The ability to predict local structural features of a protein from the primary sequence is of paramount importance for unravelling its function in absence of experimental structural information. Two main factors affect the utility of potential prediction tools: their accuracy must enable extraction of reliable structural information on the proteins of interest, and their runtime must be low to keep pace with sequencing data being generated at a constantly increasing speed. Here, we present NetSurfP-2.0, a novel tool that can predict the most important local structural features with unprecedented accuracy and runtime. NetSurfP-2.0 is sequence-based and uses an architecture composed of convolutional and long short-term memory neural networks trained on solved protein structures. Using a single integrated model, NetSurfP-2.0 predicts solvent accessibility, secondary structure, structural disorder, and backbone dihedral angles for each residue of the input sequences. We assessed the accuracy of NetSurfP-2.0 on several independent test datasets and found it to consistently produce state-of-the-art predictions for each of its output features. We observe a correlation of 80% between predictions and experimental data for solvent accessibility, and a precision of 85% on secondary structure 3-class predictions. In addition to improved accuracy, the processing time has been optimized to allow predicting more than 1,000 proteins in less than 2 hours, and complete proteomes in less than 1 day. This article is protected by copyright. All rights reserved.