Standard deviation for KD estimation was computed by Octet analysis software 9.0. Student's t-tests were performed in R.

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Acknowledged.

Generate HTML slides with this structure: Title, Motivation, Background, Methods, Results (including all figures here), Conclusion. Prioritize concise key points on each slide. Ensure space is reserved for figure inclusion.

4/4

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html Collapse Preview Save Copy

```
<!DOCTYPE html>
```

```
<div class="slide">
  <h2>Methods</h2>
  <ul class="key-points">
    <li>Assembled dataset of >5,000 HA antibodies from publications.</li>
    <li>Identified recurring sequence features (germline usage, clonotypes).</l
    <li>Developed a lightweight language model (mBLM).</li>
    <li>Trained & validated mBLM for specificity prediction.</li>
    <li>Saliency analysis for key sequence determinants.</li>
  </ul>
  <div class="figure-placeholder">Placeholder for workflow diagram of data coll
</div>

<div class="slide">
  <h2>Results: Germline Gene Usage</h2>
  <ul class="key-points">
    <li>Distinct germline gene preferences for HA head & stem.</li>
    <li>IGHV1-69 & IGHD3-9 common in HA stem.</li>
    <li>Identified novel public clonotypes.</li>
  </ul>
  <div class="figure-placeholder">Placeholder for Figure 1: Germline gene usage
</div>

<div class="slide">
  <h2>Results: Hydrophobicity of CDR H3</h2>
  <ul class="key-points">
    <li>HA stem antibodies exhibit higher CDR H3 hydrophobicity.</li>
    <li>Correlation with binding to hydrophobic groove.</li>
  </ul>
  <div class="figure-placeholder">Placeholder for Figure 2: Hydrophobicity and
</div>

<div class="slide">
  <h2>Results: mBLM Performance</h2>
  <ul class="key-points">
    <li>mBLM achieved decent performance on test set (F1 score = 0.79).</li>
    <li>Outperformed k-NN classifier.</li>
    <li>ESM2-Ab showed comparable performance.</li>
  </ul>
  <div class="figure-placeholder">Placeholder for F1 score graph and confusion
</div>

<div class="slide">
  <h2>Results: Saliency Map Analysis</h2>
  <ul class="key-points">
    <li>mBLM learned key sequence motifs of HA stem antibodies.</li>
    <li>Identified crucial residues for binding.</li>
    <li>Confirmation of known sequence features.</li>
  </ul>
  <div class="figure-placeholder">Placeholder for Saliency map heatmap (Figure
</div>

<div class="slide">
  <h2>Results: HA Stem Antibody Discovery</h2>
  <ul class="key-points">
    <li>Successful identification of HA stem antibodies.</li>
    <li>Validation rate correlated with model confidence score.</li>
    <li>Discovery of novel antibodies with high affinity.</li>
  </ul>
```

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```
<div class="slide">
  <h2>Conclusion</h2>
  <ul class="key-points">
    <li>Large-scale analysis provides valuable resource.</li>
    <li>mBLM enables antibody specificity prediction.</li>
    <li>Identified key sequence determinants of HA stem antibodies.</li>
    <li>Potential for streamlining antibody discovery.</li>
    <li>Future work: expand the dataset, refine the model, and explore polyreac
  </ul>
</div>

