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# SciScore Report

Below you will find your SciScore report containing three tables. Your score is calculated based on adherence to scientific rigor criteria (Table 1) and identification of key biological resources (Table 2). Table 3 contains statistical tests and oligonucleotides but is not scored. If SciScore makes any mistakes, please contact us to help us learn and improve.

**Table 1: Rigor Adherence Table**

| |
|---|
| Ethics |
| IACUC: The Ohio State University Institutional Animal Care and Use Committee (IACUC) specifically approved this study. |
| IRB: The study (IRB ID#201104109) was approved by the Washington University Institutional Review Board Committee, and was carried out in accordance with the principles expressed in the Declaration of Helsinki. |
| Consent: Patients gave the written informed consent, and their records were de-identified prior to the analysis. |
| Field Sample Permit: Permission to conduct field surveys on each location was given by the individual landowners concerned, and by the regulatory authority (Natural England) in those situations where the field site was afforded protected status (i.e. Site of Special Scientific Interest). |
| Euthanasia Agents: Mice were deeply anesthetized by intraperitoneal injection of sodium thiopental before decapitation, followed by brain extraction. |
| Inclusion and Exclusion Criteria |
| Subjects were eligible for the cross-sectional study if they were fluent in English and had a sexual partner (SP) in the previous 18 months and ineligible if they were post-menopausal or had undergone a sex change. |
| Attrition |
| Of these, 21 ticks could not be removed from the birds and 162 ticks were lost due to technical problems during nucleic acid extraction, resulting in 1,150 ticks available for analysis. |
| Sex as a biological variable |
| All females were of reproductive age and none were on progestin. |
| Subject Demographics |
| Age: Their age varied from 19 to 47 years (mean 26.3 , ssd 6.4) and length of relationship from 4 months to 23 years (mean 3.7, ssd 4.4). |
| Weight: Rats, weighing 200 ± 20 g at the beginning of the experiment, were housed in a room maintained at 23°C with a 12-hour light-dark cycle. |
| Randomization |

| | |
|---|---|
| Enrolled subjects on continuous suppressive ART were randomized to receive either mesalamine or matching placebo for 12 weeks, followed by a 12 week crossover period on the alternative arm. | |
| Blinding | |
| Subjects, coordinators, clinicians, and laboratory personnel were blinded to treatment assignment. | |
| Power Analysis | |
| To determine the sample size of animal experiments, we used power analysis assuming the (difference in means)/(standard deviation) is >2.5. | |
| Replication | |
| Bioassays were replicated three times. | |
| Number: Bioassays were replicated three times. | |
| Cell Line Authentication | |
| Authentication: All cells were authenticated by STR profiling and flow cytometry. | |
| Contamination: All cell lines were obtained from ATCC and tested negative for mycoplasma contamination. | |
| Code Information | |
| Identifiers: Coding sequences of all ortholog alignments were concatenated to create a single multiple sequence alignment (https://github.com/nylander/catfasta2phyml). | https://github.com/nylander/catfasta2phyml |
| Identifiers: All other scripts are available at https://github.com/plissonf/ML-guided-discovery-and-design-of-non-hemolytic. | https://github.com/plissonf/ML-guided-discovery-and-design-of-non-hemolytic |
| Data Information | |
| Availability: Sequencing data is available upon request to the corresponding author. | |
| Availability: The RNA sequencing reads have been deposited in the Gene Expression Omnibus (GEO) Sequence Read Archive of the National Center for Biotechnology Information (GSE1463966) for experiments performed at 25 °C. | |
| Identifiers: The RNA sequencing reads have been deposited in the Gene Expression Omnibus (GEO) Sequence Read Archive of the National Center for Biotechnology Information (GSE1463966) for experiments performed at 25 °C. | GSE1463966 |
| Identifiers: Experiments performed at 37 °C, previously published, reads were already deposited in GEO (GSE105133). | GSE105133 |
| Protocol Information | |
| Identifiers: This study was registered at clinicaltrials.gov (NCT-Number: NCT04371575, Date: 2020/04/29). | NCT04371575<br>Warning: study registration date April 29, 2020 is after study start date September 1, 2012 |

