## Choosing Structure Prediction Software

 There are many software tools for protein structure prediction (see <a href="https://">https://</a> en.wikipedia.org/wiki/List of protein structure prediction software)

How should you decide which to use?

Lase of use

Web server - easier for sporadic use

Downloadable and scriptable - easier for large-scale applications

Accuracy

blinded tests of the ability to predict structure from sequence. (see <a href="http://">http://</a> www.predictioncenter.org/index.cgi)

The "Critical Assessment of protein Structure Prediction" (CASP) experiments are

structure prediction in recent community-wide <u>CASP7</u>, <u>CASP8</u>, <u>CASP9</u>, <u>CASP10</u>, CASP11, CASP12, and CASP13 experiments." So let's use it!

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- "I-TASSER (as 'Zhang-Server') was ranked as the No 1 server for protein structure prediction in recent community-wide <u>CASP7</u>, <u>CASP8</u>, <u>CASP9</u>, <u>CASP10</u>, <u>CASP11</u>, <u>CASP12</u>, and <u>CASP13</u> experiments." So let's use it!

- To reproduce the key results from Garg *et. al.*, we first need to find out what to model
- UniProt (<a href="https://www.uniprot.org">https://www.uniprot.org</a>) is a comprehensive biological sequence database
- A search for "thymidylate synthase" yields 50,099 results, including 566 that have been manually reviewed. This is much more than the 110 that were included by Garg et. al. in their 2015 paper!
- The two results for "thymidylate synthase wigglesworthia" is much more manageable. Select the result that has been reviewed.



