# Article information:

Table - PMC  
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4668589/table/T1/>

# Article summary:

1. This article presents the allelic associations at SLE susceptibility loci following a meta-analysis with a replication study.

2. The study identified several SNPs that were significantly associated with SLE susceptibility, including PTPN22, FCGR2A, TNFSF4, and SMG7 NCF2.

3. The odds ratios and confidence intervals for each SNP were also reported, providing insights into the strength of the associations.

# Article rating:

May be slightly imbalanced: The article presents the information in a generally reliable way, but there are minor points of consideration that could be explored further or claims that are not fully backed by appropriate evidence. Some perspectives may also be omitted, and you are encouraged to use the research topics section to explore the topic further.

# Article analysis:

The article presents a table showing allelic associations at SLE susceptibility loci following meta-analysis with replication studies. While the table provides valuable information about the genetic variants associated with systemic lupus erythematosus (SLE), there are several potential biases and limitations in the article.

Firstly, the article does not provide any background information or context about SLE or the significance of these genetic associations. This makes it difficult for readers who are not familiar with the topic to understand the implications of these findings.

Secondly, the article does not mention the sample size or characteristics of the study populations included in the meta-analysis and replication studies. This is important information as it can affect the generalizability of the results. Additionally, without this information, it is difficult to assess whether there may be any biases in terms of population representation.

Furthermore, there is no discussion or analysis of potential confounding factors or interactions between different genetic variants. SLE is a complex disease with multiple genetic and environmental factors contributing to its development. Without considering these factors, it is challenging to draw meaningful conclusions from these associations.

The article also lacks a critical evaluation of potential sources of bias in the included studies. For example, publication bias could have influenced which studies were included in the meta-analysis, leading to an overrepresentation of positive findings. Additionally, there may be biases related to genotyping methods or population stratification that could impact the validity of these associations.

Moreover, there is no mention of any potential limitations or weaknesses in the statistical methods used for meta-analysis and replication studies. It would be helpful to discuss issues such as heterogeneity between studies and how this was addressed in the analysis.

Another concern is that only one side of the argument is presented in this article – namely, that certain genetic variants are associated with increased risk for SLE. There is no exploration or discussion of counterarguments or alternative interpretations of these findings. This one-sided reporting can lead to a biased and incomplete understanding of the topic.

Additionally, the article does not provide any information about potential risks or implications of these genetic associations. It is important to consider whether these associations have any clinical significance or if they are merely statistical findings without practical implications.

In conclusion, while the article presents a table with allelic associations at SLE susceptibility loci, it lacks important contextual information, discussion of potential biases and limitations, consideration of alternative interpretations, and analysis of potential risks or implications. A more comprehensive and critical analysis would be necessary to fully evaluate the validity and significance of these genetic associations in relation to SLE.

# Topics for further research:

* Systemic lupus erythematosus (SLE) background and significance of genetic associations
* Sample size and characteristics of meta-analysis and replication studies on SLE susceptibility loci
* Confounding factors and interactions in genetic variants associated with SLE
* Potential biases in studies included in the meta-analysis of SLE susceptibility loci
* Limitations and weaknesses of statistical methods used in meta-analysis and replication studies
* Counterarguments and alternative interpretations of genetic associations with SLE

# Report location:

<https://www.fullpicture.app/item/558786dab135a9f699bd5cbb1108e542>