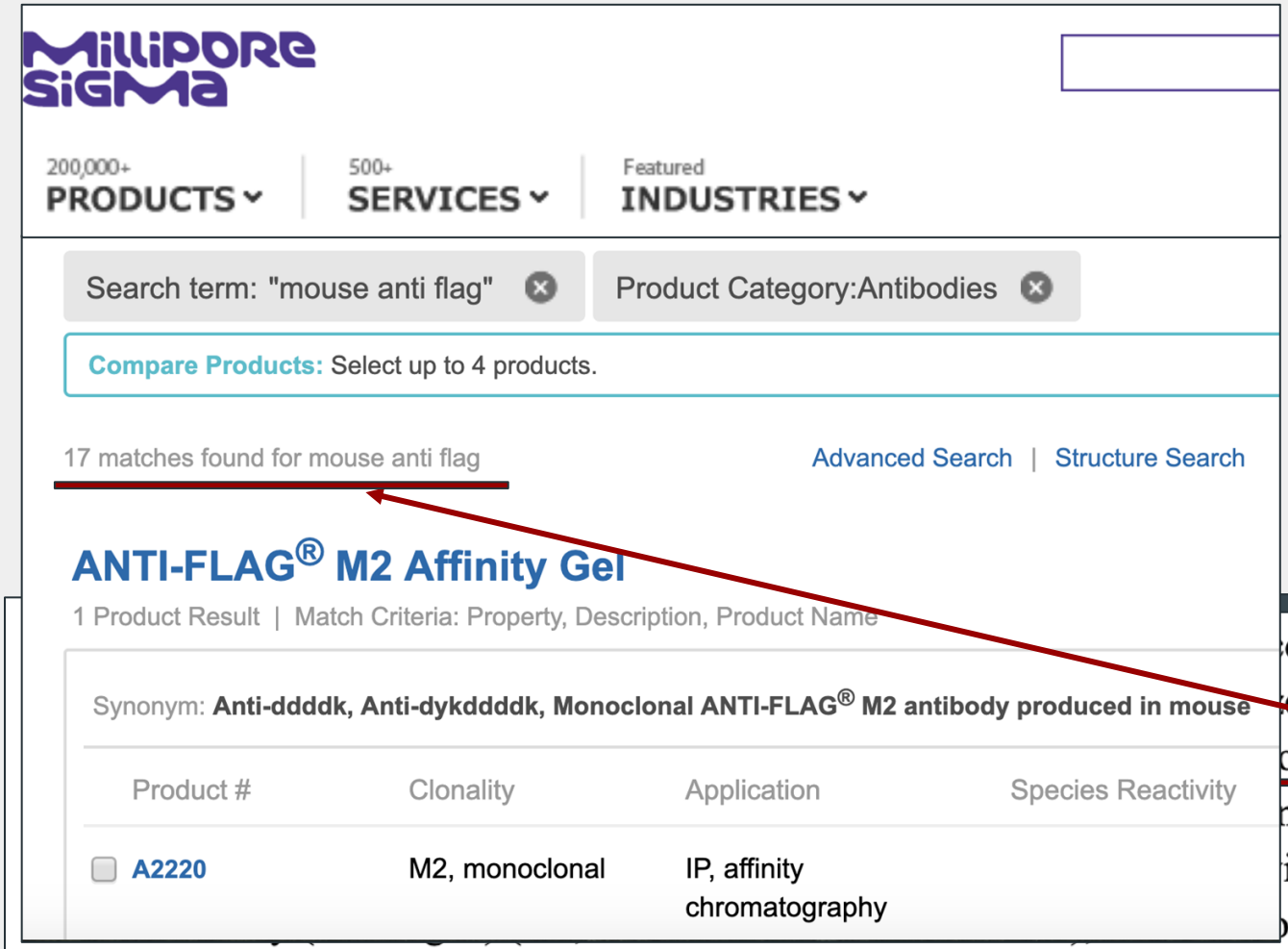
Scot P. Ouellette, Editor
Scot P. Ouellette, University of Nebraska Medical Center;

ENTREZ

RRID

Confocal laser scanning microscopy. Processing of transfected cells for confocal microscopy was performed as we described previously. Briefly, monolayers were permeabilized and fixed using 100% methanol held at –20°C for 5 min and were then blocked and labeled with mouse-anti-FLAG (Sigma) (1/200 dilution in 3% bovine serum albumin [BSA]–phosphate-buffered saline [PBS]) and rabbit-anti-Myc (Proteintech) (1/200 dilution in 3% BSA–PBS). Cells were counterlabeled with Alexa Fluor 488 anti-mouse antibody (Invitrogen) (1/4,000 dilution in 3% BSA–PBS), Alexa-Fluor 555 anti-rabbit antibody



NO IDENTIFIER FOR REAGENTS

=

NOT REPRODUCIBLE

onfocal microscopy was
ed and fixed using 100%
ouse-anti-FLAG (Sigma)
ne [PBS]) and rabbit-anti-Myc
ith Alexa Fluor 488 anti-
r 555 anti-rabbit antibody

SO WHERE ARE WE NOW?

