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Systematic Data Extraction for a Review on the Role of Cytokines in Breast Cancer Progression and Therapeutic Targeting

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Protocol status: Working

We use this protocol and it's working

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Abstract

This protocol describes the systematic procedure used to extract and synthesize data from eligible studies included in a systematic review and meta-analysis on cytokines in breast cancer. The protocol ensures reproducibility and uniformity in study selection, outcome identification, and data collection, focusing on human studies published within the last 10 years and evaluating the prognostic and therapeutic significance of cytokines.

Version information:

- 1
 - Protocol version: 1.0
 - Date: 12.07.2025
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Materials and Equipment

- 2
 - Computer with internet access
 - Reference manager (Mendeley)
 - PRISMA 2020 flow diagram template
 - Microsoft Excel and Microsoft Word.
 - Software for meta-analysis (JASP v0.19.3)
 - Access to databases: PubMed, Scopus, Web of Science

Procedure Steps:

- 3 **Step 1: Define eligibility criteria**
 - Include: Original research studies in humans, published between 2015 and 2025, that evaluate cytokines in relation to breast cancer prognosis or therapeutic potential.
 - Exclude: Animal or in vitro studies, case reports, editorials, and reviews.
- 4 **Step 2: Search databases**
 - Perform a comprehensive literature search using the following terms:

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"breast cancer" AND ("cytokine" OR "IL-6" OR "TNF-α" OR "IL-1β" OR "IL-8" OR "IL-10" OR "TGF-β" OR "IL-17") AND ("prognosis" OR "survival" OR "metastasis" OR "therapy")
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 - Apply filters for publication year (2015–2025), human subjects, and English language.
- 5 **Step 3: Export and de-duplicate records**
 - Export all search results into Mendeley.
 - Automatically and manually remove duplicate records.
- 6 **Step 4: Title and abstract screening**
 - Screen all records independently by two reviewers.
 - Exclude non-relevant articles.
 - Document reasons for exclusion.
- 7 **Step 5: Full-text retrieval and eligibility assessment**
 - Retrieve full texts for potentially eligible studies.

- Assess full texts against eligibility criteria.

8 **Step 6: Data extraction**

- For each included study, extract the following:
 - Study characteristics: author, year, country, study design
 - Population: sample size, patient subgroup
 - Cytokines evaluated and measurement method (e.g., ELISA, IHC)
 - Outcomes: survival (OS, DFS), response to therapy, metastasis
 - Statistical estimates (e.g., HR, OR, CI)
 - Type of analysis (univariate or multivariate)
 - Therapeutic interventions, if applicable
- Use a standardized Excel sheet with predefined columns for all extracted variables.
- Validate extracted data by cross-checking between reviewers.

9 **Step 7: Risk of bias and quality assessment**

- Apply Newcastle–Ottawa Scale for observational studies.
- For meta-analysis, assess heterogeneity using I^2 and publication bias via funnel plots.

10 **Step 8: Synthesis**

- Summarize qualitative findings by cytokine and clinical outcome.
- Perform quantitative meta-analysis where appropriate using random-effects models.

11 **Step 9: Documentation and PRISMA compliance**

- Complete PRISMA 2020 flow diagram detailing the identification, screening, eligibility, and inclusion process.

Expected Time:

- 12
 - Database search and deduplication: 1–2 days
 - Screening and full-text retrieval: 3–5 days
 - Data extraction and validation: 5–7 days
 - Analysis and synthesis: 5–10 days

Notes:

- 13
 - Any discrepancies during screening or data extraction were resolved by consensus or adjudicated by a third reviewer.
 - Cytokines were grouped by function (pro-inflammatory, immunosuppressive, or regulatory) to guide synthesis.
 - Studies without hazard ratios but providing Kaplan–Meier curves were excluded from meta-analysis but retained for qualitative discussion.