Abstract Submitted
for the MAR09 Meeting of
The American Physical Society

A new view on the role of intrinsic protein disorder[1] JINTAO LIU, JAMES FAEDER, CARLOS CAMACHO, University of Pittsburgh — Recent studies have found that many proteins do not have stable structure by themselves, i.e., are intrinsically disordered, which challenges the conventional view that structure determines protein function and interaction. We have analyzed the Human Protein Reference Database with the VSL2 protein disorder predictor, and find that the amount of disorder in a protein is the result of evolutionary pressure: catalytic proteins interact with substrates rapidly and highly specifically and thus exhibit low levels of disorder; transcription regulators often slide along DNA, which favors flexible or disordered structures; binding proteins have affinities that depend weakly on folding stability, and thus have a broad disorder distribution. Finally, our findings suggest that sequence/structural features such as phosphotyrosine are better indicators of multiple protein-protein interactions than disorder.

[1]Supported by NSF under grant no. MCB-0744077.

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Date submitted: 21 Nov 2008 Electronic form version 1.4