Both the surface- and interior-critical residue identification modules have been made available to the community through a new web server, STRESS. Obviating the need for long wait times, the algorithmic implementation of our software is highly efficient (running times for proteins of various sizes are provided in Fig. 5). In the surface-critical residue identification module, we use local searching to bring down the time complexity by an order comparing with a naïve implementation. After carefully profiling and optimization, a typical case takes only about 30 minutes on one typical CPU (2.8GHz) core.

We also tackle the running time issue by designing a scalable server architecture. The thin front-facing servers handle incoming user requests and the beefy back-end servers that perform algorithmic calculations. Our back-end servers are automatically and dynamically scalable. This system ensures that we are able to handle varying levels of demand in a reliable and cost-effective manner. Our scalable implementation is based on Amazon Web Service (AWS) and highly portable on cloud environment.