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INPLASY

Oxidative Stress Associated Molecular Signatures in Immune Mediated Diseases: Insights from Machine Learning and Systems Biology Approaches

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ADMINISTRATIVE INFORMATION

Support - Not Applicable.

Review Stage at time of this submission - Preliminary searches.

Conflicts of interest - None declared.

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Amendments - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 14 March 2026 and was last updated on 15 March 2026.

INTRODUCTION

Review question / Objective To systematically evaluate studies applying computational approaches, including machine learning, bioinformatics, and systems biology, to identify oxidative stress–associated molecular signatures, pathways, and biomarkers in immune-mediated diseases using multi-omics datasets.

Condition being studied Autoimmune conditions such as multiple sclerosis, systemic lupus erythematosus, lupus nephritis, rheumatoid arthritis, Sjögren's syndrome, and inflammatory bowel disease.

METHODS

Participant or population Patients with immune-mediated diseases, including multiple sclerosis, systemic lupus erythematosus, lupus nephritis, rheumatoid arthritis, Sjögren's syndrome, and inflammatory bowel disease, whose molecular datasets (e.g., transcriptomics, metabolomics, proteomics, microbiome, or multi-omics) were analyzed using computational approaches such as machine learning, bioinformatics, or systems biology.

Intervention Application of computational analytical approaches, including machine learning, bioinformatics, and systems biology methods, to analyze oxidative stress–related molecular data derived from omics datasets (e.g., transcriptomics, metabolomics, proteomics, microbiome, or multi-omics).

Comparator Healthy controls or comparative disease groups, when applicable, used to identify differences in oxidative stress–associated molecular signatures and pathways.

Study designs to be included Original research studies employing computational analytical approaches (e.g., machine learning, bioinformatics, or systems biology) to analyze omics datasets related to oxidative stress in immune-mediated diseases. Observational studies, cohort studies, case–control studies, and cross-sectional studies reporting primary molecular data will be included.

Eligibility criteria Studies will be included if they investigate oxidative stress, redox biology, or reactive oxygen species–related mechanisms in immune-mediated diseases, including multiple sclerosis, systemic lupus erythematosus, lupus nephritis, rheumatoid arthritis, Sjögren's syndrome, or inflammatory bowel disease; apply computational analytical approaches such as machine learning, bioinformatics, or systems biology; use omics-based datasets including transcriptomics, metabolomics, proteomics, microbiome, or multi-omics data; and report molecular or computational findings related to oxidative stress–associated pathways. Review articles, conference abstracts, editorials, studies without primary data, studies not using computational methods, and studies not relevant to the diseases or oxidative stress focus of this review will be excluded.

Information sources Electronic databases including PubMed, Scopus, and Web of Science will be systematically searched to identify relevant studies. Reference lists of included articles will also be screened to identify additional eligible studies.

Main outcome(s) Identification of oxidative stress–associated molecular signatures, including genes, metabolites, proteins, and regulatory pathways, revealed through computational analysis of omics datasets in immune-mediated diseases.

Quality assessment / Risk of bias analysis Risk of bias for the included studies will be assessed using the Prediction Model Risk of Bias Assessment Tool (PROBAST). This tool evaluates potential methodological bias in studies involving predictive models and machine learning based analyses.

Strategy of data synthesis Due to expected heterogeneity in study design, datasets, and computational methods, findings will be synthesized qualitatively. Extracted data will be summarized and compared to identify recurring oxidative stress–associated molecular signatures, regulatory pathways, and computational approaches across immune-mediated diseases.

Subgroup analysis Not applicable.

Sensitivity analysis Not Applicable.

Country(ies) involved United States.

Keywords Oxidative stress; immune-mediated diseases; machine learning; bioinformatics; systems biology; multi-omics; biomarkers.

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