

# 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 screenshot shows the FORTE1 web interface. At the top, there is a logo for the Computational Biology Research Center (CBRC) and its address: 2-41-6 Aom, Koto-ku, Tokyo 135-0064 JAPAN. Below this is the title 'FORTE1' in large blue letters. A red note states: 'NOTE: This is an experimental version of FORTE server. The output format is designed for CATSP1, now.' The main form area contains several sections: 'Upload your sequence file and then click "set" button:' with a 'set' button and a 'Done' button; 'OR' in red; 'Enter your sequence:' with a text input field and a note 'Please use FASTA or pure amino acid format (1400 Residue Maximum)'; 'Enter a one-liner description of your sequence:' with a text input field; 'Enter your e-mail address (where the results will be sent to):' with a text input field; and a 'SEARCH!' button with a 'Go' button. At the bottom, there is a 'Home' link, a 'A. Tomii (in preparation)' link, and a logo for 'your library' with the text '© 2002 Computational Biology Research Center'.

The submission form of FORTE1