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Below you will find two tables showing the results of SciScore. Your score is calculated based on adherence to guidelines for scientific rigor (Table 1) and identification of key biological resources (Table 2). Points are given when SciScore detects appropriate information in the text. Details on each criteria and recommendations on how to improve the score are appended to the bottom of this report.

Table 1: Rigor Adherence Table

<u>Institutional Review Board Statement</u>
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.
<u>Randomization</u>
In each animal experiment, mice were randomly assigned to each group.
<u>Blinding</u>
not detected.
<u>Power Analysis</u>
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.
<u>Sex as a biological variable</u>
not detected.
<u>Cell Line Authentication</u>
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.

Table 2: Key Resources Table

Your Sentences	REAGENT or RESOURCE	SOURCE	IDENTIFIER
<u>Antibodies</u>			
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)
<u>Experimental Models: Cell Lines</u>			
HepG2 macrophage cells were obtained from DSMZ (Braunschweig, Germany; RRID:CVCL_0027) and maintained in a 37°C with 5% CO ₂ .	HepG2	DSMZ	Suggestion: Problematic cell line: Misidentified/contaminated DSMZ Cat# ACC-180, RRID:CVCL_0027(link)
<u>Experimental Models: Organisms/Strains</u>			
Eight-week old wild-type C57BL/6 mice (initially generated in JAX Laboratory) were purchased from the Animal Center of Renmin Hospital of Wuhan University.	C57BL/6		
<u>Software and Algorithms</u>			
All analyses were performed with SPSS version 20.0 (SPSS Inc., USA).	SPSS		Suggestion: (SPSS, RRID:SCR_002865)(link)

Other Entities Detected

Your Sentences	Recognized Entity
	Oligonucleotides
cDNA templates for the sense and antisense riboprobes is specifically made using the primers M13F: GTTTTCCCAGTCACGAC or M13R: CAGGAAACAGCTATGAC and the gene-specific forward or reverse primers.	GTTTTCCCAGTCACGAC
	CAGGAAACAGCTATGAC

SciScore is an automated tool that is designed to assist expert reviewers by finding and presenting formulaic information scattered throughout a paper in a standard, easy to digest format. SciScore is not a substitute for expert review. SciScore checks for the presence and correctness of RRIDs (research resource identifiers) in the manuscript, and detects sentences that appear to be missing RRIDs. SciScore also checks to make sure that rigor criteria are addressed by authors. It does this by detecting sentences that discuss criteria such as blinding or power analysis. SciScore does not guarantee that the rigor criteria that it detects are appropriate for the particular study. Instead it assists authors, editors, and reviewers by drawing attention to sections of the manuscript that contain or should contain various rigor criteria and key resources.

Rigor Table:

In the rigor table (table 1 of this report), SciScore highlights sentences that include various elements of rigor as described by Hackam and Redelmeier in [2006](#), and by van der Warp and colleagues in [2010](#). SciScore was trained using sentences from thousands of published papers that were tagged by expert curators to indicate that the sentence described blinding (either during the experiment or during data analysis), group selection criteria such as how subjects were randomized, power analysis (statistical test), or sex as a biological variable. If a cell line is detected then SciScore ‘expects’ that cell line authentication criteria are described, a cell line is not detected this section of the table will not be visible or scored. When a criterion is expected, but a sentence that addresses the criterion is not detected by SciScore, the statement “Not Detected” is given. It is possible that a criterion is not necessary for a particular manuscript or that SciScore, an automated tool, makes a mistake. If SciScore makes substantial mistakes with your manuscript, please [contact us](#) to help us learn from our mistakes. Please see the [FAQ](#) for more details.

Scoring for Rigor Table (total 5 points):

The rigor table makes up 5 points of the total score. Those five points are split evenly among the expected rigor criteria, each criterion being worth five divided by the number of rows in the table points. Scores are rounded to the nearest whole number. For each sentence that describes an expected rigor criterion, such as blinding, SciScore adds the fractional number of points for that criterion, and if it is unable to find a statement on blinding then this section is labeled "Not Detected" and receives a score of 0. To improve detection, please make sure that your language is clear and written in standard English.

