

Functional Genomics Data Checklist:

This checklist is intended to help authors submit manuscripts that present functional genomics data such as microarray, ChIP-seq, RNA-seq, or other high-throughput data in a transparent manner that is compatible with JBC guidelines and best practices in the field, and facilitates reproducing the study.

1. Raw and processed data files have been deposited into an established depository such as GEO, ArrayExpress or the database of Genotypes and Phenotypes (dbGaP).

Yes

N/A

2. The depository accession number and any passwords if the data is currently protected has been included in the Data availability section of the manuscript.

Yes

N/A

3. The metadata associated with your genomics data complies with current standards and are Findable, Accessible, Interoperable, and Reusable (see [FAIR principles](#)) and include carefully labeled information pertaining to all samples used in the paper, such as species, tissue or cell type, number of samples, biological replicates, technical replicates, and other data such as treatment types, sex (if applicable), and antibodies used.

Yes

N/A

4. Software programs and pipelines used to process and analyze the data (with their version numbers) have been included in the methods section with appropriate citations.

Yes

N/A

5. Statistical models or tests used to analyze the data have each been named and included in the methods or results section, along with a justification including sample size, relevant comparisons tested, thresholds and/or multiple-testing correction methods employed, exact p-values calculated, etc. More details and guidelines [here](#).

Yes

N/A

6. If a third party or company has helped you with data processing or analysis, the information to what methods used have been included or cited.

Yes

N/A

7. All new methodologies, code, and pipeline programs used have been deposited into a community site (e.g., GitHub) with appropriate snapshots/doi for the exact version used in the paper.

Yes

N/A

8. All algorithms/packages used, versions of R/Python/MATLAB or similar, and other dependencies are included and cited as appropriate.

Yes

N/A