

Abstract Submitted
for the MAR11 Meeting of
The American Physical Society

BSDB: the Biomolecule Stretching Database¹ MAREK CIEPLAK, MATEUSZ SIKORA, Institute of Physics, Polish Academy of Sciences, JOANNA I. SULKOWSKA, UCSD, BARTLOMIEJ WITKOWSKI, Institute of Physics, Polish Academy of Sciences — Despite more than a decade of experiments on single biomolecule manipulation, mechanical properties of only several scores of proteins have been measured. A characteristic scale of the force of resistance to stretching, F_{max} , has been found to range between ~ 10 and 480 pN. The Biomolecule Stretching Data Base (BSDB) described here provides information about expected values of F_{max} for, currently, 17 134 proteins. The values and other characteristics of the unfolding process, including the nature of identified mechanical clamps, are available at www://info.ifpan.edu.pl/BSDB/. They have been obtained through simulations within a structure-based model which correlates satisfactorily with the available experimental data on stretching. BSDB also lists experimental data and results of the existing all-atom simulations. The database offers a Protein-Data-Bank-wide guide to mechano-stability of proteins. Its description is provided by a forthcoming Nucleic Acids Research paper.

¹Supported by EC FUNMOL project FP7-NMP-2007-SMALL-1, and European Regional Development Fund: Innovative Economy (POIG.01.01.02-00-008/08)

Marek Cieplak
Institute of Physics, Polish Academy of Sciences

Date submitted: 03 Nov 2010

Electronic form version 1.4