Development of a Novel Profile-Profile Comparison System, FORTE1

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We have developed a novel profile-profile comparison technique to increase the sensitivity of fold recognition and improve alignment accuracy. The FORTE1 program has distinct features of measuring similarity between two profiles as compared with other published methods which exploit alignment information. The FORTE1 program utilizes the sequence profiles of both a target and templates to predict the structure of target sequence. With the Magi cluster (http://www.cbrc.jp/magi/), we performed PSI-BLAST iterations maximally 20 times to prepare the profiles of both target and templates with the NCBI non-redundant database. FORTE1 is available at http://www.cbrc.jp/forte1/.

The submission form of FORTE1