**Table 2: Key Resources Table**

| Your Sentences | REAGENT or RESOURCE | SOURCE | IDENTIFIER |
|---|---|---|---|
| Antibodies | | | |
| Immunohistochemical staining for BrdU was then performed using an anti-BrdU antibody (RRID:AB_10763546). | anti-BrdU | Antibodies-Online | (Antibodies-Online Cat# ABIN336862, RRID:AB_10763546)(link ) |
| Experimental Models: Cell Lines | | | |
| The EPLC-65 cell line (RRID:CVCL_8194) was maintained in Dulbecco's modified Eagle's medium (DMEM) containing 10% FBS at 37°C in a 5% CO2 atmosphere. | The EPLC-65 cell | | Warning: Problematic cell line: Misidentified/contaminated ( RRID:CVCL_8194)(link ) |
| For the primary and secondary screenings, we used a subclone (A23) of HEK293 (ATCC CRL-1573, RRID:CVCL_0045) and mouse neuroblastoma (N2a) cells (ATCC CCL-131, RRID:CVCL_0470). | HEK293 | CCLV | (CCLV Cat# CCLV-RIE 0197, RRID:CVCL_0045)(link ) |
| | N2a | ICLC | (ICLC Cat# ATL99007, RRID:CVCL_0470)(link ) |
| Experimental Models: Organisms/Strains | | | |
| To generate PIP821bpΔ the following sgRNA was generated 5'-GCAGGAGGAGGTACAGCGGG-3' and cloned into pU6-2-BbsI-gRNA (DGRC #1363) and then subsequently injected into w1118; vas-Cas9 (RRID:BDSC_51324, Rainbow Transgenics). | w1118; vas-Cas9 | | (BDSC Cat# 51324, RRID:BDSC_51324)(link ) |
| Software and Algorithms | | | |
| ImageJ was used to analyze images (RRID:SCR_003070). | ImageJ | | ImageJ ( RRID:SCR_003070)(link ) |
| The RNA sequencing reads have been deposited in the Gene Expression Omnibus (GEO) Sequence Read Archive of the National Center for Biotechnology Information (GSE1463966) for experiments performed at 25 °C. | Gene Expression Omnibus | | Suggestion: (Gene Expression Omnibus (GEO), RRID:SCR_005012)( link) |

**Other Entities Detected**

| Your Sentences | Recognized Entity |
|---|---|
| Statistical Tests | |
| Normally distributed data were analyzed using unpaired two-sided t-tests (two groups), ordinary one-way ANOVA with Tukey post hoc analysis for multiple comparisons (≥3 groups), or ordinary two-way ANOVA and Tukey post hoc for multiple comparisons (two variables) and is shown as mean ± sem. | t-tests |
| | ANOVA |
| | Tukey post hoc |
| Oligonucleotides | |
| To generate PIP821bpΔ the following sgRNA was generated 5'-GCAGGAGGAGGTACAGCGGG- 3' and cloned into pU6-2-BbsI-gRNA (DGRC #1363) and then subsequently injected into w1118; vas-Cas9 (RRID:BDSC_51324, Rainbow Transgenics). | 5'-GCAGGAGGAGGTACAGCGGG- 3' |
| The sequences of the four strands are as follows: A (5'-GGCCCCAGTGCTGCAATGAT -3'); B (5'-GTGAGCGTGGGTCTCGCGGTATCA TTGCAGCACTGGGGCC-3'); C (5'-GCCCAATTTACTACTCGTTCTGGT GTTTCTCGTACCGCGAGACCCACG CTCAC-3'); and D (5'-ACGAGAAACACCAGAACGAGTAGT AAATTGGGC-3'). | 5'-GGCCCCAGTGCTGCAATGAT- 3' |
| | 5'- GTGAGCGTGGGTCTCGCGGTATCA TTGCAGCACTGGGGCC-3' |
| | 5'- GCCCAATTTACTACTCGTTCTGGT GTTTCTCGTACCGCGAGACCCACG CTCAC-3' |
| | 5'- ACGAGAAACACCAGAACGAGTAGT AAATTGGGC-3' |

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For a full description of scored criteria and tips for improving your score, please see https://www.scicrunch.com/sciscorereport-faq