WE ARE CURRENTLY IN 5TH YEAR OF A 3-MONTH PILOT

NIF, INCF, members of the NIH, and about 25 major journal Editors in Chief, began to talk about research resource reproducibility

- 2012: 1st meeting at the Commander's Palace @ Society for Neuroscience
  2013: 2nd meeting at NIH
- 2014: Pilot project started; 25 journals would ask authors to provide RRIDs for 3 months, 2 journals started on time

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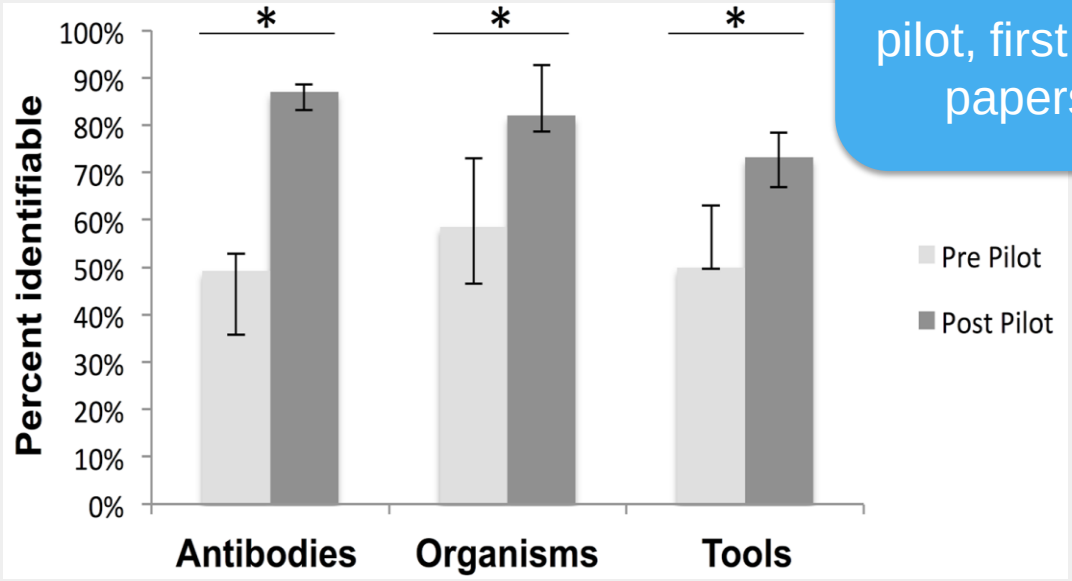
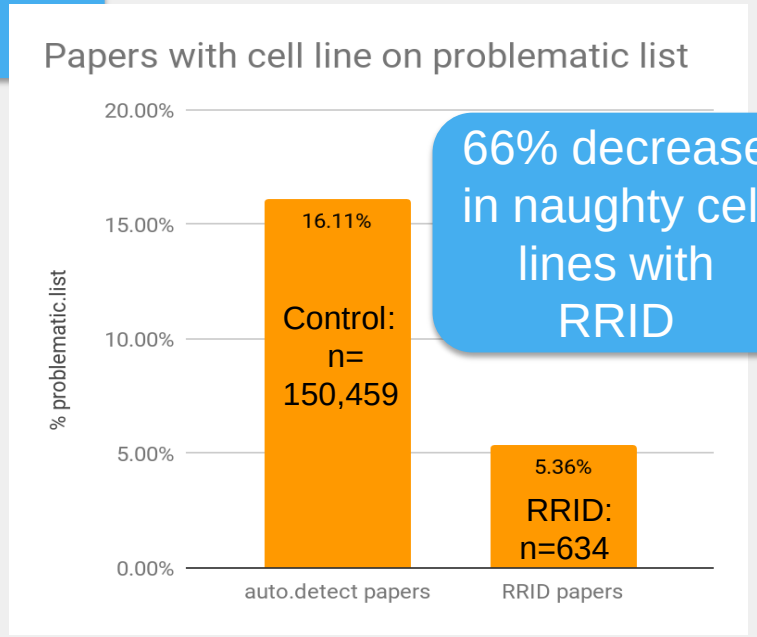
RRIDS = BETTER PAPERS

