Supporting Information

Mining Proteomes for Zinc Finger Persulfidation

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The PDF file includes:

- Figure. S1, S2, S3
- Table S1 to S12
- SI references

Other supplementary materials for this manuscript include the following:

- Table S1 and S9 (.xls files)

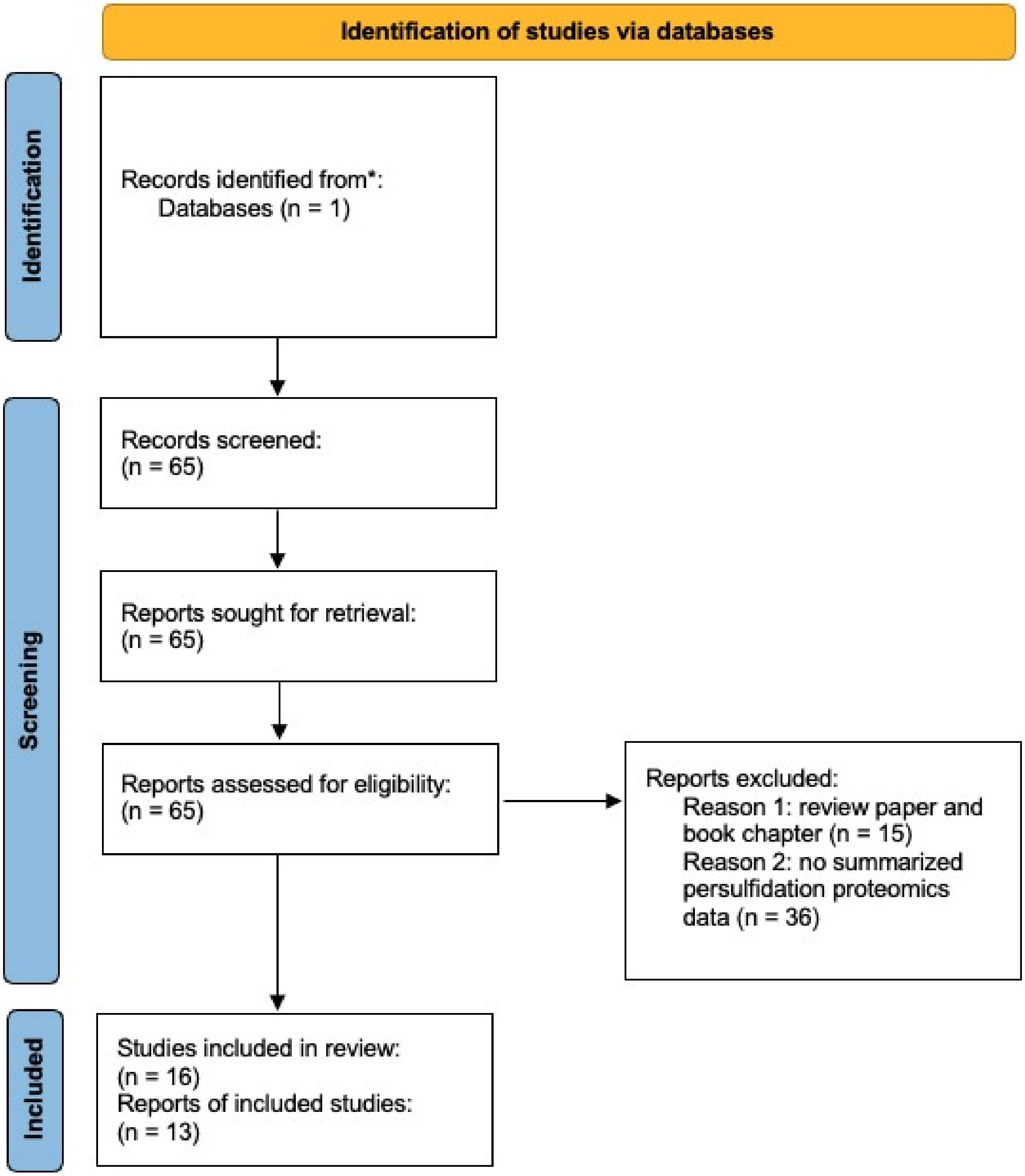

Figure S1. PRISMA Flow Diagram for Study Selection. Flow diagram showing the process of the selection of the studies from the PubMed database for inclusion in the meta-analysis. The diagram follows PRISMA 2020 flow diagram with three phases: Identification, Screening and Included.[1] The number of records at each stage is recorded. *Database is PubMed.

