

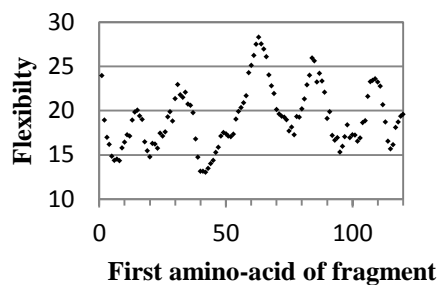
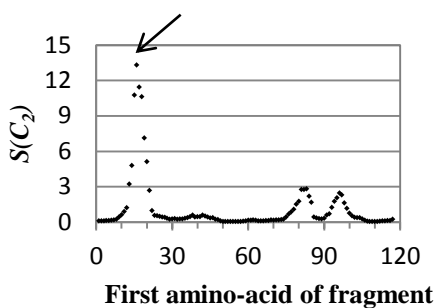
# The enigma of the near-symmetry of proteins: Domain swapping

Maayan Bonjack-Shterengartz David Avnir

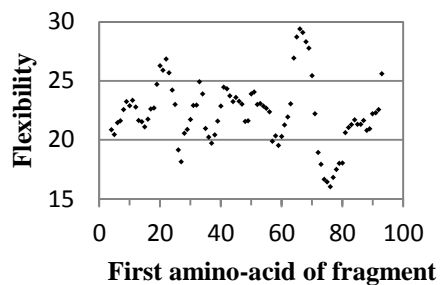
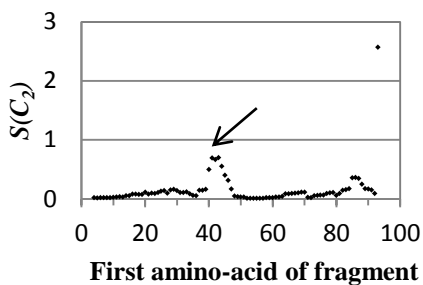
Institute of Chemistry and the Lise Meitner Minerva Center for Computational Quantum Chemistry, The Hebrew University of Jerusalem, Jerusalem 91904, Israel

## Supporting Information

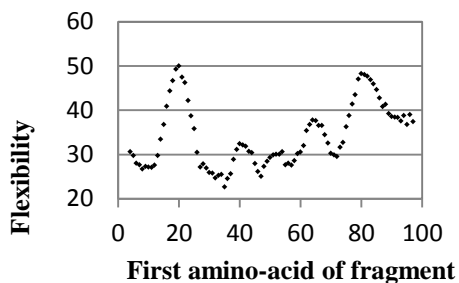
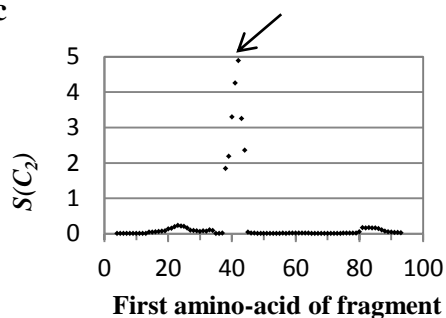
**a**



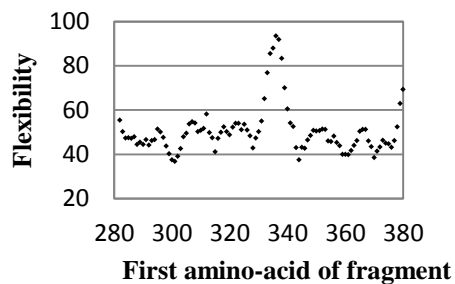
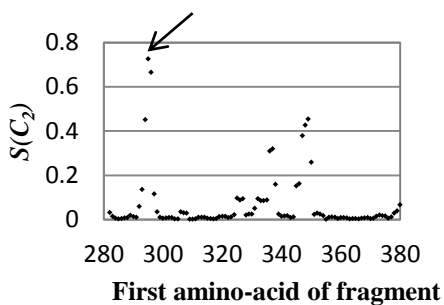
**b**



**c**



**d**



**S3 Fig. Comparison of the CSM running ruler symmetry analysis with the average atomic displacement factor (ADP) flexibility parameter.** The black arrows indicate the hinge regions. PDB codes of analyzed proteins: (a) 1A2W, (b) 1CDC, (c) 1A64, (d) 1WWA.