Data is based on the RRID pilot, first 100 papers

Resource Identification Initiative



Bandrowski et al, 2015a,b,c,d



66% decrease in naughty cell lines with RRID

Babic et al, eLife, 2019

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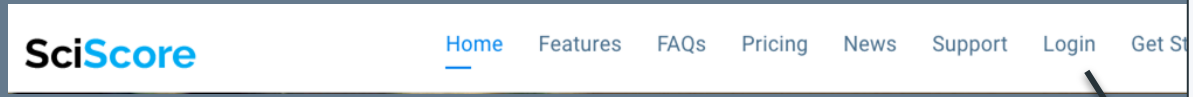
NEXT STEP: SCISCORE - THE TOOL THAT MAKES RRID'S A REALITY

SciScore checks whether the authors address sex, blinding, randomization of subjects into groups, power analysis, as well as key resources.

The tool produces a score that roughly corresponds to the number of criteria filled in vs the number that were expected.

SciScore

SCISCORE.COM IS FREELY ACCESSIBLE FOR AUTHORS AND IT IS INTENDED TO IMPROVE MANUSCRIPTS



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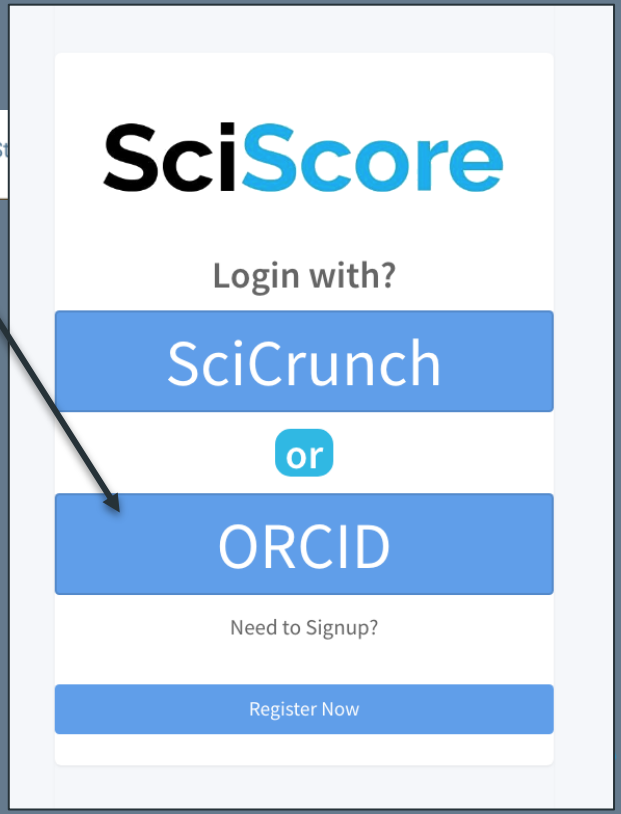

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SCISCORE TAKES AS INPUT THE METHODS SECTION OF MANUSCRIPTS

JBC JOURNAL OF BIOLOGICAL CHEMISTRY
Published by the American Society for Biochemistry and Molecular Biology

J Biol Chem. 2018 Sep 14; 293(37): 14444–14454.
Published online 2018 Jul 27. doi: 10.1074/jbc.RA118.003681
PMCID: PMC
PMID: 3

Role of a conserved glutamine in the function of voltage-gated Ca^{2+} channels revealed by a mutation in human *CACNA1D*

Edgar Garza-Lopez,‡ Josue A. Lopez,‡ Jussara Hagen,‡ Ruth Sheffer,§ Vardiella Meiner,§ and Amy Lee‡

Author information · Article notes · Copyright and License information Disclaimer

Experimental procedures Go to:

Genetic analysis

This study abides by the Declaration of Helsinki principles and was approved by the Institutional Review Board at Hadassah-Hebrew University Hospital. Affected patients' guardians gave informed consent for exome sequencing and to publication of this study.

Whole exome sequencing was performed as described previously (51). Briefly, exonic sequences were enriched using SureSelect Human All Exon 50 megabase kit (Agilent Technologies, Santa Clara, CA). Sequences were determined by HiSeq 2500 (Illu
analysis including read alignment and variant ca
CA) using the default parameters with the huma
analysis of the analyzed individuals yielded 44.
Following alignment to the reference genome (h
were off-target (>8 bp from splice junction), syn
frequency >0.01 in the ExAC database (Exome A
http://exac.broadinstitute.org)[3] or in our in-house exome database comprising ~2500 exomes. All potentially causative variants were confirmed using Sanger sequencing.