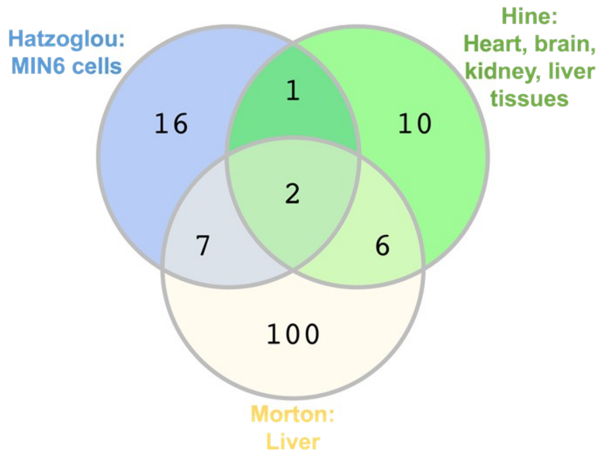

Figure S2. Venn diagram depicting the overlap in the types of persulfidated ZFs from *Mus musculus* with the same persulfide specific proteomics method: biotin thiol assay (BTA).

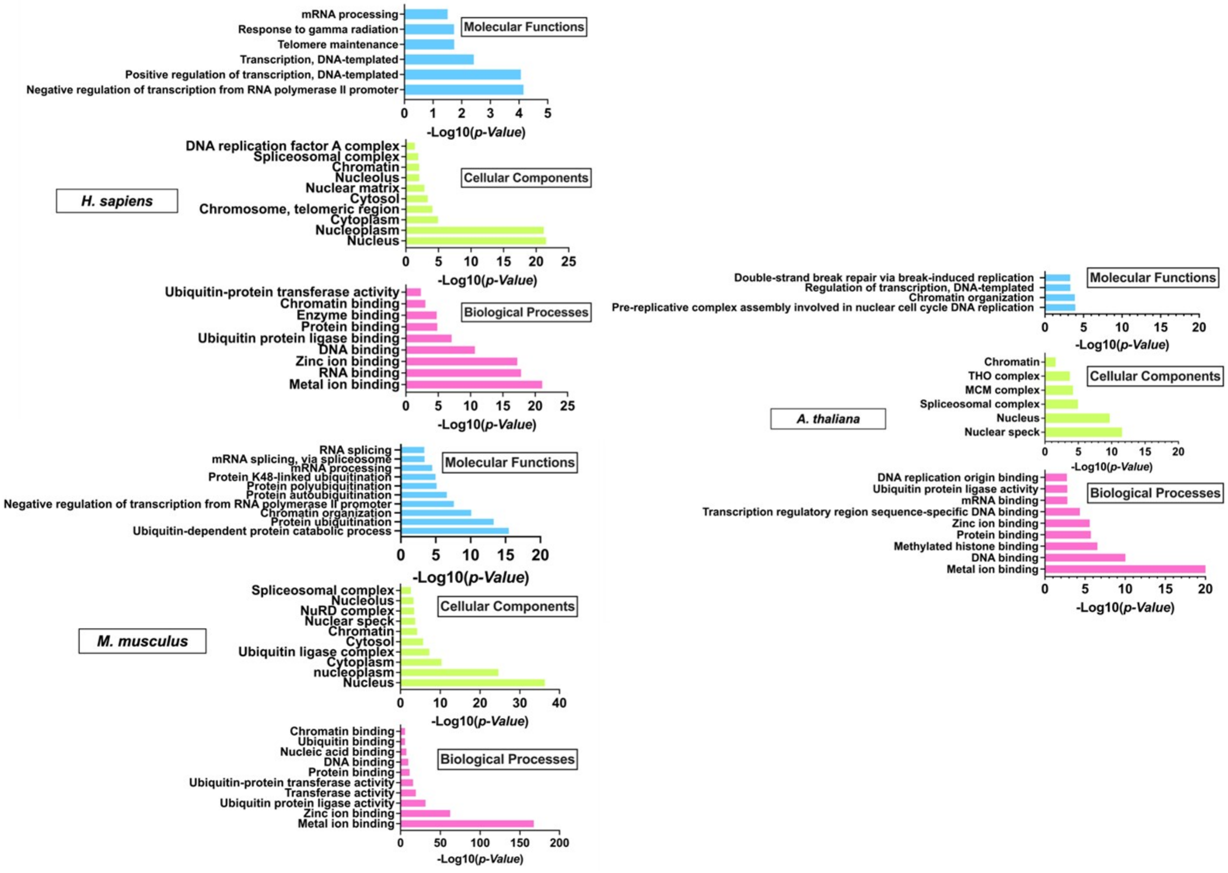

Figure S3. Gene Ontology (GO) enrichment for M. musculus, H. sapiens, and A. thaliana using DAVID. Bar graphs of the distribution of GO terms as a percentage of associated genes, with a significance level of $P < 0.05$, categorized into molecular functions, cellular components, and biological processes. The background protein list is the whole proteome.

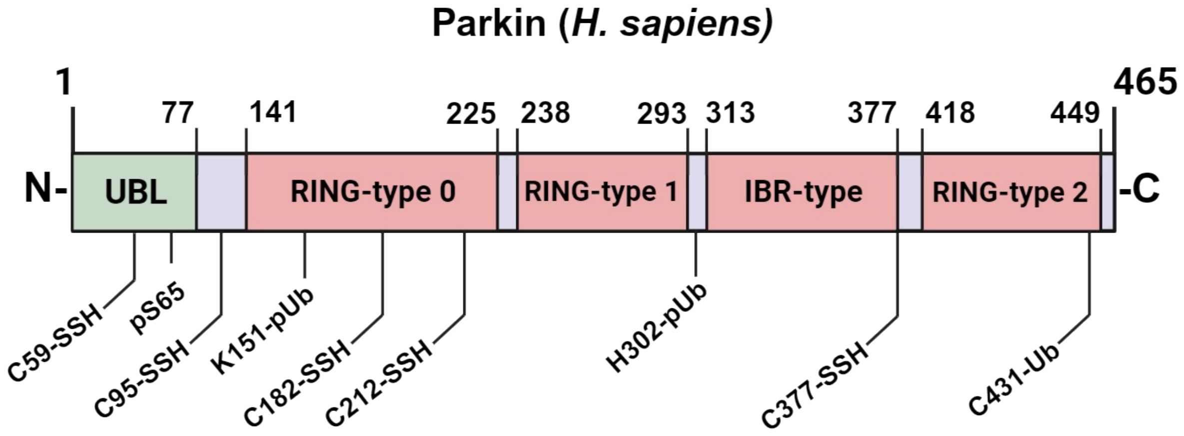

Figure S4. Cartoon depiction of Parkin sequence and relevant PTMs. Phosphorylation of Parkin at S65 (pS65) in the Ubiquitin-like domain (UBL) by PTEN induced kinase 1 (PINK1) and binding of phospho-Ubiquitin (pUb) to the RING-type 0 ZF domain (pK151) are required for full activation of Parkin E3 ligase activity. These PTMs induce a change to Parkin's resting-state conformation, where the multiple ZF domains (above, colored in pink) self-associate and obscure the catalytic C431, to an open conformation where the RING-type 1 ZF domain can bind the E2 enzyme in ubiquitin transfer. C431 of the RING-type 2 ZF domain is accessible for ubiquitin binding and transfer to Parkin substrates. Additionally, persulfidation of Cys residues (Cys-SSH) enhances Parkin's E3 ligase activity, with most modified residues located in the domains responsible for the protein-protein interactions with PINK1 or E2 enzymes.

Table S1. Total persulfidated ZFs (n= 267) from *Homo sapiens*.
This file provides a comprehensive list of all persulfidated ZFs identified from published persulfide specific proteomics datasets in *Homo sapiens*.