Key Resources Table

The key resources table (table 2 of this report), contains two types of things that are detected automatically by SciScore:

1. RRIDs, research resource identifiers
2. Sentences that “should” have RRIDs

RRIDs, are unique identifiers for reagents and other resources that largely overlap those resources that have been labeled as particularly problematic by the National Institutes of Health in recent changes to grant review criteria, please see ["key biological resources"](#), e.g., antibodies, cell lines and transgenic organisms. The RRID initiative is led by community repositories that provide persistent unique identifiers

to their resources, such as transgenic mice, salamanders, antibodies, cell lines, plasmids and software projects such as statistical software. RRIDs are described in a primer by Bandrowski and Martone in [2016](#).

RRIDs are unique numbers that resolve to a particular database record, for example the RRID:CVCL_0063 resolves to this record for a cell line:

https://web.expasy.org/cellosaurus/CVCL_0063

The information in that database is structured and curated by Cellosaurus staff, the authority for cell lines. If authors use this RRID then SciScore will ask the database about the number. Once an RRID is found in the database, SciScore attempts to match text in the sentence with the database record, most often it attempts to find the name of the resource, in this case HEK293T, and information about the company or catalog number to verify that authors have put the right RRID in the sentence. If a typo is made by authors, that renders the RRID not valid, the RRID column will be blank (table 3 will contain the RRID in the unresolved RRID column in red). If an RRID was submitted to the authority by authors, it often takes a week or more to become available in the resolver database, thus exercise caution in the interpretation of the SciScore report in cases of newly minted RRIDs.

Sentences that should have RRIDs are detected by SciScore, by looking for patterns in a sentence that are similar to how cell lines or antibodies are described in published papers. A sentence that describes one or more antibodies may be detected by SciScore and this will be placed into the table without a corresponding RRID. SciScore will attempt to find the name(s) and catalog numbers of the resource. In cases where the tool is relatively confident, it will suggest an RRID. The suggested RRID appears in gray with a link to the RRID website where **authors must confirm** that the RRID found by SciScore is the correct RRID.

Note of caution:

Please verify all RRID suggestions, only the author can know whether suggestions are correct.

Scoring for Resources Table (total 5 points):

Each resource that is detected is scored, and the total is 5 points, with scores rounded to the nearest whole number. For each RRID detected, points are awarded, but for each sentence that is detected that does not contain an RRID, points are not awarded. If SciScore detects catalog numbers or relatively unambiguous resources, partial points are awarded. For each RRID that does not resolve properly only partial points are also awarded. Therefore, the way to maximize the points from this section is to add RRIDs, and proper citations that include vendor names, catalog numbers, lot and version numbers into the methods section of the manuscript.

Incorrect sentences:

SciScore is a text analysis tool, and it is therefore susceptible to making two types of errors, false positives or false negatives.

False negatives: The most common error occurs when the algorithm fails to detect a sentence that contains an antibody or another resource. False negatives generally occur either because the sentence is complex or in a less common syntax pattern. Generally simple sentences in clear standard English are simpler to process and result in few false negatives. If a truly complex sentence structure is required to describe reagents, a table may help not only SciScore, but also human readers. If an RRID is detected in a sentence, SciScore will be triggered to take a look at the sentence, which may have been skipped otherwise.

False positives: This type of error includes cases where a sentence does not contain an antibody, but the algorithm asserts that this sentence does have an antibody. If many resources are used and all have RRIDs, a single false positive will not reduce the score substantially. But if only 1-2 resources are used, then a false positive can reduce your SciScore needlessly. False positives are most often seen in the tools

portion of table 2, as the algorithm detects company names, where it should not. We try to minimize these false positives using several strategies. If this impacts your score, please contact our team (<http://sciscore.com>) and include the sentence where SciScore made the error. While we can't fix the score, we can learn from our mistakes.