Copy methods section, paste into sciscore.com to create a report

Molecular biology

The following cDNAs were used: $Ca_V1.3$ (GenBank™ no. AF370009), $Ca_V2.1$ (GenBank™ no. NM_001127221), $Ca_V3.1$ (AF190860), β_{2a} (GenBank™ no. NC013684), and $\alpha_2\delta_1$ (GenBank™ no. M76559.1). The Q558H mutation was inserted into the corresponding regions of the domain II S1–S2 linker (IIS1–S2L) in $Ca_V1.3$, $Ca_V2.1$, and $Ca_V3.1$ using the NEBuilder HiFi DNA Assembly cloning system (New England Biolabs). Channel fragments were amplified by PCR with appropriate primers and ligated into the parent plasmid ($Ca_V1.3$/pcDNA6, $Ca_V2.1$/pcDNA3.1, $Ca_V3.1$/pDsRed Express-N1). For the FLAG-tagged $Ca_V1.3$ WT and Q567H constructs, a FLAG epitope with spacer sequences (TRH-DYKDDDDK-VTFDEMQT) was added to the extracellular loop just C-terminal to residue Gly-693 by

THE SCISCORE REPORT CONTAINS 2 TABLES:

RIGOR & RESOURCES

Table 1: Rigor Adherence

Institutional Review Board Statement
IRB: The study was approved by the institutional review board of Cedars-Sinai Medical Center.
Consent: All subjects were informed about the study and signed written informed consent before the study took place.
Randomization
In each animal experiment, mice were randomly assigned to each group.
Blinding
Not detected.
Power Analysis
Power analysis was performed using an alpha error probability of 0.05 and a power level of 0.8 to select sample sizes for behavioral experiments.
Sex as a biological variable
Not detected.
Cell Line Authentication
Authentication: All cell lines were authenticated using short tandem repeat (STR) profiling.
Contamination: All cell lines used were regularly tested negative for mycoplasma contamination throughout the whole duration of this study.

Author's sentence detected

The **rigor table** pulls sentences from the methods section that fit the criteria.

For example, in this paper SciScore detected that power analysis was present. +1

Statements on Blinding or Cell Line Authentication were not detected by SciScore. +0

SciScore

THE SCISCORE REPORT CONTAINS 2 TABLES:

RIGOR & RESOURCES

Table 2: Key Resources Table

Your Sentences	REAGENT or RESOURCE	SOURCE	IDENTIFIER
Antibodies			
Primary anti-GFP antibody was obtained from Santa Cruz Biotechnology (USA; Cat# sc-9996, RRID:AB_627696).	anti-GFP		Unresolved: RRID:AB_627696 Suggestion: (Santa Cruz Biotechnology Cat# sc-9996, RRID:AB_627695) (link)
Experimental Models: Cell Lines			
HepG2 macrophage cells were obtained from DSMZ (Braunschweig, Germany) and maintained in a 37°C with 5% CO2.	HepG2	DSMZ	Warning: Problematic cell line: Misidentified/contaminated (DSMZ Cat# ACC-180, RRID:CVCL_0027) (link)
Experimental Models: Organisms/Strains			
Eight-week old wild-type C57BL/6 mice (initially generated inJAX Laboratory) were purchased from the Animal Center of Renmin Hospital of Wuhan University.	C57BL/6		Not detected.
Recombinant DNA			
Not applicable.			
Software and Algorithms			
All analyses were performed with SPSS version 20.0 (SPSS Inc., USA)	SPSS		Suggestion: (SPSS, RRID:SCR_002865) (link)

Expected Information is recognized (+1)

Expected Information is missing (+0)

Expected Information is missing but retrievable

The **resources table** pulls sentences from the methods section that contain some resource, organized by type.

When information matches the wrong identifier or a problematic resource SciScore warns authors.

SciScore

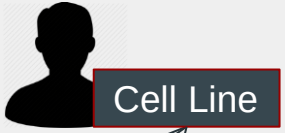
SCISCORE - HOW IT WAS MADE

- ~30 algorithms that work in concert to
  - identify named entities
  - classify papers / sections
- Lookup tables for reagents
- Classifier types used:
  - neural networks
  - standard NER
  - POS, sentence diagrams
- Reports are assembled by rules,
  - if a cell line is detected -> detect cell line authentication
  - If a cell line is contaminated -> red error message

SciScore

SCISCORE - HOW IT WAS MADE

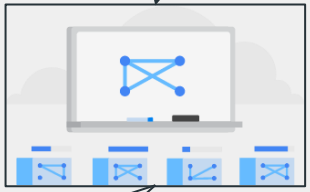
Step 1: annotate sentences:



Sentence 1 (methods sentence line 353; PMID:26012578)

For luciferase activity assays, **HeLa** or **HCN-A94** cells were grown in 24 well plates and transfected with 0.1 µg phRL-TK-10BOXB plasmid, 0.1 µg of pGL3 promoter plasmid and with 0.7 µg of one of the six pCl- λN-HA-tagged UPF3B expression constructs.

