

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

- | | |
|-------------------------------------|--|
| n/a | Confirmed |
| ☐ | ☒ The exact sample size (<i>n</i>) for each experimental group/condition, given as a discrete number and unit of measurement |
| ☐ | ☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| ☐ | ☒ The statistical test(s) used AND whether they are one- or two-sided
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☐ | ☒ A description of all covariates tested |
| ☐ | ☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| ☐ | ☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals) |
| ☐ | ☒ For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| ☐ | ☒ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| ☐ | ☒ Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i>), indicating how they were calculated |

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection	We conducted a systematic literature search across six academic databases: PubMed, Web of Science Core Collection, Scopus, GreenFile via EBSCO, Bielefeld Academic Search Engine, and ProQuest Theses & Dissertations. The R computational environment (version 4.4.0) was used for deduplication of bibliographic records. We used Rayyan’s proprietary function (https://www.rayyan.ai/) to perform an additional deduplication. We extracted relevant data from the included studies in the meta-analysis. We employed the metaDigitise R package (version 1.0.1) or its graphical user interface shinyDigitise to extract the x- and y-axis coordinates (i.e., trophic levels of organisms or stable nitrogen isotope analysis and PFAS concentrations).
Data analysis	We scripted our analyses in the R computational environment (version 4.4.0) using the metafor package and log all preprocessing.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

The raw and generated data used in this study are available in the GitHub repository under accession code https://github.com/ThisIsLorenzo/PFAS_Trophic_Magnification. Raw data is also provided in Supplementary Materials (Data S1-S5). Source data are provided with this paper.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender [Research not involving human participants.](#)

Reporting on race, ethnicity, or other socially relevant groupings [Research not involving human participants.](#)

Population characteristics [Research not involving human participants.](#)

Recruitment [Research not involving human participants.](#)

Ethics oversight [Research not involving human participants.](#)

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☐ Behavioural & social sciences ☒ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	A meta-analysis synthesizing data on over 1,000 trophic magnification factors (TMFs) for per- and polyfluoroalkyl substances (PFAS) from 64 studies encompassing 119 global food webs and 72 individual chemicals. Multilevel meta-analytic models were used to estimate overall PFAS biomagnification patterns and to compare TMFs across chemical types, food web characteristics, and study designs. Key findings include evidence that PFAS concentrations generally increase with trophic level, identification of chemical-specific magnification trends, and quantification of the main sources of variability in TMFs.
Research sample	The unit of analysis in this meta-analysis is the individual effect size (i.e., trophic magnification factor) extracted from eligible studies. The research sample comprises published and unpublished studies that met predefined inclusion criteria, representing a subset of all possible research on PFAS trophic magnification. Within each study, underlying species-level sampling is reflected in the reported variances or standard errors, which were used to weight effect sizes in the meta-analytic models.
Sampling strategy	We employed a systematic search and screening process to identify relevant studies reporting trophic magnification factors (TMFs) for per- and polyfluoroalkyl substances (PFAS). Studies were identified through multiple bibliographic databases. Inclusion criteria were pre-specified and applied during screening. From the eligible studies, individual TMFs were extracted as the unit of analysis. No random sampling was used; all eligible studies were included.
Data collection	Data were collected through a systematic literature search of primary studies relevant to the research topic. We extracted specific data items from the literature and stored them in a relational database. A detailed data collection process was pre-registered it is available at https://doi.org/10.32942/X2SP92 .
Timing and spatial scale	We did not impose any time restrictions on our literature research strategy.
Data exclusions	Studies and data points were excluded if they did not meet predefined eligibility criteria established prior to screening (Method S4 in Supplementary Information).

Reproducibility

We assure computational reproducibility providing raw extracted data from the included studies in the meta-analysis and the analysis code (including all models and model parameters used in this meta-analysis). Raw data and analysis code can be found in our GitHub repository: https://github.com/ThisIsLorenzo/PFAS_Trophic_Magnification. We assure methodological reproducibility providing transparent search strategy, documented inclusion/exclusion criteria, inclusion decisions justifications, clear data extraction rules and coding decisions. We used the PRISMA flow diagram to show the literature search process and PRISMA-EcoEvo guidelines for reporting systematic reviews and meta-analyses. We pre-registered the research protocol on EcoEvoRxiv (DOI <https://doi.org/10.32942/X2SP92>). A permanent, citable reference to the GitHub repository hosting the code used in this study is provided with this paper (<https://doi.org/10.5281/ZENODO.17293157>).

Randomization

Randomization in the traditional sense does not directly apply to our meta-analysis. However, elements of randomization principles appear in our study. Studies were randomly assigned to six different reviewers for screening to reduce reviewer-related bias. Our random-effects meta-analytic model assumes that the included studies are considered a random sample from a larger population of possible studies and food webs.

Blinding

Blinding was applied during the selection of studies to reduce bias in inclusion decisions. Six independent reviewers screened titles and abstracts using the Rayyan platform. Two authors performed a blinded pilot assessment on a 10% subset of records to ensure consistency in full-text screening, after which one author completed the remaining full-text evaluations.

Did the study involve field work?

☐ Yes

☒ No

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

Methods

- | n/a | Involved in the study |
|-------------------------------------|--|
| ☒ | ☐ Antibodies |
| ☒ | ☐ Eukaryotic cell lines |
| ☒ | ☐ Palaeontology and archaeology |
| ☒ | ☐ Animals and other organisms |
| ☒ | ☐ Clinical data |
| ☒ | ☐ Dual use research of concern |
| ☒ | ☐ Plants |

- | n/a | Involved in the study |
|-------------------------------------|---|
| ☒ | ☐ ChIP-seq |
| ☒ | ☐ Flow cytometry |
| ☒ | ☐ MRI-based neuroimaging |

Plants

Seed stocks

Research not involving plant samples.

Novel plant genotypes

Research not involving plant samples.

Authentication

Research not involving plant samples.