Table S2. Total persulfidated ZFs (n= 548) from *Mus musculus*.
This file provides a comprehensive list of all persulfidated ZFs identified from published persulfide specific proteomics datasets as well as data from our group in *Mus musculus*. [2]

Table S3. Total persulfidated ZFs (n= 172) from *Arabidopsis thaliana*.
This file provides a comprehensive list of all persulfidated ZFs identified from published persulfide specific proteomics datasets in *Arabidopsis thaliana*.

Table S4. Total persulfidated ZFs (n= 23) from *Rattus norvegicus*.
This file provides a comprehensive list of all persulfidated ZFs identified from published persulfide specific proteomics datasets in *Rattus norvegicus*.

Table S5. Total persulfidated ZFs (n= 4) from *Emiliania huxleyi*.
This file provides a comprehensive list of all persulfidated ZFs identified from published persulfide specific proteomics datasets in *Emiliania huxleyi*.

Table S6. Results of Gene Ontology (GO) in Homo sapiens using full zinc finger list as background.
This table presents the results derived from conducting GO on *Homo sapiens*, utilizing the DAVID bioinformatics resource. [3, 4]

Table S7. Results of Gene Ontology (GO) in *Mus musculus* using full zinc finger list as background.
This table presents the results derived from conducting GO on *Mus musculus*, utilizing the DAVID bioinformatics resource. [3, 4]

Table S8. Results of Gene Ontology (GO) in *Arabidopsis thaliana* using full zinc finger list as background.
This table presents the results derived from conducting GO on *Arabidopsis thaliana*, utilizing the DAVID bioinformatics resource. [3, 4]

Table S9. Comparative Analysis of Persulfidated Zinc Finger Proteins (ZFs) Across Multiple Species.
This table depicts the results of a Venn diagram analysis identifying shared persulfidated ZFs across four species: *Homo sapiens*, *Mus musculus*, *Arabidopsis thaliana*, and *Rattus norvegicus*, and analysis identifying shared persulfidated ZFs using the same persulfide specific proteomics method (BTA method).

Table S10. Results of Gene Ontology (GO) using full proteome and Kyoto Encyclopedia of Genes and Genomes (KEGG) Pathway Analysis in *Homo Sapiens*.
This table presents the results derived from conducting GO and KEGG pathway analysis on *Homo sapiens*, utilizing the DAVID bioinformatics resource. [3, 4]

Table S11. Results of Gene Ontology (GO) using full proteome and Kyoto Encyclopedia of Genes and Genomes (KEGG) Pathway Analysis in *Mus musculus*.
This table presents the results derived from conducting GO and KEGG pathway analysis on *Mus musculus*, utilizing the DAVID bioinformatics resource. [3, 4]

Table S12. Results of Gene Ontology (GO) using full proteome and Kyoto Encyclopedia of Genes and Genomes (KEGG) Pathway Analysis in *Arabidopsis thaliana*
This table presents the results derived from conducting GO and KEGG pathway analysis on *Arabidopsis thaliana*, utilizing the DAVID bioinformatics resource. [3, 4]

Reference

1. M. J. Page, J. E. McKenzie, P. M. Bossuyt, I. Boutron, T. C. Hoffmann, C. D. Mulrow, L. Shamseer, J. M. Tetzlaff, E. A. Akl, S. E. Brennan, R. Chou, J. Glanville, J. M. Grimshaw, A. Hróbjartsson, M. M. Lalu, T. Li, E. W. Loder, E. Mayo-

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2. A.T. Stoltzfus, J. G. Ballot., T. Vignane, H. Li, M. M. Worth, L. Muller, M. A. Siegler, M. A. Kane, M. R. Filipovic, D. P. Goldberg, S. L. J. Michel, *unpublished work*., 2023.
3. D. W. Huang, B. T. Sherman and R. A. Lempicki, *Nucleic Acids Res.*, 2009, **37**, 1-13.
4. D. W. Huang, B. T. Sherman and R. A. Lempicki, *Nat. Protoc.*, 2009, **4**, 44-57.