Step 2: algorithm training



Step 3: check different sentences

Sentence 2 (methods sentence line 125; PMID:28638484)

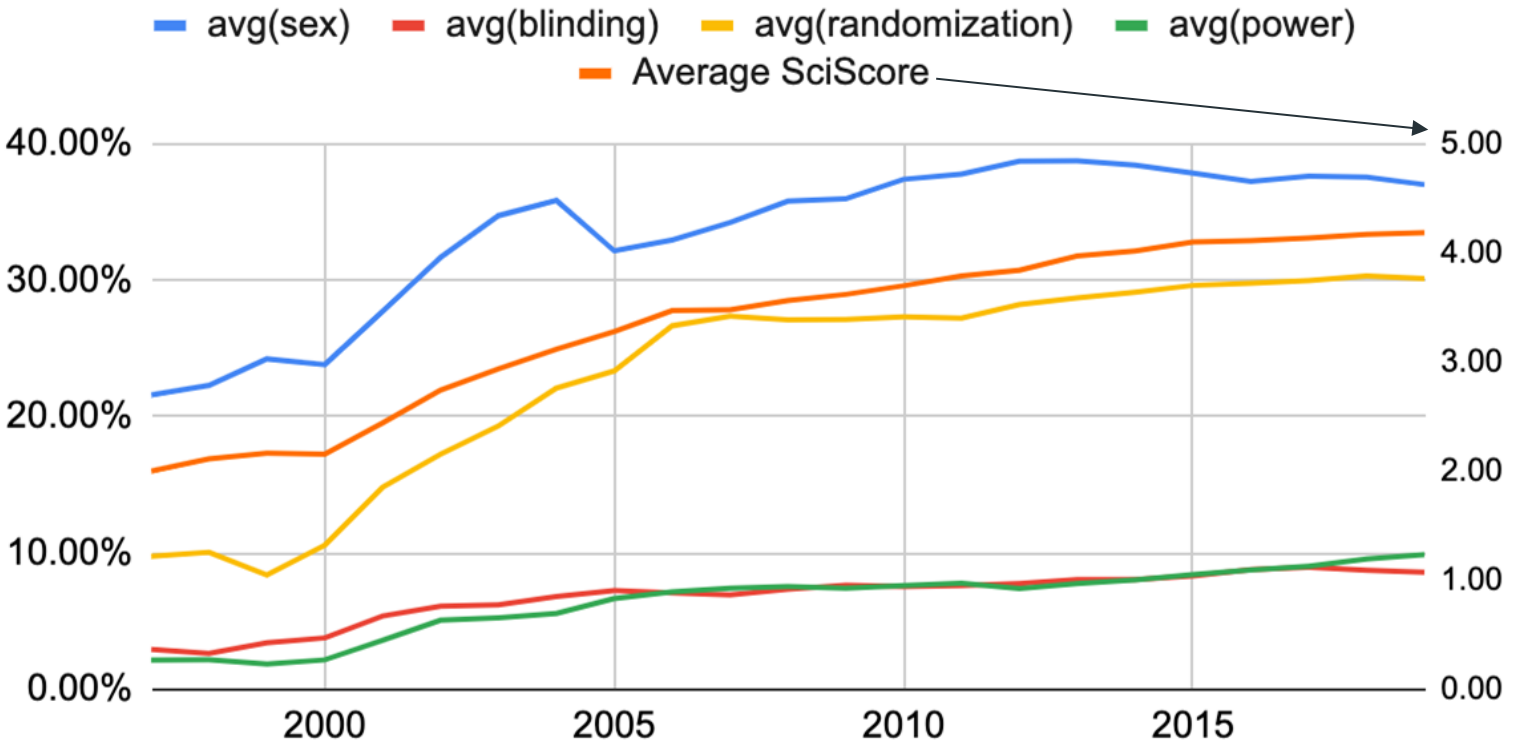
For cellular uptake kinetics study, **HeLa** *(false negative)* or **RAW264.7** *(correct annotation)* cells were seeded into 96-well plates and allowed to attach for 24h.

