- 1. What is identified with CLIP-seq?
- 2. How is the protein of interest isolated in CLIP-seq?
- 3. What sources of bias are addressed in PureCLIP?
- 4. Based on which two signals is the most likely hidden state concluded?
- 5. On which datasets was the performance evaluated?
- 6. Name one main advantage of PureCLIP compared to previous methods.