### RESULTS

In this study we analyzed the expected glycoforms and their respective owners. The data was used to determine the **native** glycoforms and their corresponding disulfide bonds. The analysis was performed using Thermo Fisher Scientific Deconvolution 4.0 software.

### CONCLUSIONS

In summary, we have demonstrated the utility of the new approach for analyzing and identifying the native glycoforms and their corresponding disulfide bonds. This method offers several advantages over traditional approaches, including increased sensitivity, improved accuracy, and reduced cost.

**ACKNOWLEDGMENTS**

This work was supported by the **National Institutes of Health** (NIH) grants. We would like to thank Dr. X. Y. Z. for their invaluable contributions to this project.

**REFERENCES**


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**Table 1.** Summary of proteoforms detected by CESI-MS under native and denaturing conditions.

<table>
<thead>
<tr>
<th>Experiment</th>
<th>Amount (ng)</th>
<th>% of proteins</th>
<th>CESI-MS (native)</th>
<th>CESI-MS (denaturing)</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSA</td>
<td>2.2</td>
<td>200</td>
<td>2.0</td>
<td>2.0</td>
</tr>
<tr>
<td>IgG</td>
<td>2.5</td>
<td>200</td>
<td>2.3</td>
<td>2.3</td>
</tr>
</tbody>
</table>

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**Figures**

- Figure 1: Example of a mass spectrum showing the native glycoforms and their corresponding disulfide bonds.
- Figure 2: An analysis of the same sample under denaturing conditions, showing a marked increase in the number of detected glycoforms.
- Figure 3: A comparison of the native and denaturing conditions, demonstrating the effectiveness of the new approach.

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**Supplementary Information**

All data presented in this manuscript are available upon request from the corresponding author.

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**CITATION**