Classifier Type	F1	Precis.	Recall	Training Set Size
Rigor Criteria				
Institutional Review Board	76.9	88.2	68.2	340
Consent Statement	96.8	97.8	95.7	373
Animal Care Statement	77.9	82.2	74.0	591
Randomization of subjects	80.6	86.2	75.8	368
Blinding of investigator or analysis	96.3	100	92.9	183
Power analysis for group size	90.9	83.3	100	81
Sex as a biological variable	92.6	98.9	87.0	862
Cell Line Authentication	66.7	76.9	58.8	155
Cell Line Contamination	85.7	90.0	81.8	151
Key Biological Resources				
Antibody	78.8	87.2	71.9	16,772
Organism	71.6	81.6	63.8	4,439
Cell Line	72.1	79.2	66.1	1,763
Software Project/Tool	89.8	94.1	85.8	10,161

SO WE GOT TO THINKING, IF EVERY PAPER IN BIOMEDICINE CAN BE SCORED, WHAT WOULD THOSE SCORES LOOK LIKE?

WE RAN SCISCORE ON THE OA CORPUS* AT PUBMED CENTRAL

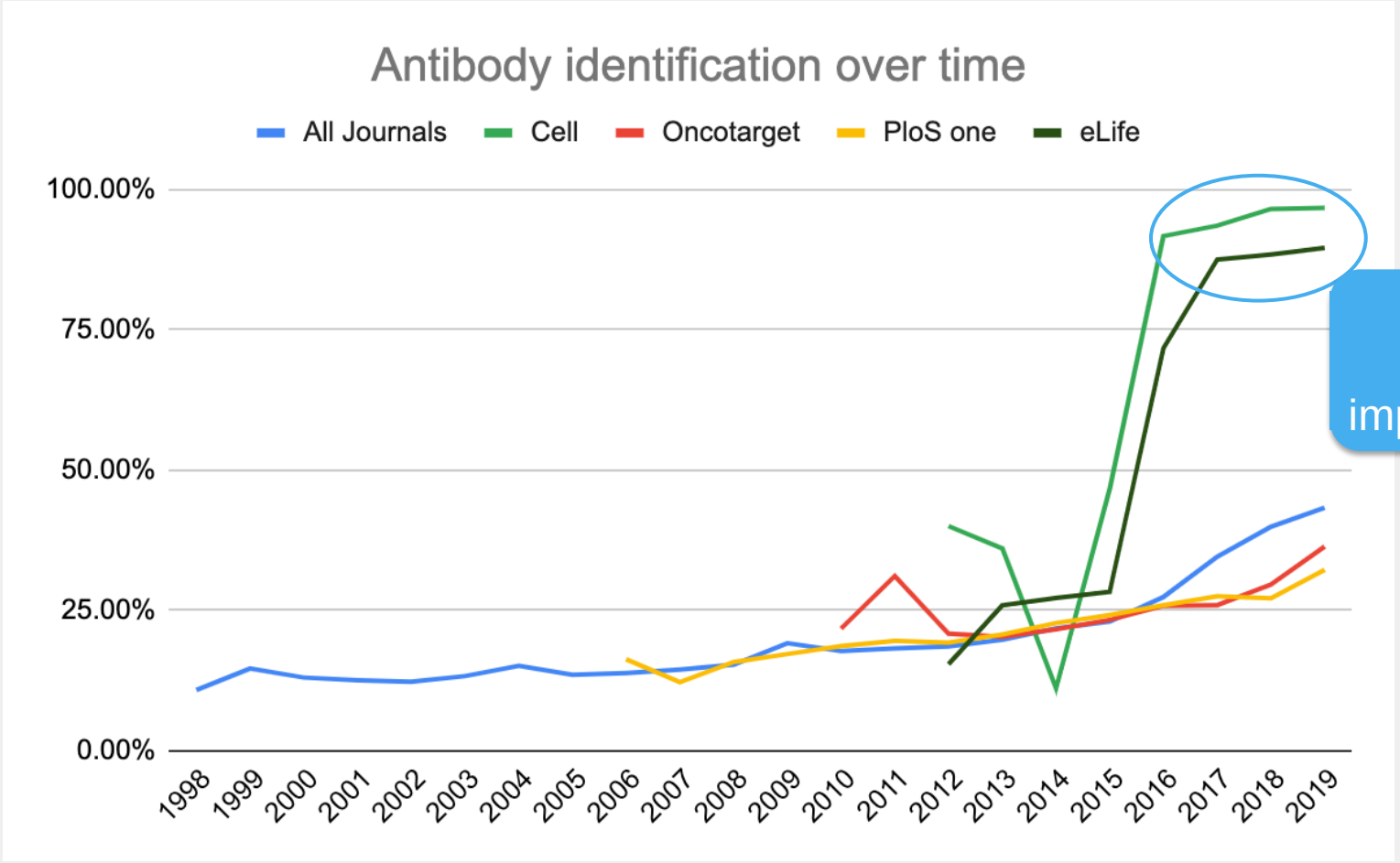
Papers addressing sex, blinding, randomization of subjects, and power analysis