</body>
</html>
```

Collapse Preview Save Copy

Explanation and Key Features:

- **HTML Structure:** Uses basic HTML tags for structure. I've avoided complex styling for maximum compatibility.
- **CSS Styling:** Minimal inline CSS for basic readability. You can easily expand this to customize the appearance.
- **Slides:** Each `div` with class "slide" represents a separate slide.
- **Key Points:** Uses `ul` (unordered list) for concise key takeaways.
- **Figure Placeholders:** `div` with class "figure-placeholder" provides space and a reminder to insert figures. The `text-align: center` and `line-height` properties are used to center the placeholder text.
- **Conciseness:** Key points are kept short and to the point.
- **Figure References:** I've included a comment referencing the figures mentioned in the original text (Figures 1-3, etc.). Replace the placeholder text with actual image tags (e.g., `<img src="figure1.png" alt="Figure 1: Germline gene usage">`).
- **Comments:** I've added comments to help you understand the purpose of each section.
- **Easy Customization:** You can easily modify the text, styling, and layout to suit your needs.
- **Clear Organization:** The slides follow the structure you requested (Title, Motivation, etc.).

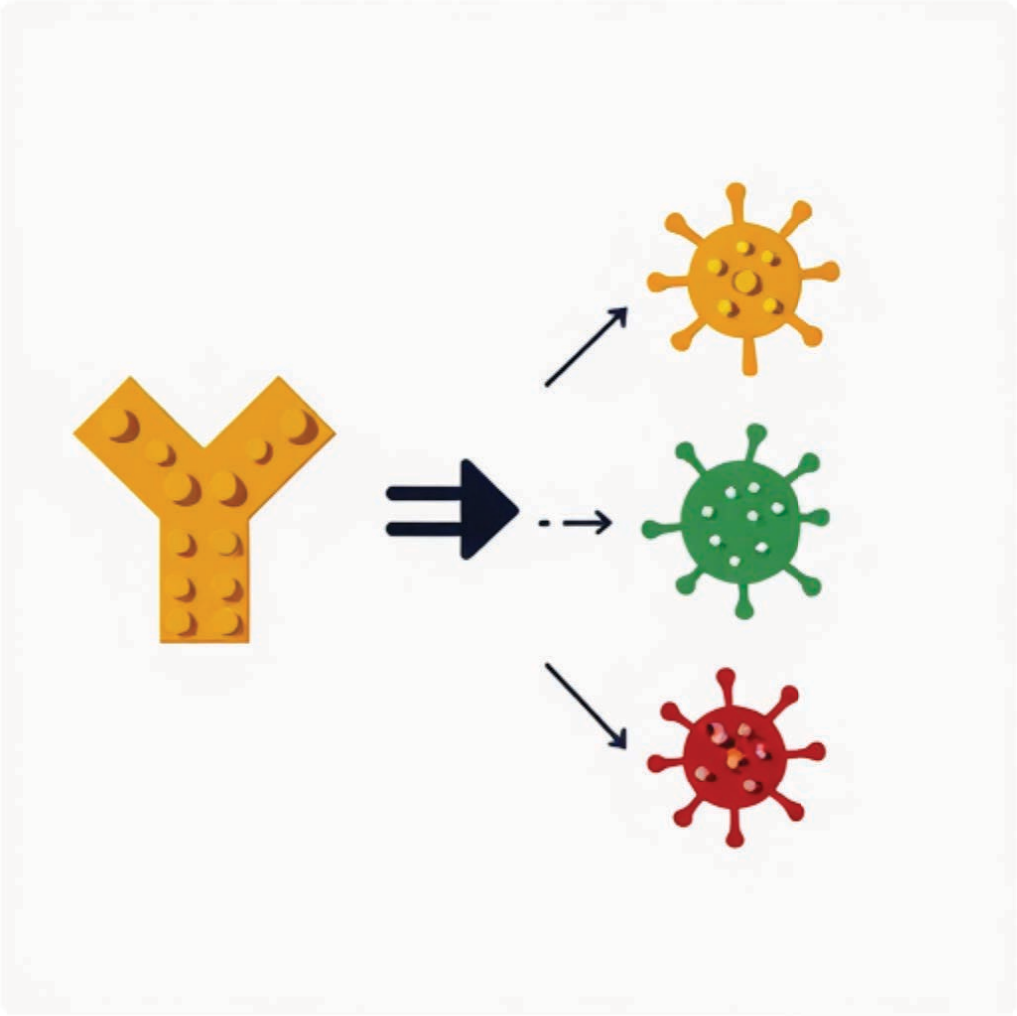
How to Use:

1. **Save the Code:** Save the code as an HTML file (e.g., `presentation.html`).
2. **Open in a Browser:** Open the file in a web browser.
3. `<img src="your_image_file.png" alt="Your image description">` ke sure the image file paths are correct.
4. **Customize:** Modify the text, styling, and layout to your liking.

This provides a solid foundation for your presentation. You can further enhance it with animations, transitions, and other interactive elements using JavaScript and CSS.

can you write one simple prompt for motivation section so i can generate image for it. only reply prompt.

Gemma3



Generate an SVG illustrating: a Y-shape lego on the left, another three different color viruses on the right vertically, an arrow in the middle.

can you write one simple prompt for background section so i can generate image for it. only reply prompt.

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Title: Deep Learning Identifies Key Features of Human Antibody Specificity

Motivation

Understanding antibody specificity is crucial for vaccine design and therapeutic development.

- Current methods for epitope mapping are time-consuming and expensive.
- Deep learning offers a powerful approach for predicting antibody specificity.
- Aim: Develop a model to identify key features of human antibody specificity.

Background

Human antibody repertoire diversity.

- V(D)J recombination generates immense diversity.
- Germline gene usage influences antibody specificity.
- CDR3 is the primary determinant of antigen binding.
- Hydrophobic score of CDR3 may correlate with binding affinity.

Methods

Data Collection and Preprocessing

- Gathered antibody sequences with known specificities.
- Identified clonotypes and public clonotypes.
- Performed germline gene usage analysis.
- Calculated hydrophobic scores of CDR3 regions.

Methods

Model Development

- Utilized a pre-trained memory B cell language model (mBLM).
- Fine-tuned the model for antibody specificity prediction.
- Implemented saliency score analysis for feature interpretation.

Results: Germline Gene Usage

Results: Hydrophobic Score Correlation

Results: Model Performance

Results: Saliency Score Analysis

Conclusion

Deep learning successfully predicts antibody specificity.

- Germline gene usage and CDR3 hydrophobic scores are key determinants.
- Model reveals important residues for antigen binding.
- Future work: Incorporate biophysical knowledge to improve accuracy.