

Title

Alberto Perez², Ivet Bahar¹, Ken A. Dill², and
Justin L. MacCallum²

¹Department of Computational and Systems Biology, and Clinical
& Translational Science Institute, School of Medicine, University
of Pittsburgh, 3064 BST3, 3501 Fifth Ave, Pittsburgh, PA 15213

²Laufer Center for Physical and Quantitative Biology
Stony Brook University
Stony Brook, NY 11794-5252

April 26, 2012

Abstract

Abstract¹

1 Introduction

[Figure 1 about here.]

2 Methods

2.1 ENM

[Table 1 about here.]

See figure 1.

See table 1.

References

- [1] MacCallum, J. L.; Perez, A.; Schnieders, M. J.; Hua, L.; Jacobson, M. P.; Dill, K. A. *Proteins: Struct., Funct., Bioinf.* **2011**, 79, 74–90.

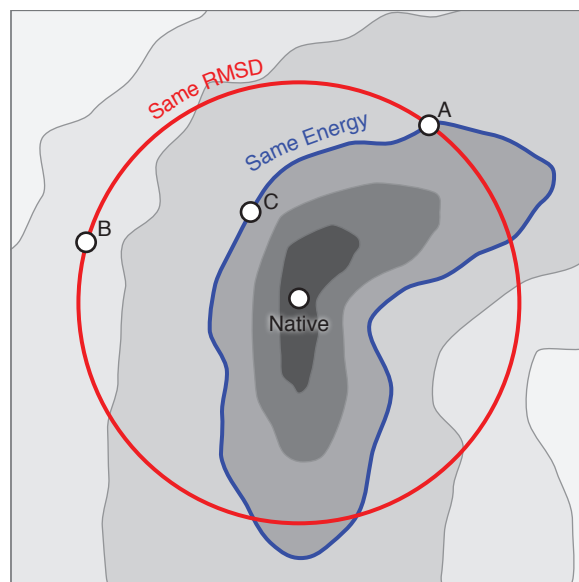


Figure 1: Schematic

Table 1: Structures used for large motions

Target	PDB1	PDB2
Scallop myosin	1kk7	1kk8
Acyl Carrier Protein	1acp	2fae
Aspartate Aminotransferase	1ama	8aat
Bcl-xl	1bxl	1ysn
Calcium Sensor	1k9k	1k9p
Calmodulin	1c1l	1ctr
Cyclin Dependent Kinase Inhibitor	1dc2	2a5e
Cystatin	1a67	1cew
Hydrolase	1qz3	1u4n
LacRepressor	1lcc	1lqc
LambdaCro	5cro	6cro
Lupin Hydrolase	1f3y	1jkn
Maltose Binding Protein	1omp	3mbp
Pin1	1f8a	1pin