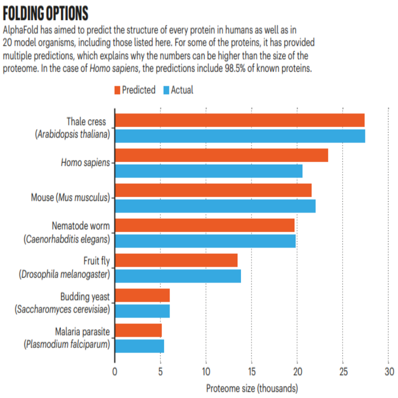
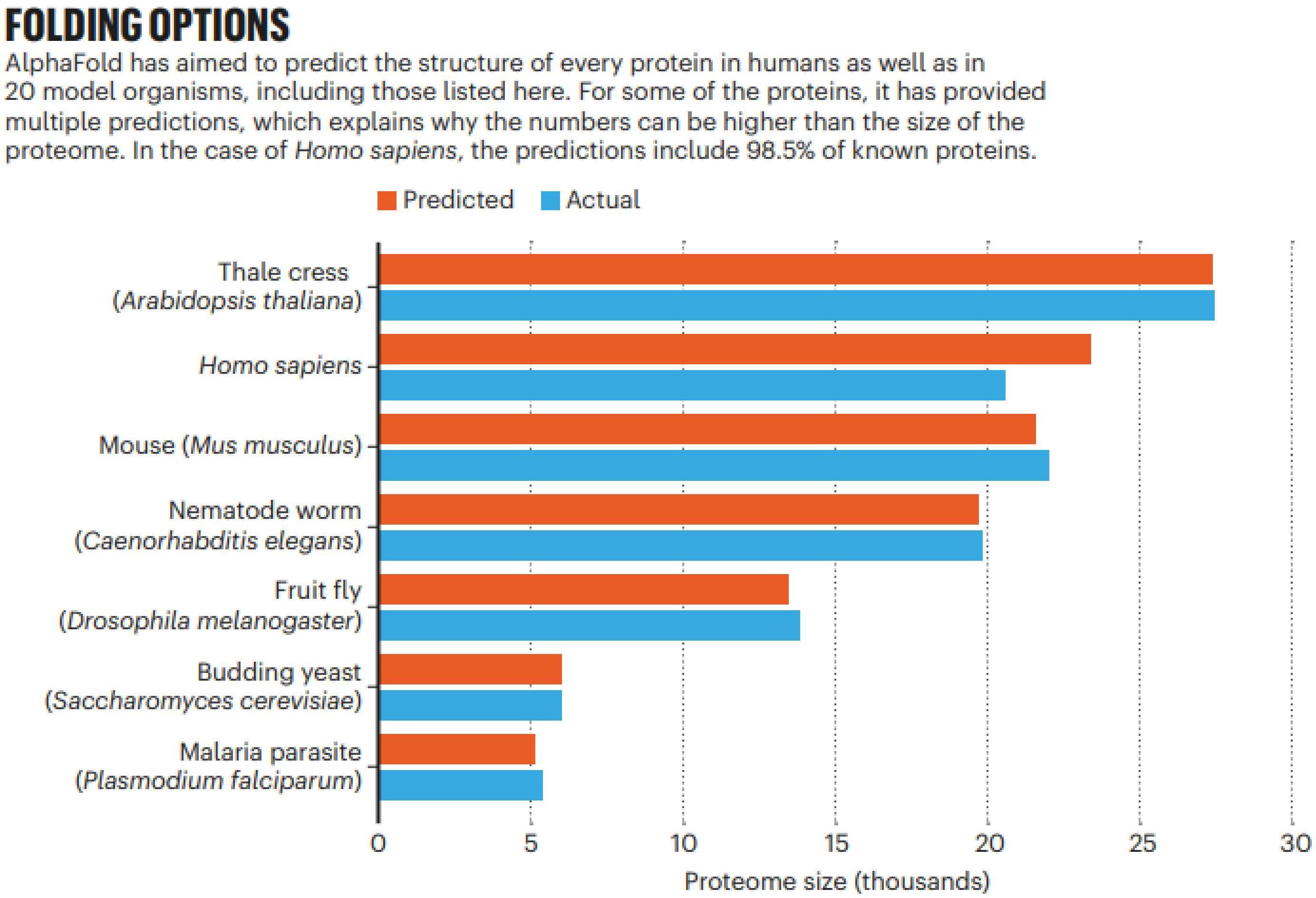


Highly accurate protein structure prediction with AlphaFold

Description

The transformative artificial intelligence (AI) tool called AlphaFold, has predicted the 3 dimensional structures of nearly the entire human proteome (98.5% of human proteins). The resulting dataset covers 58% of residues with a confident prediction, of which a subset (36% of all residues) have very high confidence. Furthermore, the tool has predicted almost complete proteomes for various other organisms, ranging from mice and maize (corn) to the malaria parasite.



FOLDING OPTIONS

AlphaFold has aimed to predict the structure of every protein in humans as well as in 20 model organisms, including those listed here. For some of the proteins, it has provided multiple predictions, which explains why the numbers can be higher than the size of the proteome. In the case of *Homo sapiens*, the predictions include 98.5% of known proteins.

The predicted 3 dimensional structures are freely available to the community via a public database hosted by the European Bioinformatics Institute at https://alphafold.ebi.ac.uk/.

Category

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