* 1.6 million papers from 4,686 journals

SciScore

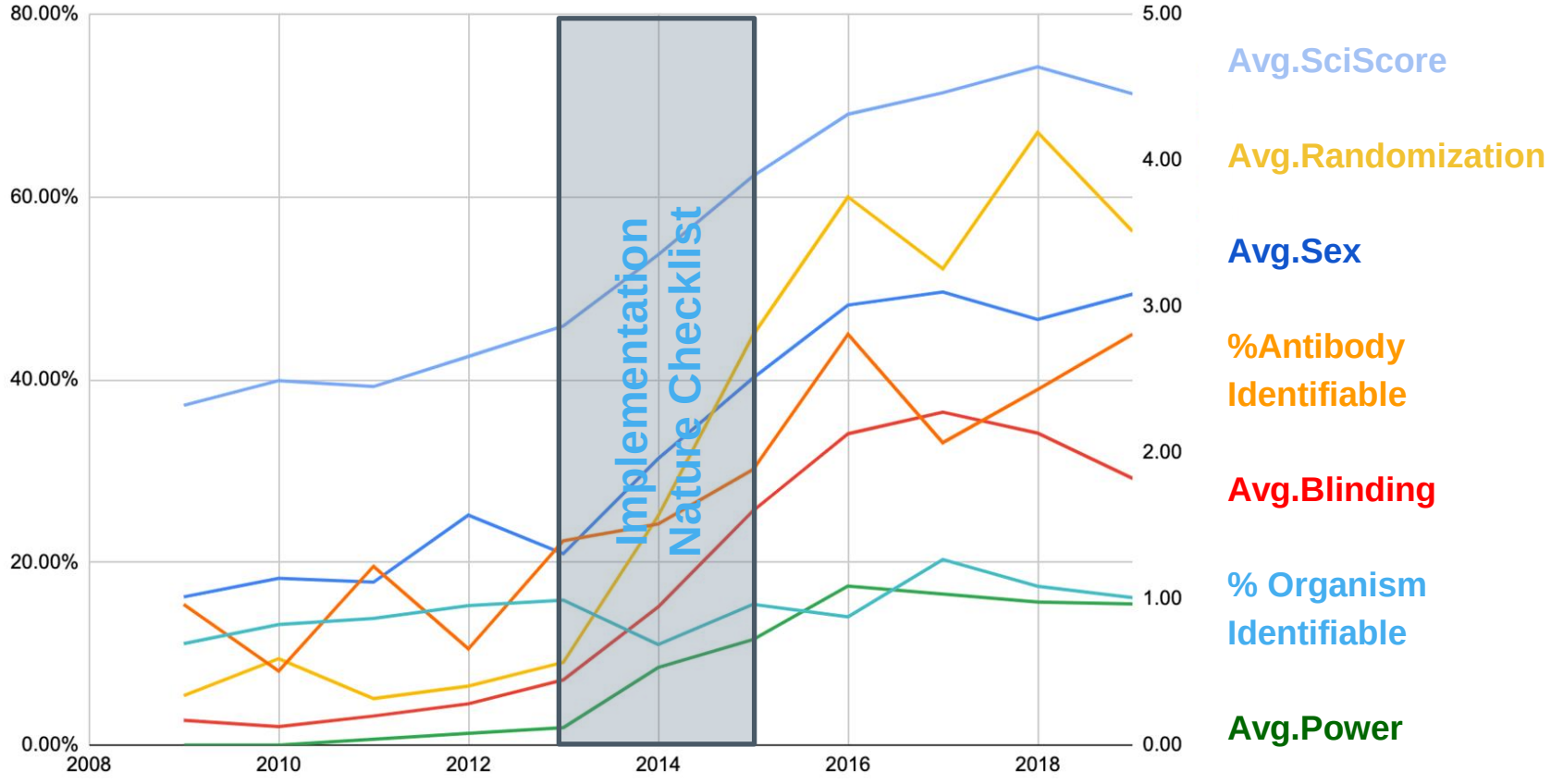
STANDARDS HELP TO IMPROVE ANTIBODY



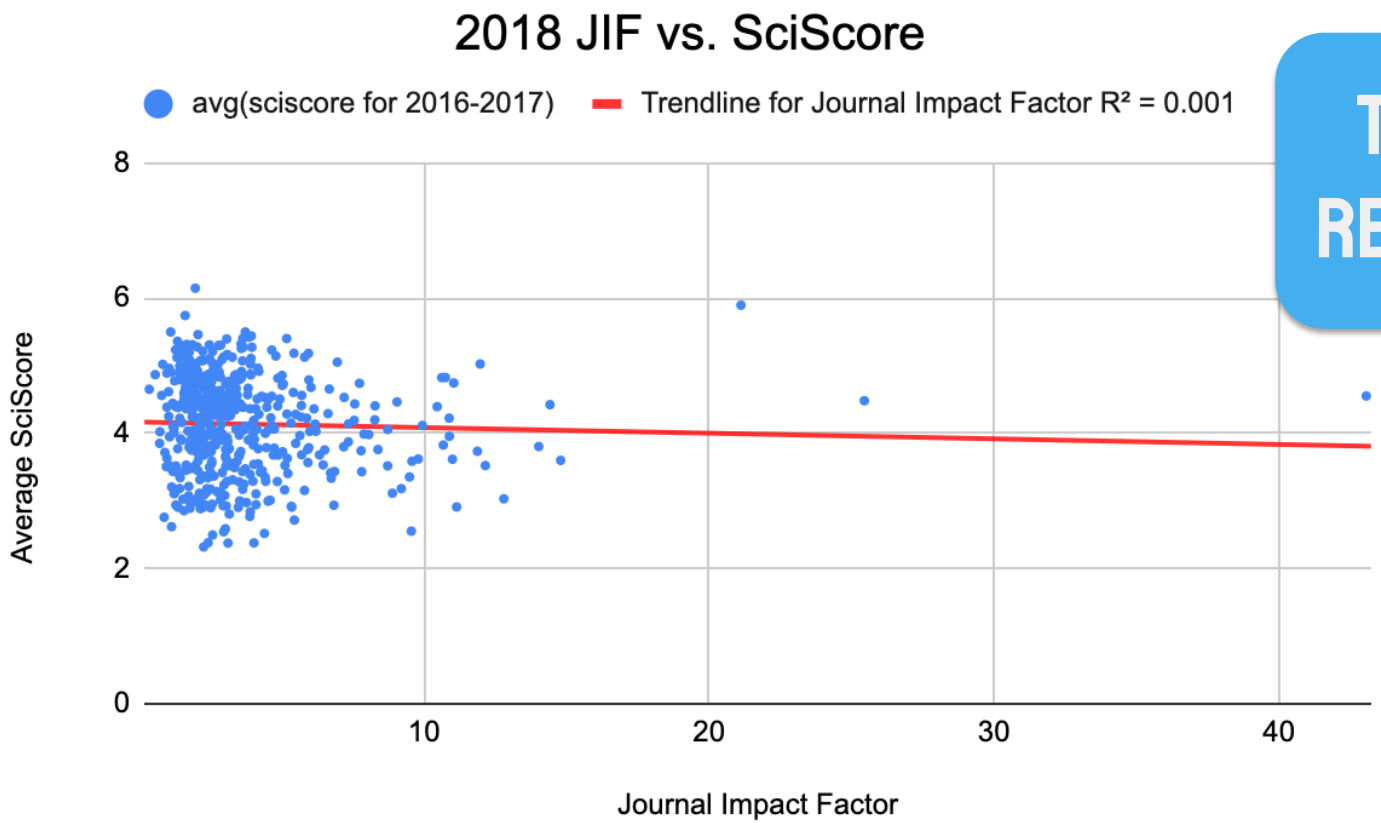
Effective standards implementation

SciScore

IMPROVEMENT OF NATURE SCORES



WHAT ABOUT THE IMPACT FACTOR?



THERE IS NO RELATIONSHIP!

SciScore

Current Pilots:

British Journal of Pharmacology (8 mos/2019 SciScore: 6.28)

Brain & Behavior (5 mos/2019 SciScore: 5.46)

10 Springer Journals *New Pilot*

eLife *New Pilot*

OUTLOOK

****Coming soon****

Additional MDAR support

eJournal Press Integration

Aries Integration

Aggregation of scores on university / funder / researcher level

Exploring integration with other disciplines / tools

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"Did you check how MIT is doing in your analysis? I bet they're worse than we are."

—COUNCILOR OF A US UNIVERSITY

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